

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
3863	34231	A	3903	174	1599	VLHAVGNQVQCGPGPEVHVCG WRPGCVRLQLHVVGRADGPE CDLCAVWPGGGDV*PAVPGAV PHVTQCEPQGHYPYEGTGAGA YCAALCGPPGARGHCGQEARQ PQVRTCQGGERRRDCQDLL*E AGGQEAQGAERFSAQ*ASRGTP RAAATHPPRTASPGEGQH*VP AHVGGARPGAWQRHPGLHQY HRPQHLEPPAQDEPHQDP*HL PGQRPAPAVEAEPGQQAPS/KP CPPPEPSAQDGVPAENGLPQG DP/GAIAAPRAQAPDSPCGRCTSP GQQ*YWLGPAGPQRGSSPEWD RP*ATQDGRPRPRTTAAACDP G*PREPRGGAPQWAGWGRRR **RLRNPQ*PGQPSGSSGRPG PRRPSVASSVSE/RVLRGERALS PSPEAPLRASGQRANPTTAA ECPPYNPRDLCWTPGWLPMGP ESGKRRCVEEDAGPALHRQ GGTDGET**TGRGNNRPGPYGR
3864	34232	A	3904	331	1120	HKDRFWQLQNDSCFLHSPGER QWLGGPRSDTFGPQVLFGHVGI CSQRA/HPAGPGHRLPEGR*PP HRSQRHPPRSRKPYLE*PPDMC VATDRRTQTTPRDFPPLGR*KPH GTLRSAACPAGRVSPSPRPRGL PAPPPKSHLC/PGVRGR*QLLP PHPGSPKGERGWTASPGAARG GPGPAPAPRPRASWSQSPSVTFP LPLAGLA/GHPGSRTEPAWKAG GAAARPGPELPRDLLQAGSTDT ASGEQLAAGPWTGKEISGRARP RL
3865	34233	A	3905	2	415	YTILTEK*KLSKLS*WVHQDQ LQKREELSMELNK*DQDSEAY PQRTVTGEETWLYQYDPPPLPR SLPPPQTHTAPVGA*S/DWGG*E LPPGLNGDKLAHHSPTPFLSFG LLFVDWL*SQLLSLGLFTQGV/ RIFI

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3866	34234	A	3906	1	4527	MGFCCRRCRPRLKGRPCIQHA GPVAAFVATPYSLYVCEPQ NVTLTCLRLGPVDKGDVTFY KTWYRSSRGVEQTCSERRPIRN LTFQDLHLHHGGHQAANTSHD LAQRHGLSESADHHGNFSITMR NLTLDDSLYCCLVVEIRHHHS EHRVHGAMELQVQTGKDAPSN CVVYPSSSQDSESNHGNFRH VSNGLLMRGPRPLDRERNSSHV LIVEAYNHDLGPMRSSVRMRK LRQSTALAQHWGTGALDR
3867	34235	A	3907	1	2180	MALTFPCRKFWEYGRQRPEVR YSVPASHQLKATDADEGEFGR VWYRILHGNHGNFRHVSNG LLMRGPRPLDRERNSSHVLIVE AYNHDLGPMRSSVRMRKLRS TALADSTGQAQHWTESRSGSPG SPVAPTCSART*QTSASVHLCL SGKSHHAWPP*TPFKLYYVHIE YSAHHKENLVIVYVEDIND EAPVFTQQQYSRLGLRETAGIG TSVIVVQATDRDSDGGGLVNY RILSGAEGKFEIDESTGLIITVNY LDYETKTSYMMNVSATDQAPP FNQGFCSVYITLLNELDEAVQF SNASYEAAILENLALGTEIVRV QAYSIDNLNQITYRFDAYTSTQ AKALFKIDAITRILGTQMDTKM NKTLSPQRVLRLEVEMLIQD ANQSATRRCAENYNRGVVEPL RAQQSYLAGEAGRLHGRGGFP VECEREEGIQTECPGEVMPDR GSDMEGVITVQGLVDREKGF YTLTVVADDGGPKVDSTVVS TRVYITVLDENDNSPRDFDTS AVSIPEDCPVGQRVATVKA WD PDAGSNGQVVFSLASGNIAGAF EIVTTNDSIGEVFVARPLDREEL DHYILQVVASDRGTTPRKKDHI LQVTILDINDNPPVIESPFGYNY SVNENVGGGTAVVQVRATDRD IGINSVLSYYITEGNKDMTFRM DRISGEIATRPAPDRERQSFYH

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3868	34236	A	3908	603	1395	RGRPRGSPFIPTAPREKKR*EE VGGHKREQTG*GGGERKKPPN PQHEPKERGWCSRVPPEEPQ/RK RRSARARPKKL*REKRRRGRPK RCLW*TRRHPSHHPRTIIQC*F* WRK/REEGKERKKEQPAHAGQ KRRKAARHRRRRRRRERTDEK NRTWTRRRREKAGQDEKREGE HGQKRSQQGRESRRDGRARTR KERRQKRENDNRARRRQQAER EKTYSVKRRQTTTQAAEEVRA RENEAREPQRRQHSRRRKEKE EMRAPRSKQ
3869	34237	A	3909	1	548	
3870	34238	A	3910	1	1803	
3871	34239	A	3911	1	279	
3872	34240	A	3912	1	506	MCYSRQSNLGTGEGKIKGSEV IDECPRSSRYQDLQELQNKTKL TVLEGDILDESCLKACQDMSV IIHTTSIIDIGVTHRESIMNINVK RTQLLLEACVQATVPVFIYTSTP EVAGPNSYKEIINSHHEEPLN TWCSPP/PYKKA/LARSGI*ATL QLGGSQEECT
3873	34241	A	3913	3	621	AGQQTVEIDLRRRIQLPDLENQ RNFNELSRIVLEVRERVRQEQQ EGGHEAGEGRGRQGPRESQSP AQPRAEAPSKGPDGTPGEDGGE PGDAVAAAEQPAQCGQGPFV LPVGVSSRNEDYPRTCRMWNS TFQTYKKEVCLPRHSMHPGPW AICCECQTRFGGRLPVSVEAA LPYWVPLSLRPKQHPWCWMA AGTAGGSVMMS
3874	34242	A	3914	1	430	RHRIQLPDLENQRNFNELSRIVL EVRERVRQEQQEGGHEAGEGR GRQGPRESQSPAQPRAEAPSK GPDGTPGEDGGEQPNVAAAAE QPAQCQGGQPFVLPVGVSSRNE DYPRTCRMW*GCGGYWGLKV GQHGLQRGQPHT
3875	34243	A	3915	2	1175	
3876	34244	A	3916	1	256	HLRIHTQESSYVDCDEGKALTS KRNLIHQHRIHTGEKPYCESKY IG*PFGLLPQLGHLHEHVSGEKP VLDIRCFGLPEFFTPFW

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3877	34245	A	3917	1	1396	MRPOLAGRDHHRGAATLLER PGRLVTHFRQRRGAVRYGGGK STTQHLSSQRRLSGPNDHTKGLV WLLLEHILQRLVSFVKLQATRTF TRTYITYAWFLPWGFSGLVCGT PVDTCWALKHQRIHTGEKPFEC SFCGKAFNGNSLIHQRIHTGE RPYQCEECGRAFNANLIRHQ RIHSGDRPPYCTECGNSFTSSSE FVIHQRIHTGEKPYECNECGKA FVGNSPLL RHQKIHTEKPYEC NECGKSGFRTSHLSQHQRHTG EKPYSCKVCGQAFNFHTKLTR HQRIHSEKPF* ¹ /CVD CGKA FS AQEQLKRHLRHTQESSYVCDE CGKALTSKRNLHQHQRIHTGE KPYEC SKYEKAFGTSSQLGHLE HVYSGEKPVL DICRFGLEPFFTP FYWKEEKCCGRKMRNEVVHK VSFFLVVPIALSSLLKKKWKML KKEKAQDPTVEYGNLEDDNSQQ
3878	34246	A	3918	1	547	MDSQRPRERQREERQSERQR HTQRMHREAETEDERD WKGH DTKTRRQRQRKRAEEGQCREH DRERRRD RTGERREKQKSTQ QSRKPSEEPHREKTQIKRERGPE QGELERGQCTERNRKA/GTPEC *TDPHIWTPHARSAPAHPPDH TAAKYRPPYRSHHSITHQHPR AASLKLWPKP
3879	34247	A	3919	1	399	
3880	34248	A	3920	3	872	KSKLKSEQDGISKTHKLLRRTC SSTVKTTDDVCVTKSHRTFGRLS SSDPRAEQAMTAIKSHKLLNRP CPAAVKSEECITLTKSHRLTRS WSGDP RCEHNTNLKPHKLLSRS YSSNLRMEELYGLKNHKLSSKS YSSAPKSSKT*/VFSKEP**RRRG RKALSLPQGLFGYP**HHLHPSSS QLAPNGAKCIPVRDRGFLVQTI EFAEQRIPLVNEVCEVCDEPHV FQNGPMLRRGRDVCWEAKKY ANSVVRKKFCRLSIARRSRYRA DMDLLRMSNFILTHYKQKQLNL
3881	34249	A	3921	3	218	CCRSHQGAGEGGHLSVQLLWQ YRWMCWCSWGPV/FQFHTDLEL VAWRVCGLDPGCGQLDIGMQT LIGDHICVF
3882	34250	A	3922	1	1055	

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3883	34251	A	3923	3	962	RSMRQKVNKDIQDLISALPQAD LIDYRTLHPKSTEYTFFSAPHR TYFKIDHIVGSKALLSKCKRTEI TTNCLSDHSAIKLELRKIKLTQN RTTTWKLNNLLNDYWVHNE MKAIEIKMLFETNENK/DETYQN LWDTFKA/PSILNGQKLEAFPL KTGTREGYLLPLFNIVLEVL AMAIRQEKE/IKGFQLGKEEVK LSLFADDMIVYLEDP/ISAANLL RLISNFSKVSQYKINVSQSQTFL YTNNRQTESQIMSELPFTIATKR IKYLGIGLTRDVKDLLKENYKP LFNEIKEDTNKWNIPCSWIGRI KIVKMAILPK
3884	34252	A	3924	1	1452	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSKEYTFFSALHHTYSKIDRT VGSKALLSKCKRTEITNSLSDH RAIKLELRKIKLTQNRSTTWKL NNLLNDYWVHNEMKAIEIKM FFETNENKDTTYQNLWDTFKA VCRGKFIALNAHNRKQERSKID TLTSQLKELEKQEQTSKASRR QEITKIRAELEMEIETQKTLQKSN ESRSWFFERJNKIDRPLARLIKK KREKNQIDVIKNDKGDITDPT EIQTITIREYYKHLNANKLENLE EMDKFLDITYTLPRLNQEEVESL NRPTGSEIVAIHNSLPTKKSPGP DGFTVEFY/QEGN*AGEGNKGY SIRKRRSQIVPVWR*HDCISRPK HRLRPKSP*AGKQLQQLRIQN QCTKITSIFIHQ*QANRKSNEH* TPIHNCFKENKIPRNPYPKGCCEG PLQGLQTTAQ*NRKGYKQME EHSMLMGRKNQYRENGHTAQ

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3885	34253	A	3925	1	1251	MKAEINMFFETNENKYTVYQN LWDTFKAVCRGKFIALNAHKR KQERSAMNTLTSQLKELEKQE KTNKSKANRRKQETTKIRAEKKEI ETQKTIHQKINESRSLFFFEKTNKI DRPLARLVKKKREKNQIDAIAIN DTGDIITDPTEIQTITIREYYKCL YANKLEYLEEMDKFLDITYTLQ RLNQEKVESLHRPITGSEIEAIIIN SLPT/KKSPGPDRTAQFYQRYA DGMYLKIHRAIYDKPTANIMLN GQKLEAFPLKTGTROGCPRLSL LFNIVLEVLRARVROEKEINGIH LGKQEVKLSLFDGMMIVYLENP IVSAQNLLKLISKFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTITTTKRIKYLGIQLARDVKD LFKENYKPLLNNKIKEDPNKWK NIPCSWIGRINIMKMAILPK
3886	34254	A	3926	1	1203	
3887	34255	A	3927	1	1233	
3888	34256	A	3928	1	951	MKREKNQIDAINKDKGDIITDP TEIQTITIREYYKPLYTNKLENLE EMDKFPDITYTLPRLNQEEVESL NRPTGFIEIA/TNSLPTK*SPGAE GFTAIFYQSVGSSGQGNQARE RNKGYSRKRGTQIVPVCRW DCIFRKLHGLSPKSP*ADKQLQ QSLRIQNQCAKITSIPHQ*QTYR EPNHE*TPIHNCYKENKIPRNTT YKGCERPFQGELOTTAQ*NKRR HKQMEEHSMMLMDRKNQYREN GHATAQGH*IQCHPHQATNYFL HRIGKNYFKLHMEPNKSLHSQ DNPQKEQSWRHAT*LTQILQ GYSHQNSI
3889	34257	A	3929	1	814	

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3890	34258	A	3930	1	1545	HQLKVFQRIHSIRSSCDGSAWGV VAPTFKTRGARSRRAAIRLGA ADLDEVKSSLVNESENQSSSD SEAERRPQPVRDTTFQKPRDYFA EVRRPQDSAFFKGPPYPGPFL MIPDLSSPYLSNGPLSPGGARTN SSPAPKETWICARFGGVSLSFLE IGSRVLLGRDVRNSSLLPAQI PIACHFAVDGGNFIRKGAYLL TFDLFGNWGLFFLIEIAVWELS AHSSGQSEDALELSRGTCSSSL QLCWTAKALVGKGLDGGPVC KNSGICSTRKTQEQMSFMEAL YQEGFLRETVVQAVRKVPQTP RKAVLEVLAARAIHQEIKIGQL GKEEVKLSLFADDMTVYLENPI VSAQNLLKLISNFSKVSQYKIN VQKSQAFFPYTNNRQTESQIMSE LPFTITTKRIKYLGIQFTKDVKG LFKENYKPLLNEIKEDTNKWK NIPCSWIGRINIVKMAILPKVIY RFNAIPIKLPLTFFTELEKTTLNF IWNQKSRIGKKILSKKNKAGGI
3891	34259	A	3931	693	1464	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFPIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATK/DQKS FCTAKETTIRVNRQPTWEKIF AIYPSDKGLIS

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3892	34260	A	3932	211	2519	ENRKSNCCLCQMA*LYI*KIPSS QPKISLS**ANLAKSQDTKSMC KNHHKHSYTLITDKQRAKS*VNS HSQLQRE*NT*ESNLQGM*RT SSRRTTNHCSTK*KRTQTNGR TFAHG*EESIS*KWPYCPSK/K RTEITNSPSDHSTNKLRLRIKKL TQNHITWKLNNLLNDSWVN NEIKAEIKKFFETNENKKTYY NLWDATAVLRGKFIALNAHI GNLERSKIYTLISQLKEPERQEQ TNPKASRRQETKIRAELEIET QKTLQKINESRSWFFENIKIDRQ LARLIKKKREKNQIDTITNNKG DITTDPIEIQTIREYYKYLYAN KLENLEEMDKFLDYTLPRLNQ EEVESLNTPTTGSEIKAIINSLPT KRSPGDRSTAE/FYHRYKEEL VLFLKLQFSTEKEGGRDITK KENFRPISLMNIDAKILNKILAN RIQQHIKKLIYHDQVGFIPGMQ GWFNICKSINVIFQYTNNRQTES QIMSEL PFTIASKRIKYLGIQLTR DVKDLFKENYKPVLEIRGHK QMEEHSMMLMDRKNQYCENGH TAQGNL*IQCHPHQATNDFLHR IGKEEVKLSLFADDMIVYLENPI ISAQNLLKLISNFSKVSAYKINV QKSQAFRYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYRPLLNEIKEDTNKWKNI PCSWVGRINIVIMAILSKVIYRF
3893	34261	A	3933	2	1304	
3894	34262	B	3934	141	2008	

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3895	34263	A	3935	1	1845	MVISVDAEKTENKIQQPFTLKT LNKLGIDGSYLKIIRAIYDQPTA NIILNGQKLEAFPLKTGRRQGC PLSPLLFNIVLEVLAIRIQEEI KGILQKGEEVKLSLFADEMIVY LENPIVSVQNLLKPIRNFESVLG YKINVQKSQAFLYTINRHTESQI MSELPTIATKRMKYLGIQVTR YVKDLFKENYKPLLNEVKEDT NKWKNIPCPWIGRINILKMAIL P/KELEKTTLKFIVNQKACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYQNRDIDQWN RTEPSDIIPIYNHILFDKPKKNK KWGMGSLFNKWCWENWLAI RKLKLDPFLTPYTKINSRWIKD LNVRPKTIKLEENLGNTIQDID MGKDFMSKTPKAMATKAKIDK WDLTKLRSFCTAKETTIRVNRQ PKEWEKIFAIYSSDKGLISRIYK ELNFRKINNPIKKWAKDMNR YF*KEDIYAANRHMKCCSSLA IREMQIKTTMR/YHLTPVRMAII KKSNNRTRENYFKIHMESKKS QNSQGNRKEKEQSWRHATRL QTIVQGYTVAKTACYWYKNRP TDQSNRTENQEIRLHTYNHLIF DKPDKSNGEITTPYSINGARITG
3896	34264	A	3936	1	700	
3897	34265	A	3937	1	3489	MKSGHPEKEQDNSDVQETREIT IRGLLCTALMRHSTGAIAIYLVG LSGSASLKLAVPLRCEGDKD AGHPLETQTALCERGRGARS LV GNTIMTSQVPVNETIIVLPSNVIN FSQAEKPEPTNQGDLSKKHLH AEIKVIGVNLQNVLERGWGKC QEMIYVVLGLDICRPFVSRVSEE GRMGQRGEEDANSDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRS

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3898	34266	A	3938	120	1331	TSLGPIYCAVRHTSSCRKVGSSR CQIIGCQLSVRLQLDQAHHKQL PWLAPKNAVVPKSLFDPQGRK EGVTALTPEAPRSGPPKRLQLFP PSLCPNCSKQGAFFSPFVGTAT LLATPFSSRSRVLVLPGRMRYA DKWRVSKMKRCCIEQWNSSEK THSARASHSLQRQGGPRVGGG SLQAGCHIVISAALSKEEALWV ASFCRQIVQSYLRPLLCSGADP GAFMDLRLGEELRSLLESLSYTP PSNEFKISMKLEAQDPRNTTST CIATVVGLTGARLRLRLDGSND KNDFWRLVDSAEIQIGNCEKN GGMLQPPLGDSFHCDDVRVSILD LFCFLLELPFTIDTKRIKYLGIQ LTKDVKDLFKENYKPLLNE/IK/ EDTNKWKNIPIRSRIG*INIVKMA ILPKDFG
3899	34267	A	3939	1	1421	MDSMSGGGQYRKINGNPTSVK CPLLLLPAILTPEPVNRWRQSC KAFARHSPLAFRVTISTSTFFDG LLVTGLYTSTSVQASQSIGGSSA FGFVLEVLARAIRQEKEIKGIQL GKEEIKLSLFAGDMIVYLENPV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGHQLTRDVKDL FKLENYKPLLKEIKEDTNKWK IPCSWVGRINIVKMAILPKNWK KLKFIWNQKRAHIAKSILSQKN KAGGITLPDFKLYYEATVTKTA WYWYRNRRDIDQWNTTPESEIM PHIYNLIFDKPEKNKWKGD LFNKWCWESWLAICRKLKLD FLTPYTKINSRWIKDLNVRPKTI KTLLENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQTTKWEKI FATYSSDKGLISRICNELKQYK KKTNNPIKK

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3900	34268	A	3940	3	1566	IQTTIGEEYKHLTYTNKLENLEE MDKFLDITYTLPRLNQEEGESLK RPMAGSEIEAIINSLPTKNSPGP DRFTAIFYQRYKEELLISNFSK VS/VIQNQWEKITSPIHQ*QTNR EPNHE*TPIHNCFKENKILGIQL TRDVKDLFKENYKPLLSEIKED TNKWKNIPCSWIGRTNIVKMAI LPKDKTSKYIDVDENEGSHCGK RKYKYGMEKALEILARAIQEK EIKGIQLGKEEVKLSLFADDMI VHLENPIISAQNLLKLISNFSKV SGHKINVQKSQTFLYTNNRQTE SQIMSGLPFKIATKRIKYI.GIQL TRDVRDLFKENYKPLLNETKED TNKWKNILSSWIGRINIVKMA ILPKVIYRFNAILINLPMFTFTEL EKTTLKFIWNQKRACIAKTILSQ RNKAGGITLRDFKPYKATETK TASEMKYYLENKIPFKVLHVM YNVPTHPFFIGDLHPNTKVVS LPNITSLIEPMNQGVISAFKDCY LRKTFVQAVATPEGETEMTVM QFWKDYNT

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3901	34269	A	3941	1	2580	MVKGSIQQEELTLNRYAPNTG APRSIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVKSDI QELNSVLHQADLIDIYRTLHPK STECTFFSAPHRTYSKIDHIVGS KALLSKYKRTEIITNCCSDHSAT KLELRINKLTQNRSTTWKLNLL LLNDYWVHNEMKAQIKMFET NENKDTAYQNLWDTFKAMCR GKFIALNAHKRKQERSKIDTLT SRLKELEKQEQLHSKDSRRQE INAEKAFDKIQPFMLKTLNLT DIDETYLKIIRAIYDKPTVNIILN GQKLEVFPLKTGTQGCRLSPL LFNIMLEVLAIRIQEKEIKGIQ LGKEEVKLSLFADDMIVYLENP IISAQNLKLLISNFSKVSQYKIN VQESQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVI YRFNAISNKLPMFTFFTELEKTTL KFI*KQKRACIASKLSQKNKA GGITLPDFKLYYYKAIIVTKTA WYWYQNRDIDQWNRTEPSEIIP HIYNHLIFDKPDKNKKWGNDS LFNKRWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLHVRPKT IKTLEENLGNTIQDIGMGKDFM TKTPKAMATKS/KIDKWDLIK KSFCTAKETTIRVNRQPTQEWK KIFTIYPSDKGLISRIYKEPKQIY

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3902	34270	A	3943	5	2130	QRLRRQHRLEQKTRSTTCHMR QSTTRSAERADTRIESMPT*ITP *HTDDVP/SHCTNSTHTATTSPS TIHHQQLTRVANVAQIRRTDI SSIAATEWISTINTHNYACRTRA VSQRRYVSDFEKERPTSNTP PRFRLVVSPTPLVGTTCGTYP PPARSISIASHLPLPLSLLPSSL DLDGRLTACSSVSQFSGSRGS PSSYIVATTRVISDVYDMTTY YNSTITPIS/PSARS*QORSVHLL LSSHRTYRHLVSRHTSQEHSL GGPLHRH*YNPVGSRAAAWAS KSALV/SVSEALVVSALI*LVA TRQRLVGICRTTPIRARSSVVR* VTRYQPNQRAPLIHATYHLLDR GQHPQSMQTIHWTTPPCWCL VCGKKSSLPCCSSTSMSTRNQ YDTLSLTTSWVL*SSIFWLAFIL LPRTSLPWPTVS*LAANA\SSGS TPVNSSFRT/SVRRSKLVVPANE IETPSFVVVTKFSRSASSYDCSIE YASTYAINITIVNSYVFA/PTHHT REHTISYALTSPGQPQNKTRIP LQWAF*AVRPSTQ/PSTVIYHAP TSQAIAASCALHSLGCLLGSAT APLPPTWTTPPPPPQLRTT*STG SLPHPPSC*TRP*PLAPRN*PFTG MSSQHCIPT*PQLASHSIALRG/S RARPTTSQTSIAS/SHSHS*LSHV Q*RPLSDQRSPLDHAHSHSILYA RASRISCLRVCV
3903	34271	A	3944	254	884	MTPNYTSRLFLHMGVLFYPFYR RLT*HIRTHINLKGWK/NRHF QMDTKNAEKALDKIQHRFMK TLKISIQGTHFKIKAIYKGSTT NTILNGEKLKAFPLRTGIKQGC LLPLPFNIVLELLARAIHQEKEIK GIQIGKEEVKLTFLFADDMIYLE NSKDSRKLPELIKEFSKVSRYK VNLHKSIALLYTNSDQAEQIK NSTSFTI
3904	34272	B	3945	52	843	

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3905	34273	A	3946	1	831	MEMLYCLIAEAGHISRRMATNT ANSAGLKPTCVCVALPLPPGRS APHRSCSQAGRELPGQGPRYYR HLPQLSILHSIGEGQCGFWSER SFKGYPERPAGAAGVCRLQGC GRRGRGAPFRTTDFSSRPRGAA ERADQGPRAAGSPWPRTTSGAQ RGRAQQGHTARRRGNNSNPGP SRARQASRRRRPATSGPPRGSP RPDRPRRRSPFYKSSSRETSRPP EGPRRPRAPALSAPAPGQPARP RPREPVPCGAVFTARDRLRPPA ATSHAPFSAANPRR*HRPGGPG ARRLGDAQLSRRST/SGAPRCS QTRSR*PTCVCVALPLPPGRSAP HRSCSQAGRELPGQGPRYYRHL PQLSILHSIGEGQCGFWSERSF KGYPERPAGAAGVCRLQCGGR RGRGAPFRTTDFSSRPRGAAER ADQGPRAAGSPWPRTTSGAQRG RAQQGHTARRRGNNSNPGPSR ARQASRRRRPATSGPPRGSPRP DRPRRRSPFYRSSSRETSRPPG PRRPRAPALSAPAPGQPARPRP REPVPAGVFTARDRLRPPAAT SHAPFSAANPRR
3906	34274	B	3947	250	281	
3907	34275	A	3948	3	639	DHTRCLRQLRLRLVLGVGPVPG AGPAG*KGCYGGRSANHHGAP ASCHLARSSCGPRLPGRYSAQQ PRARCAASGLCGWTAADPV PSEVLASQEVQLLCAGE*SGSC GPTHADLQPSGGTGEDGAAR AKRDLPGSVGERAAAPASGRL RACPGRPAGAGPGRARPPGGTA ALAQPPRPQGAARPPSGIGWP GNNSAQSKGRALMEQAAG

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3908	34276	A	3949	161	2377	SLFHGKVCHEFLHEPLPLVYLSL CTGYQLFKPSLISWLEEEELST LPRVLQEWKMLCKTKGPALW QDNFCLKTLNGIQLARNQNGEE LYDCKQCEDVFCKHPCLKTNM STQNRGNTSECIQYAKDLLSLY NKTSTIRKVSFVKHGKSFRL/F *MFRSRESVHKINPLK/CTDYGK AFIYQSYLEAHRKTSQSGEKLNE WKQCGEAFTHSTSHAVNVETH IINKNPYECKEKGDFRYPTHLN NHMQTHIGIKPYKCKHCGKTF VPSGFLEHVRTHTEGKPYGCKE CGKAFGTSAGLIEHIRCHAREK TFKCDHCGKAFISYPSLFGHLR VHNGEKPYEHKEYGKAFGTSS GVIEDRRSNTGQKRFDQCG KVFVSFSSLFAHLRTHTEGKPF KCYKCGKPFSSACLRHMRTH TEERLYQCKKCGKAFKCSYLT KHLRTHAGEKPYECMKCGKAF TERSYLTKHLRRHSGEKPYECK KCGKAFTERSDLTKHLRRHTG DKPYEYKDCGKAFVVSSSLVD HLRTHTGYPYKCNACEKAYS RSCVLTHLKTAAEKTSECN ACGNSFRNSMCFHDLRLTLTKI KPYKCKDCGKAFCHSDLTNH VRIHTGEKPYKCKEKGKAFRTS SGRIQHLRTHMGKPFECDCQG KAFVFSQVLVHI*KHTREKPCG CEECGKTFVVSSSLTEHVKIHR
3909	34277	A	3950	6	455	GLLHERQAEARCSICLDYLRHP MTTDCRHYI*SARIHQCW*ELQ DISPCPVCLQHCPDKNLKRNQ LCHMTDIAKQLLTARRKRKL QGEPPVCRKSDVALFCEKDP LCHQYRVSLDH*DH/SPMPIEQ AAAKHRKQFESYIEPLEKQV

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3910	34278	A	3951	2	1009	WNGHRMN*MQSSNGLEWN/QS SNGKEWNHRIESNGIIIAWN/Q WYQHQTTEKNGIFEWNRRSSN GPEWNHVMWNG/DNPWTRM QSSSNGIEWNHRMDSNGIIFQW NGNGNHRIGIEWNYDQ/SNEW/ QWNQHQTTEKNGIWKWNRRESS NGPEWNHLMWEN/ENNPWTR MQSSSNGIEWNRMESNGLEW NNH*TESNGSVSSDGNR/QS SSNGIAWNHHKMESNGINIKW NQMESWN/WN*MNRMLSSNG IEWNQHQTEKNGIIEWNRRESS NGPEWNHLMWEN/ENNPWTR MQSSS/NWNRMESSNGLEWNN/ QLNGIEWNHHRMEMNGIIIEW NRJELWN
3911	34279	A	3952	1	1494	MASLLGAPRLAGWASGAGALS RGWAIRPADTGGNLPVPRVPL PPDPVLRTARWAPGVNSGSQFSC HCQAPILEMGHGSSPGLGDAE VRAITVQCIRPIDGPQPQGGGS AGRRLTIPASTQEWALPLVGRV LANVLTGGDTGNQPIQRSLC RPQPCSHAETWGEVEAQVPAQ SNREQPAAAPGCGPGRGETGA RPETTFSPRRAPPNPYDEEGVR WSLEFMLCGTDGPVQPVQHQE GPAARLQLIRGGSLILESEGTLR G/SPVLQTDQPASHLLHTQGF A/AALSAVCL/HQNIHSGSALL APATRAAWEQIQRSSEGTALQ LRRLEGYFSNVARNVQWYTLQ PFVIVTTNMILAVDIFDKFNFTG ARVPWFDAIHEAFPRELESSISF PANFFKPPEEKEGLVVRPASK TTPQTTRPGPTEREAPISR*KR HPDDTG*FTFTLGIVYCTPGQLP PEPYDPNRRSLWLPHWPIINTS MVSALVYSEGAPLPSPL
3912	34280	A	3953	1	681	MGQLLDKNTPSHGARTREECG RERLCVSPSQGTDPRTSAAYLC VGGPAWSPLSESRPAGSSGCPW IKPPDPYRSPIGLCSLLTTEMMS RQPRTDLRGQTNPAAPSAVPVL SCSQNLVWPSLMAGTTWHSPL LSPSCFWHSPPGHN*H*CCVSKD *KSLFEWPTA/YSPLL PSTSP/SS KSMQPPKPRSNADSSVQASLIP RAMSSPTVSPWIMGNQSQGF HIAVSMWDD

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3913	34281	A	3954	136	420	RESRNLNRGESEDPAPPSIRNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPSPAPPPEHTHTGSPRPPSGRSR IRAYLH
3914	34282	A	3955	1	1782	
3915	34283	B	3956	1	3070	
3916	34284	A	3957	104	279	STTHPSVHE/QEEEEEEEEEEEE EEEEEEEEEEEEEEEEERKKKEC SKAQCKHFPLSEVL
3917	34285	A	3958	1	252	MTVCIHASEDLPVGRDVEVED SDIHDRDPGLGDKSETPSE/EKK EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE NFLQHYLHL
3918	34286	A	3959	2	368	
3919	34287	A	3960	239	432	CLWLQEEEEEEEEEEEE*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEKIFLGHVRGI
3920	34288	A	3961	1	577	MQIPSLHLKKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE/EKKKKKEKKKKEE EEFERRRKKKKERKEEEEE/G KEEEEEEGEEEEEEEEERRK EEEEEEEEEEEEEEEEESCLMGP MCVHIHPDKDLYSLGPPAQR TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3921	34289	A	3962	327	559	PKGRTPSPSCIHRYPCQTPRPHE P*GCHCPEEK/PRPRVWGPSCR MPLGVSQEKRPCAPGGVQGSF RVSLMMLTRL
3922	34290	A	3963	1	577	MQIPSLHLKKKEEEEEEEEEEE ERRRRIGRGREKKEEEEEEEEE EEEEEEEE/EKKKKKEKKKKEE EEERRRRKKKKERKEEEEE/G KEEEEEEGEEEEEEEEERRK EEEEEEEEEEEEEEEEESCLMGP MCVHIHPDKDLYSLGPPAQR TGSHAELPT*KARRSSSWTAAS RGCAARDPPRRCSPA
3923	34291	A	3964	157	272	WCNGSLPSYGW*LVGMESLGR MHKDLWTRQPNQDQLQ
3924	34292	B	3965	1	3723	
3925	34293	B	3966	1	573	

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3926	34294	A	3967	3	424	AGGQALQGGPQGRGSGVVG/ PGTGSSGAQHGLKHYPVLSGGS ERSWGRSHTPAGAGC*VRGRR AGGRPGTGHSRPPGGSCLSPAP PNSARWLGLGAPWQAGAGLR DPGDWRRGQGGPGWAWCPGQ PPAQHTCPPNSTARY
3927	34295	A	3968	3	1238	RGAERRAWSRGPACTRRGPAD WAAAGAGRPCPQRRGVCCTAA VPGAARLSCPIGPGDPRGRS LTGQGS*GLGAAGGGWTGALP SWHS*SQGWQTDVPR*VRGTE RDICTGL*QCPPPGGLQTGSGG LEHSLPWPBGIGIQA*GNHPCR LPRS*ALSAGGSGGQALQGGP QGRGSGVVG/PGTGSSGAQH HCCPPYTPG*HPISLLALGPQ SLQPEWAHSGTASGEQHSAGE HGMGTTGH*LPLGCSRCLVGLK HYPVLSGGSERSWGRSHTPAG AGC*VRGRRAGGRPGTGHSRPP GGSCSPAPNSARWLGLGAP WQAGAGLRDPGDWRRGQGGP GWAWCPPGPPAQ*HTCPPAGS LPGAAPGVLCAL*GPAAGV*A GPGPGGSR*TRGSPGAPRPA
3928	34296	A	3969	3	415	ETGRHRSQSVSSPPVQPRGKR AMYHSAELVSRGFFRPPVQAP AEPAGAAEGVHSQPASRQEA/G S/TEVRGQAHRFVSPNAAAGAG DG/PDPQSLAPTNRPCPPGGISP ARSEPVPPAPGRAAP*CFPDLP LAPPLC
3929	34297	B	3970	1	657	
3930	34298	A	3971	125	524	EAEALENSQPCDTG/PQSAFSP PGSTQHPRSQLSQCKQRYQDLQ EKLLSEATVFAQANELEK*RV ILSIGEPLLKQDSKQVQVDLQD LGYETCGQSKNEAQEETTSPE HEEHSSRKEMVLVEGLCSEQG
3931	34299	A	3972	1	648	MGQVWGLVHFTLEVHTGDDEE EQEYSEVTEDVTEHVYLP KVAKEEEAGIQQARQEGDLEA WQFPVRIHPPDQENITATFEPF PFKLLKELKQAINQYGPSPFV MGLLKNVTYSSQMIPTDGDPLT RACLTPAQFLQFKTWWADEAS IQAARNAWAQPIQINITADQLLG VGGWAGLDAQFVMQDDAIEQ LRGVQIRAREKIIT*CGEQYPSF

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3932	34300	A	3973	350	1078	GSNRRSNRAEQLRGVCIRAW KUTSGEEQYPSFSIVKQGP TDFIAWLQESLKKVIADSA IVLWLLAFDNANPDCQAAL RGKAHLVDYIKACDGIRG RLSWLSLQGRPAGAACTSS DWKAQLAPGPHAGPLRCP ARQPRLPAVLSAGAAFRDC CVQALLGGSAGPGDRLPG ALVALSLPFVKEATMNRW HRSAFFLFSANAHGAEGV VASR
3933	34301	A	3974	2	630	WDNCGLWFIPSWNLFTLM KESLMK*QKK*QSRFVCL /PAKEGEVYPYPSAPPYF WPDPPDLSFLEDAGQKVI VQAAPQAIALSSIQAGIQ EGDLEAWQFPRIHPPDQ ATFEPFPFKLLKESQAIN QYQGSGSPFMELLKNVAV SSQMIPTDWDALAQACLT LTQFLQFKTLWADEVSIQ AACNA
3934	34302	A	3975	264	634	WSSRCQHSSRPQASESW FPG*G PSFWPRIQGDEK TGAGGHP*LG C*PGMT QGQFSTKCQHTCLMW GSHWAQEAEPENAPGTSC PGSSG SWVLRSSLQRQK SAWSPG/ASM PAPKMPFL TPSSGFS
3935	34303	A	3976	3	410	KKKVWREEKERLLKMT LEERRKEYLRDYIPLNSIL SWKEEMKG QGPK*EENT QETSQVKKSLTEK VSLY RGDI/*VDAIVNAANASL LGGGGVDGCIHRAAGPCL LAECRNNGCDTGHAKITC GYDLP AKCEYN
3936	34304	A	3977	74	432	MLHNLRPRTLTRTRCP STPTT*ATPPTTHGSAGP RAAHLRTGTRRWAPRRAR SCTRSSPR RARAASTPPLA PARELRSPASP SCEQSAAP PSGRNGGNFPESIFV KTINSN

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3937	34305	A	3978	2	894	WGGYGMRTGPRTLTTTRCPSTPS*TTT*ATPPTTHGSAGPRA RTCAAQRTSGSHPSQRRSSAA PGV*RVNVPWAH*MKRV*TT LENLTA/PEMAMPAPHVIFAT DDWAAMVHPSARVPGLDGTG ALLVPTGVCAPGCKCPLTSSS VTHTRLKTTLSVPPSARQTGRG RSPDLRCSYPPDEQPVCPVKC GSPWVSVLVAVIQSESALVDP HPQHPYLYPVDMMQNLTLNLGE PQARALAAKLLGRPSSSQSGS RVPAVWAQAGNATYITVHTLC SHNTHMSPVRVKRFTHLG
3938	34306	A	3979	157	570	
3939	34307	A	3980	1	936	
3940	34308	B	3981	257	3934	
3941	34309	A	3982	210	4286	MPLKTRTALSDDPDSSSTSLGN MLELPGTSSSSTSQELPFCQPKK KSTPLKYEVDGLIWAQFKRRP WWPCRICSDPLINTHSKMKVSN RRPYRQYYVEAFGDPSESAWV AGKAIVMFEGRHQFEELPVLRR RGKQKEGYRHKVPQKILSKW EASVGLAEQYDVPKGSKNRCKI PGSILKLDSEEDMPFEDCTNDPE SEHDLNLLNGCLKSLAFDSEHSA DEKEKPCA\KSRARKSSDNPKR T*L*KRATYNFEAH
3942	34310	C	3983	163	309	
3943	34311	A	3984	72	424	RNCGTARSOHEPLGSWLQDTP QPP*TELAGNLPGD/F*PGPGK EQGMFVCHPIRQPLPRPLPGSSH QSMPTAQPLSSSSALLPALPAG FPVTTGGQWTKLQVQAPAPFHL PPQVEAV*AFYQKQMLVPCSL* SMPTAQPLSSSSALLPALPAGF PVTGGQWTKLQVQAPAPFHL PQVEAV
3944	34312	A	3985	1	347	KWQRFVLTGIDTYSRYEAYPA CHASTKTTIHGLMEFLIHHGIP HSIASDQGTMLMAKEVQRWAH AHGIHWSYHVPHHPEVAGLIER WNEIGLLKSQLQHLVNLRLRE LQCWLQ
3945	34313	A	3986	1	1716	

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3946	34314	A	3987	1	737	MSSVLLRLIYQLTKQTASFEGG PEQKALQQIAAVQAALPLGPY DPANPMVLEVSADRDVTVWSL WQVPIGESQLGFWSKALPSSAD NYSPPERQLLACYWALVET EY LTMGHEVTMLPELPIMTWVLS DPSSYKPAPMASWGVYPYQLT EEEKTRAWFTDGSARYTETTR KWTAVAIQPLSRTSLKDSNEGK SSHQQA KNGITVLAGVIDPDYQ DEISL/LTPQWRCHPGSSVWRAS SLGISHPP
3947	34315	A	3988	2	384	CGRSGYWHSSVATKITRLRML RPREGRKLP PGDIMIPLN*KLRL PPGS/FLLLSHQAKKGVMTLAG VTDPDYQDEISLLHNGGTGKS PHISDTFYGSKVASCQNTGPEK QDETQAQETAVYKSQIFGS
3948	34316	A	3989	3	1273	
3949	34317	A	3990	3	341	GLGRRQPAGSWPERRPGPSA/R RSTAPRRCGQAES*TERGSQPH QVQGGQGRWGVCMMKIPSHSGKS PDVSEVSKSRNSIISTAVTHAVV APEGLKRNGGGSHLRSSRGHR AVIF
3950	34318	A	3991	44	243	
3951	34319	A	3992	40	558	LGSIQVMQAVRNAGSRFLRSW TWPQTAG*QMTAPSSPPPPGL CSYSCPLSHP/SLPVTVRPWPSPS FSSQQGRGQNA/APGPSAQALD SSKTLRPSRKLNRTLPA TPSSG EPHLDQPSGDPQLTLARHPPE EPVNFQLCHLLSVGPYANKSEP QPSHLKMRIMLREVVRIT
3952	34320	A	3993	335	581	RRHLFLQWQRAWRLQVAAA GTTRPTSAMGIRCSEGAARAT AARA*TAGPEPLE/PAANPPPL TASALRAPPSFVLPOCTR

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3953	34321	A	3994	216	1159	SWHGPPGANTVAAAAPPEEK AALKLRPTHGWVPVRATDVH ILKASGESEWRGGSRAHQMS VAMATALGEGVPVRGPAAAGSL RLLPGSSAPLGRDAISSCNGVN GLETTGGRCRHNAPNKRHGD LLEGAAAR/AQAARA*TAGPEP LE/PAANPPPPLTASALRAPPSF VLPQCTAAPRDPASAAGAN*G KAQSRNC*NEPFA YGGGTHGT GAGAAVTVAADGN*LGSIQVM QAVRNAGSRFLRSWTWPQTAG PWPSPSF/VFPAGSWPERRGPS AQALDSSKTLRPSRKLNRTLR ATPSSAFTLPFQERRAL
3954	34322	A	3995	1	738	MTKRGHGTAWAVASKSASP WQLPHSVFPGTEKSRIE VWE LPRFQRMYGNTWMSGSSLLQG NQNLHAERYCNSTLERNDTPIE SLPKPRESEDLGEHNGSTMEE VGAETRVQRHWVRVSMTELAL ASDAHMWGSNPGQRTVGMV GECGTMLGDTQVLLSNPCGDR ARRAYSTAPDYAVCGNGGKVK LNEQRFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGDS*AIPIVTE LGERIAQLLIMLYVVKWGKSEIK RT/G/GFGSTNKQGKAAYWME ALRPEPLCWQSNYPEAAAVGK PKAAYTKKLHGDS
3955	34323	C	3996	87	329	
3956	34324	A	3997	3	122	
3957	34325	A	3998	1	156	
3958	34326	A	3999	1	353	
3959	34327	A	4000	1	201	
3960	34328	A	4001	56	207	EEKKEKEKEKEK/EEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
3961	34329	A	4002	1	174	MNRC*RIHYSNEVH*KEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
3962	34330	A	4003	1	278	MTSYKFTEPKNGIWQLHEAAQ LDTTYKNKLNKKEEEEE/EEEE EEEEEEEEEGEGEEEEEEEE EEEEEEEEEEEEEEEEEGVIL
3963	34331	A	4004	144	429	DLPREYALPAGPRRRCRHTH RYEPNPEFGAKHSCPA*HRAA PATSDTQE*HRSNAFEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEETLFSNM

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3964	34332	A	4005	3	122	TEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
3965	34333	B	4006	1	300	
3966	34334	A	4007	1	1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIIDSNFEPELVLEFFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHETIYILNQDAQNKSP SAVMSHESDAHSDSARSSSSK LELSPDVNKKIRSEAMVKEKKK ADKKGEKSARSPPSLSDNDFS KQDGNITTRQEMSPAGVPLGGM QLNEVKPKKDRQNVQQNEDAT QYEEISILTKLIVESYEGEKVRGL YEGEGFAAFQGGCTYRVSCPFE NLQEGEEGRLEECPEPRRVH VAGRSMYEGEVVNGMRNGFG MFKCSTQPVSYIGHWCNGKRH GKVGVEVATWRAEKKKKEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEKIRP
3967	34335	A	4008	453	705	LLSIVQAEAVSENSHPILPRVSR SGWGQKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE SCYSITPELSCKLGHR
3968	34336	A	4009	93	705	ESSTQTCSGFWTGCTALHRWR GMPERCPPESTRDS*TRFPQSSLP GHKT/SEKEEENRKEEEEEKE KEK/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEQEEEDDEE EEEEKSCSVNLSIELPWPDKA YSRLAPLSSQGPVAVKVPTHEL AKLEDVCVQFTYLTVEKRRWAR AVTGAQELGVDYPRNECKPH NNGYDND
3969	34337	A	4010	1	3189	
3970	34338	A	4011	1	5127	
3971	34339	A	4012	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLR*KKC*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFEKINKIDRP ARLIKKREKNQIDTIKNDKGD ITTDPTIEIQTIREYYKHYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRNITGSEIATNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASH LIPKPGRDITTKGNFRPISLMNI DAKIL

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3972	34340	B	4013	1	3570	
3973	34341	A	4014	1	2347	MELKTKARELHDECTSLSSRF QLEERVSVMEDEMNEMNLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRDTTKKENFRPISLMNI NAKILNKM LANIQQHKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIIISIDAEKAF DKIQQHFM LKTLNKLVLVLA RAIRQKEIKGIQLGKEEVKVS FADDMIVYLENPTVSAQNLLKL IGNFSKVSYGKINVQKSQAFY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYWYQNRDIAQ WNRTEPSEIMLHIYNLIFDKPE KNKQWGKDSL FNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPV RMAIHKSGNNRKIQ/GGIWCD RIL*R*TTCTRVAKIEQSL*RRI/W KRLQRTL SIPVLDAV*PPMF*AS
3974	34342	A	4015	1	5073	
3975	34343	A	4016	1	3297	
3976	34344	A	4017	1	3514	MELKTKARELREECRLSRSCD QLEERVSADEDEMNEMKREG KFREKRIKRNEQSLQEIDWYVK RPNLRLIGVPESDVENGTKLEN TLQDIIQENFPNLRQANIQIEI QRTPRQYSLRRATPRHIVRFTK VEMKEKMLRAAREKDRSTRQK VNKIDTQELNSALHQADLIDYR TLHPKSTEYTFSPHHTYSKT DHIVGSKALLSKCKREITHTNYL SDHSAIKLELRKLNLTKSRSSTTW KLNLLNDY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
3977	34345	A	4018	1	2666	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKAULSKCKRTEIITNYLSDHS AIKLELRRIKNTLQSRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDKGDITDPTETIQT TIRESYKHLAYANKLENLEEMDT FLDITYTLPRLNQEEVESLNRPI GSEIVAIHNSLPTKKSFGPDGFTA EFY/PESYL*QTHRQYHTEWAK TASIPFENWIKTGMPSLTTPIQH SVGSSGQGNQPGEGNKGYISIRK RGSQIVPVCRRHDCLSRKPHRL SPKSP*ADKQLQQLRIQNCQT KITSILIHQQQTNREPHE*TPIH NCFKENKIPRNPTYKGCEGPLQ GELQTTAQGNKRGHKQMEEHS MLMGRKNQYRENGHTAQGNL QIQCHPHQATNDFLHRJGKNYF KVHMEPKKSPHRQVNPKPKEQ SWRHHTT*LQTLQGYNSQNSM VLVPKQYRSMQNRALRNNA AYLQLSDL*QT*EKQAMGKGFP I**MVLGKLASHM*KAETGSLP
3978	34346	A	4019	824	3693	AWKGTDDRSTRQKVNKDTQEL NSALHQADLIDYRTLHPKSTE YTFFLAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNLL NDYWVHNEMNAEIKMFFETNE NKDDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
3979	34347	B	4020	1	3765	
3980	34348	A	4021	1	4791	
3981	34349	A	4022	1	3297	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3982	34350	A	4023	1	3170	MVKGSIQEQEELTILNIYAPNTG APRFIKQVLSDLQRLDSDHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTI.H PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEITNYLSDHS AIKLELRINKLNTQSRSTTWKLN NLLNDYVWHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQKLELEKQEQRHSPSRQEQE ITKMRAELKEIETQ
3983	34351	A	4024	281	3030	KPRLENYMKNAEASRADAINW KKGY/LVMEDKMNMEMKREGKF REKRIRKNKQSLQEIWDYVKRP NLRISVPESDRENGTKLENTL QDIIQENFPNLARQANIQIEIQ RTPQRYSSRRATPRIIIVRFKSV EMKEKMLRAAREKEIQTNIREY YKHRYANKLENLEEMDKFLNI YTLRRLNQEEVESLNRPIRGSEI VAIINSLPTKSKSPGPDGFTAEEY QRYKEELVPFLKLFQSIKEGI LPNSFYEAII
3984	34352	A	4025	1	3290	MGELITPLSTLDRSTRQKVND TOELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRINKLNTQNRSTTWKLN LLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKRE KNQIDTIKNDK
3985	34353	A	4026	1	3573	
3986	34354	B	4027	1	4251	
3987	34355	B	4028	1	3065	
3988	34356	A	4029	965	4089	TWKGTTSTRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTF/LAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRINKLNTQSRSTT WKLNNLLNDYVWHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQKLEKQEQTHSKA SRRQEI TKIRAELEIETQKTLQ KINESRSWFFERINKIDRPLARI KKKREENQID

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3989	34357	A	4030	523	3981	
3990	34358	A	4031	1	3429	
3991	34359	A	4032	1	3156	
3992	34360	A	4033	2	4943	
3993	34361	A	4034	1	6747	
3994	34362	A	4035	1	3928	MAAWNLLKSYAYWGGLRKE DFHCLDRKTLRTVSFLAALLSY ESIGGKGKGLTTRKDIYTENPSV HHHHQRPKLVDTTKMGKKQN RKTGNSKMQSASPPPKERSSP ATEQSWMENDEELREEGFRRS NYSELREDIQTGKKEVENFEKN LEECITRITNTEKCLKELMELKT KARELREECRLSRCDQLEER VSAMEDEMNMKREGKFRDK RIKRNEQSLQEIWDYVKRPNLR LIGVPESDVENGTKLENT
3995	34363	A	4036	1	3638	
3996	34364	A	4037	3	3585	SNSHITILTLNVNGLNAPIKRHR LANWIKSQDPSVCCIQTHTLTC RDTHRIKIKGWREIYQANGKQK KAGVAILVSDKTDFKPTKIKRD KEGHYMMVKSGSIQEEELTTLN YAPNTGAPRFIKQVLRDLQRDL DSHTLIMGDFNTPSLTLDRSTR QKYNKDIQDLNSALHQVDLIDI YRTLHPKSTEYTFSSALHHIYSK IDHIVGSKALLSKYKTTEITNC LSDHSAIKLELRIKKLTQNRSTT WKLNNLLLN
3997	34365	B	4038	877	8907	
3998	34366	A	4039	1	450	QGSPPSGSRE*NSQSAGPQCALP PAMA*VPLSWRSMGKWWKRT SCTSDST*PPSERRHWSRKS SPSAMPASFRCSASAREMLP*KKG RCAAGSGIAPPPETWGRGTGGC PGKQATCGVSGPNANGEPVL/K YPPSSSEAHGGPGRNGRSD
3999	34367	A	4040	2	522	
4000	34368	B	4041	102	186	
4001	34369	A	4042	2	5417	

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4002	34370	A	4043	45	1585	KQPSGLLKFGNLIKCHPPSLTH MLSQPCA/EAPTPDPNWELA/LY IHPSSGIMSATVSFWSIGTA/YLE AQGIWEPFRRRLSFEASNPPFD VGRPFDLRRIVGISSEGNLNTLS CDPGHSRGFCGAGGSSSRPSAG SHKQ*GPSGHPHSSHSNRNSAD VDDVRAVNSGRTSSMTSAQAA SSQPANKTRPLVLDNSTGAQGH SAGRKSKGAKQSQHSQHHAH SPLEQHQPPLPPVPQPQEPQP ERLSPAPLAHPSPERASSARHS SESDITSLIEAMDKDFDHHDSP ALEVFTEQPPSPLPKSGSTEGG PASTFTQAVDGGIQFFTDWCWE GPSSLLAVAREVQLALCIHELL IHGFSQLQVSGGPGAMPDPAAH LPFFYGSISRAEAEIILKLAGM ADGLFLVRQCLRSLGGYRQLN GTYAAGGAHCGPAELCEFYS RDPDGLPCNLKPCIPPSGLEPQ PGSSTACETPWARPSRPSARP RRWRSSLLRRTTSGCGPTTAA
4003	34371	A	4044	1	1773	
4004	34372	A	4045	1	663	MALWTLRPTLLVTCMLICAPG VMGAVVAPLTILGGPLLIRAAW YTAGIVGGLSTVAMCAPSEKFL NMGAPLGVGLGLVFVSSLVDQ MGRWFVAGGA/VGLGALCYY GLGLSNEIGAIEKAVEYWFNSF VCHSNQQNACSHELHDERLLG DMGLPILHAMLLRRLPSVDSQN ALSSIMLLHTALP*QSAERLFS* TS**EALG*YGFAYPACNASAK TTIRGLTECLIQHIVTPHSIASD QGTHFTAKEVQQWAHAHGIH WPYHVPHHPEAAGL
4005	34373	B	4046	147	330	

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4006	34374	A	4047	485	1568	GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLPSWEGQRFVLTGIDT YFRYGFAYPACNASVKTTIHGL TECLVHHHGVPHGVASVQGTH FMA*EVQQWAAHGHHSYH VPHHLEAAGLIEQWNGLLMSQ LQHQLGDNTLQGWGKVLQKG VYALNQCSIYGTVSPRIHJGSR NQGVEVAPLKITPSDPLAKCLL PFPKALHSACLEVLVPEGGTLP PGDTTTIPLNWKLRLLPPRHFL LLPLSQKAKKGATVLAGVIDPD YQDEISLLLHIGGKEEYAWNTG DPLGRLLVFPCHVIKVNGLQKQ PNPGKTANDPDPGSMKV*VTPP GKKNPRPAEVLAEKG
4007	34375	B	4048	182	662	
4008	34376	A	4049	1	2250	
4009	34377	A	4050	1	1326	
4010	34378	A	4051	1	1614	
4011	34379	A	4052	1	2586	
4012	34380	B	4053	1	1954	
4013	34381	A	4054	1	705	
4014	34382	A	4055	1	1833	
4015	34383	A	4056	1585	4128	
4016	34384	A	4057	1	1425	MARG/NAITLPV/CGRVAKFT/L EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLTGQQT PAFGRRVSGVIEIADGSRRRKA AALTESDYRVLVGELDDQMA ALSRLGNDYRPTSAYERGQRY ASRLQNEFAGNISALADAENIS HKAHKYFVEANTGTETGYQG EESLFNKAYYGGGTNFRKESQ KLQQSAAKKRDAELANGALGIIIE LNNDYTLKKVMKPLITSNVTVD EIERANVFKMNGKWDFAFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKITL APNTQTASPRALADSLMQLAR QVSRLESQQSSQKKAIAITAI RKNKEANAVLARLNSELQQQL KGFADFREPPKQDFRLLGQTS VDRLLQLSQGQAITELCGAKRV GYFGPTQFYIALKLIAAAQSGLP VRIESIKCGNSYDHDYEFELGTL VLPRLSEGFALSNCGEHYWL

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4017	34385	A	4058	1461	2496	NKRNHQSVCHAFIRIPAAAPMV DSLIRVGVGMARGNAILTPVCG RDVKFTLEVLRGDSVEKTSRV WSGNERDQELLTEDALDDLIPS FLLTGQQTAFGRRVSGVIEIAD GSRRRKAAALTESEGTPAFGRR VSGVIEFADGSRRRKAAALTES DYRVLVGELDDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAENISRKIITRCI NTAKLPKSVVALFSPHGELSAR SGDALQKAFDKEELLKQAS NLHEQKKAGVIFAEVEVITLLTS VLKTSASRTSLSSRHQFAPGA TVLYKGDKMVLNLDRSRVPTE CIEKIEAILKELEKPAP
4018	34386	A	4059	340	2067	
4019	34387	A	4060	1	1959	
4020	34388	A	4061	1	2319	
4021	34389	A	4062	1	1587	
4022	34390	A	4063	964	1757	GYSGSKPDVITLLEQKEPCVV ARDVTRRQCPAAPMVDSLIR VGVGMARGNAILTPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADANN ISRKNITRCINTAKLPKSVVALF SHPG/ELSARAASRQRCQGYHK LHDKQRLLRG*KGNICAKLLNE
4023	34391	A	4064	1	1554	
4024	34392	B	4065	1	1599	
4025	34393	A	4066	1	682	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIRVGVGMARG NAILTPVCGRDVKFTLEVLRGD SVEKTSRVWSGNERDQELLTE DALDDLIPSFLLTGQQTAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDDEQMAALSRL GGATQAFAKENNQKHTKKRT ASLILHAMICCRSLNSSKTKNT KCLNSINQRLKILSLQKDLMSG TAGRCKTLTEQ
4026	34394	A	4067	1	2448	
4027	34395	A	4068	1	2541	
4028	34396	A	4069	1	828	
4029	34397	A	4070	1	1899	
4030	34398	B	4071	1	1686	
4031	34399	A	4072	1	1437	

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4032	34400	A	4073	1	3417	
4033	34401	A	4074	1	3826	
4034	34402	A	4075	812	2578	FIRDFADFGTTIKQDFRLLGQTS VDRLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGHNGN GQVSPHFHQTSSSTIRSCSCHLLT LNFLTLQLNTSDIAVFHSTPKLL LVTSTITHMGLNTSQAQSVPI NSVAGSLAALQPVQFSQQLHSP HQQPLMQQSPGSHMAQQPFMA AVTOLQNSHKFSHRSHGPGQS NDACSEPTNKKMRRNRFKWGP ASQILYQAYDRQKNPSKEERE ALVEECNRVWQARRLGAFGKE DVHVSFAARRGAKFRHQTLLG RRSSIPAAPMVDLIA RVGVMA RGNAITLPVCGRDVKFTLEVL GDSVEKTSRVWSGNERDQELL TEDALDDLIPSFLLTQQTPAFG RRVSGVIEIADGSRRRKAAALT ESDYRVLVGELDDQMAALSR LGNDYRPTSAYERGQRYASRL QNEFAGNISALADAENISRKIIT RCINTAKLPKSVVALFSPHGELS ARSGDALQKAFDKEELLKQQ ACKLHEQKKAGVGDNDSIDSW KNAGR VFKDSKFDANDPILK DQTQEWSGSATFTSDGKIRFIL

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4035	34403	A	4076	1474	3367	REEGANSECLGRHGFKKMLYV KRDEVGKGQIRLETVFEQAIDQ RFSTDTSLSIPAAPMVDSLIARV GVMAAGNAITLPCVGRDVKFT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDIPSPLLTGH KTPAFGQRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGKCMVPTESAPH VTVLGCQCGLGLENGLKEY LGRSTLDMEAWQPLQEFYLNH LITGQMFEIAVTQNNKINSSP TTEQSWMENDFDELTEVGFR SVITNFSELKEHVLTHRKEAKN LEKSDGENTKLENTFQDIIQE NFPNLARQVNIQIEIQKTPQRY SSRRATPGHIIVRFTKVEMKEK VLRAAREKASLAPENLNSKIR PVVILFHYGESWNLRLADQRLI FAKSWPRASRYQQGHQDLFILR SDLPSQVFIRDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA VAAAAADGVTFSPVTPHTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYVTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
4036	34404	A	4077	794	4235	RVSRGRKWFIFIALKRMMPAMKK AMNLFGLSNVRTVHPEGFTV YISTHISFPLSGYRTGLRSFGLV KQKKSPIRMPVCVYTNLTLCQYR KPDGSGIVSLKIDWIIERYQLPQ SYQRMPDFRRRFLQVCVNEINS RTPMRLSYIEKKKGRQTTHIDL ALKGLRVLLVEGNDPQGTASM YHGWWPDLHIHAEDTLLPFYLG EKDDVITYAIKPTCWPGLDIIPSC LALHRIETELMGKFDEGKLPTD PHLMRLAIETVA
4037	34405	A	4078	1	2574	
4038	34406	A	4079	1	536	

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4039	34407	A	4080	368	1449	LKSTNLITLRLFLVPMPLAYM KFTPSGLVAACAPWLRQRRVV QLGQIAFSAP/YLSQMVRQEMY NRYGESAYEDGYRYTTITRKV QQAQAQAVRNVLVDYDMRHG YRGPANVLWKVGESAWDNNK ITDTLKALPTYGPLPAAVTSA NPQQATAMLADGSTVALSMEG VRWAPYRSDTQGGPTPRKVT DVLQTGGQIWRQVGDAWWL AQVPEVNSALVSINPQNGAVM ALALLNNARPWYLGAPRDSTI IFCQFGAHLPLDPKTQPVGCRN AARKSCAEIRLVDPARANSGL VRRYRKYRRQYHKSRSRQPL RQQQPVRLDWRNVNDQYALT TRFLYQSLQRHAQLNVPLFHV
4040	34408	A	4081	1420	1842	
4041	34409	A	4082	407	1347	GRIRVHIHKDGRADGGSQPGVT AIQQQLPFAFAFPN*SY*TESAW AQSIK/GPWWRDQVDGPAGR LAALPQR/SLINAVSTRMEGIG AFNTANPACST*FLCSLLILPSLF STALPNFRLSAMVSDCTISNMV WST/SAVTDWCTPLD*ERKHR GTARLTGTGKGVGMDRDKQVST LFLGFCYAHQWNEDVFIARH VHLHIALFLDQRAQTASYLQYH IFFARFVPHRTGVFATVARLK HNDNRTIAPCFTRLWTLRLWR HLLFEVAFVVLQQRQRLHI LCIGRIEVHHQTLFKPGDRRG KQLRFYVLL
4042	34410	A	4083	1	649	MRHGYPARANVLVKVGESAW DNNKDYRYAKALPTYGPLPA AVTS/ANPQQATAMLADGSTV A/LSMIEGVWRWAPYRSDT/QQG PTPRKVTVDVLQTGGQIWRQV GDAWWLAQV/PEVNSALVSINP QNGAV/MALVGGDFNQSKFN RATQALRQAGAHLPASQSGH HQQTAR*KSNFCARM*TPDQLS W**KNCPFLSPT*QRQWSLRR YRPVSQRTSF

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4043	34411	A	4084	2	551	WRAAGPEPCPTGRQLRP/AGDL ACSAAGPGEFPTAPLALAGR SKCGAAEPATQNSRWPMSPH LSLHASPQAEAGAGSGL/VPAPR AAAG*RAPQMRP/VVGAEEAE APGP*EPCRHAPHASQHRVGC HPS/AEEPCHRPAPHASQHRVY CHPSGLNPAGTQHPMPASTGTA AIHRG*TLAPSSP
4044	34412	B	4085	1	1029	
4045	34413	A	4086	1	2157	
4046	34414	A	4087	1258	1838	TQVVFITSAWGLGEMVVQGA NPDEFYVHKPTLAANRPAIVRR TMGSKKIRMVYAPTQEHGKQV KIEDVPQEQRDIFSLTNEEVQ LAQQAQVQIEKHVYGSMD/IEW/ AKDG/HTGNGHVQALRNRCPE ARQHRMRIPGRILPRPIGRMAG PKTRIEHTSVTVISNRKKIKTEN RGHKGYEDRKLHEDQLRHQS
4047	34415	A	4088	2806	3540	
4048	34416	B	4089	1	1251	
4049	34417	A	4090	341	946	GLSSVGQSVNDHLPWT*GLSSV GQSVNDHLPWT*GLSSVGQSV NDHLPWT*GLSSVGQSVNDHLP WA*VLSSVRQSIDDHLPWT*VL SSVRQSIDDHLPWT*GLSSVGQ SVDDHLPWT*GLSSVGQSVDDH LPWT*VLSSVRQSIDDHLPWT* GLSSVGQSVDDHLP*M*GLSSV RQ*VT*AKVNPKISAVTRNRGS VESPHLEGRSLKQVFIQVED MSWGPPWLWVEGESWT
4050	34418	A	4091	426	706	VLGGGSEKAPLWWSGPMVLP GAHSMKT*LPHTHVEFGFACLA SAGAQDVGMEGPRHTTENSVT GSPSHFPPRASQHRGICRPHAG RATADF
4051	34419	A	4092	596	905	GLSSVGQSVNDHLPWT*VLSSV RQSIDDHLPWT*GLSSVGQSV DHLPT*GLSSVGQSVDDHLP WT*GLSSVGQSVDDHLPWS*G LSSVGQSVDDHLPWT*GLSSVG QSIDDHLPWA*VLSSVRQSIDD HLPWT*VLSSVRQSIDD/HSSMD VRSV*CRTISR*PSSMDVRAV*C RTINR*PSSMDVSAV*CKTINR* PSSMDVRSV*CRTISR*PSIP*T* GLSMSLIPSQCLGSAVTPFSAV TRNRGS/ENHPILKAAASRSKSS FPRLKT

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4052	34420	A	4093	3	1194	SLGPRSHSCCRSDYRSGTTVPL VLLPVCVGPALLVFALLSPLCV VCSALCGGLLPVLRASLFLWCV AFLAGLVFVFGFAFFGSLVRGR FLVVVPFFLLFALCRLFLVCW LRSFGACPVSVCVAGFACFAGL FLVLVSLSSGFGRLSFSCVVG SLCLPGFAFRAFCLFFLPCVGPA LLAFPGFCGPSSPSLSYGGLFAP WSCALLGFFGCLGWSAPGLSS FGLSVRVLSLPCASGLRSLSGC ALVPGLFLPWVFSRSLRPLVSF GCLLCFSVSHNMDWIKESAG KVIQGN*WLPVILFFGSVPLTS KAATAKPLMRMG/RALTVSQL T/AVASFAAVYGLFILPT*PTLV GAVQMDDTGTTTRIGKLVSNNHP FFIRVLLGVALTVCFGFVLGSF
4053	34421	C	4094	70	1950	
4054	34422	B	4095	262	4347	
4055	34423	A	4096	2	458	
4056	34424	A	4097	2	445	QPTERGLCASLKPSRAAIKSQSS KVISFDSMSHIQGTVVQGVGSQ GLEQQYRSGVAVFRLHSFSHRL LSACEFSRCRVQAVSRSIILGSG RWQPPSHSSTREWPSGHTVWG LQPHISPLHCPSKDLS*GLCLCN KLPPENLGFSYVL

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4057	34425	A	4098	1	2589	MVWFLKNVNHGTHINAKEYN DVENKERTGWKVGSTYELLCA RPLRKGNVGLSGDVFLTVFVM KTGHSSSLPSTTTSDSTAQEGY ESRGGMLDWKHLDDSPDSTD LGAVSSHNHQDKKAMLDGEE RPFNEPGVFHLLADHQLTQKV ASIPGSAVCAYDMLDIASVFTG RFKEQKSPDSTWTPVDERVPK PRPGCCAGSSSLERYATSNEFPD DTLNFIKTHPLMDEAVPSIFNRP WFLRTMVRYRLTKIAVDTAAG PYQNHTVVFLGSEKGIILKFLAR IGNSGFLNDSLFLEEMSVYNSE KKWSTAKPVRVTIILNPGQASF CITLRETVC*RRKHWCPPYRC TLQ*HFCPC*HCLSGKETLCRVT GGMKVKADRDSELPYAAMLA AQDMAQRCKELGITALHIKHR ATGGNRTKTPGPGA\SRPSSPCP LGCLK/WQTLFPRRLRWPGGG RRKRSQLEAQRVIRESYLKGHD QLVPVTLIAIVLAFVMGAVF SGITVYCVCDHRRKDVAVVQR KEKELTHSRGSMSSVTKLSGL FGDTQSKDKPEAILTPLMHNG KLATPGNTAKMLIKADQHHLD LTALPTPESTPTLQQRKPSRGS REWERNQNLINACTKDMPPMG SPVIPTDLPLRASPSHIPSVVVL ITQGGYQHEHYVDQPKMSEVAQ MALEDQAATLEYKTIKEHLSSK
4058	34426	B	4099	1	1299	
4059	34427	A	4100	95	502	FPEIPQSCREGAPGPAKPGGPRA REPCPNRTAASWGVHCEDEGGS TVRTGGPL*GRGVHREDGASSP QHPPRRGRGLGHLGPRPL*GGQ DAAAAPGHRGKS/GGKGFLPAL RVQGERGRVSRRAVCMWTS CASVPS
4060	34428	A	4101	2	653	DSFGMSVLKINPRTLFGGKPY VCRECGRGTWKSNIHQRT SGEKPYVCKDCGRGFTWKSNI FTHQRTSHGLKLYVCKECCGQSF SLKSNLIHQRAHTGEKPYVCR ECGRGFRQHSILVRHRTSHSG EKPYICRECEQGSQKSHIRHL RTHTEKPYVCTECGRHFSWK SNL.KTHQRTSHGVKPYVCLC GQCFSKSNLNKHQ\RSHTGEK

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4061	34429	A	4102	8	389	LPASASQSVGTTGVISFENTCNI CHFFFLLLFFSSSSFFFLPFSFS FRVSLF*IQPLKTTASTVQGRQH SGGYRASPERRADQRAHTGEK P/YVCRECGRGFRQHSLLQLSV YPHSFWTQDKRSNH
4062	34430	A	4103	1	740	EGKGRGPRFRPRAHPFPHELQS RLCILKLPHHPTPSSCPSS*TPVA PLPSHPCAPH/SARSCPVSDEAA LP*SMALWARAGLLEAPTLL PAADASSPA/MPFSRKLPPPLP L/CPEPLGPSAAPSPPAPPGPNA AARPP/PPSPSAAPGPRRPGAIR PVGPSRGP/PRNSRSLRAPDVH TAPMRCLPSVRPPLPVLAL/PD PLPRPPSFVPSLPSP/PSSGPSCPP TSAPPGSPRPGFVRLPCLLFWGS
4063	34431	B	4104	48	272	
4064	34432	A	4105	2	622	CPLSPLLFNIVLELLARAIKEK */LKGIGIEEEVKLSLFGDDLIV YLENPKYSSKKLLELVNEFNKV SGYKIYVHKSVALLYTNSDQAE NQIKNSTPFTTATSSSSSSSSSP QGIFLTAKRLKNF*RGKFKTLVK KNQGDPKKGKNPPGPKMGKN NFGKTPFWAKKI*KFHSNPKKT PPFFQKLKKTGVKFFWAPKGP KGFLSKK
4065	34433	A	4106	39	1043	QKQPVWQRCREIGTLGYCGWK WTLDIHGRGHRILSGGVEIPGP WTEGFIQGRDVGELQEPGLSGR ESIH*GKSYEYECSEDEGEVFRV RASLTNHQVIHTAEKPYKCTEC GKVFSRNSHLVEHWRIHTGQK PYKCECDKVFNRNSNLARHQ RIHTGEKPHKCNECGKAFRECS GLTTHLVIHTGEKPYKCNECGK NFRHKFSLTNHQRSHTAEKPYK CNECGKVFSLLSYLARHQIHHST EKPYKCNECGRAFHKRPLMA HLLIHTGEKPYKCNECDKVFGR KFNLTNHQRIHTGERPYKCNA CGKVFNQNPHLRHRKIHAGE NSLRTIQME

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4066	34434	A	4107	3	941	QQHQQQQHFGVQVAIQQQQQ QGPVQVTNQLGPKPQGLMPP SSHQDLLVQQVSPRPQGPQG MVGPAQVGVLIQIQLHGALGP QGLH*QVFM*QSRVFSSPQLA QQGQGLMGHRLVTAQQQQQQ QQHQQQGSMAGLSHLQQLMS HSGQPKLSAQPMCSLLQLLQ QQLS*QQLHQQQQQQLQQQ QQL*QPQLHQQQQQQLQQQ PQQLQQQHQQQLQPQINSQ/HL FSPRRPPNHMGLLTHSPNLTA LRLTSTHKAALGPGLQAALGHP KDGLLWKTGLTWRARGLICTG GIISYFTQHSWEVKVFTTL
4067	34435	A	4108	1	2255	MEKNKVVKREAEANSINLSVY EPFKVRKAEDKLEKNSDNVLE NRVLDGKLSSEKNDTCLPGTAP SKTKSSSKLSSCSAIMALSAKK AASDSCKEPVANSRESSPLPKE VNDSQARAPLQSTVMTNAVSP AELTPKQVTKPVA TAFLPVSA VNEMKTAGSRVINLKLANTTT VKATVISAASVQSASSAIK AAN AIQQQTVVVPAPSRANAKLVK TVHLANINLLPQGAQATSELQ VLTKAQQIKQAIINAASQPP KKVSRVQVVSSLQSSVVEAFN KVLSSVNPVPVYIPNLSPTNAG ITLPTRGYKCLECGDSFAVEKS LTQHYDRQSMRIEVTCHNGTK NLIFYNKCSLLSHARGHKEKGV AADTRGQKTCTICQMLLPNQCS YASHQRIHQHKSLEYTCPEGAI CRSVHFQTHVTKNCLHYMRRV GFRCVHCNVVYSDVAALQSHI QGSCHCEVFKPICPMACKSAP STHSHTYTQHPGKIGEPETIYKC SMCDTVFTLQTLRYRHFQDHI NQKLSVFKCPDCYLLYAQKQL MMDHIKSMHGTLKSIEGPPNLG INLPLSIKPATQNSANQNKEDT KSMNGKEKLEKSPSPVKKSV ETKQVAPGWTCWECDRLEFIQ RDVYISHVRKEQGMKKHPC RHLQCHNRHKGIRKVVYACSH CPDSRRFTTKRLMLEKHVQLM
4068	34436	B	4109	1	411	
4069	34437	C	4110	54	146	
4070	34438	A	4111	1	1937	

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4071	34439	A	4112	1	1830	MCIEVTCNHCTKNLIVYNKCNL LSQARGHKEKGVMQCSYSIL KPVSAAGHIVSPSSNSSSSSTLQ SPVGTGIHTVTKIQSGITGTVISA PSSTPSTTAMPLDEDPKLCRHH NLKCLKCNEIFQDKRSLATHFQ QAADMSGQKTCCTICQMLLPNQ/ CQRHGHKSPYTCPECRAICRK KRTQIHEWERETGKEISISFEKK SMETKKVASPGWTCWECDFHLF MQRDVYISHLRKEHGKQMKK HPCRQCDKPFSSSHRLCWHNRI KHKGIRKVVYACSHCPDSTGTFT KGLMLEKHVH*CMASRTLTK K*QTTPMRRKQK*K*TSRAVP SGVERTGSGVQASQRSNNSTT EKAENQCF*GSQAPLCCTQVKG TSASAQAKWGWR*PTGEQTQ PRGRISQWVMSDRCKVCAKT FETKAALNTHMQTHGHAEGCL KQPCRSLLSQPRIKTEARNLIRN ADFLNSILRNGEGYSKEKKNGT GFLGRSARLALGAQGGKSWRF LFWVLLPNVLRVGMHDVN HRLINAAGCVQLAVTLSTEPH GISSAISRVPRHCHPSGENSMAT SLNVNRSISRLAAGSGVLAAMD PIPAHGRAIETGLGTEDTEQ
4072	34440	C	4113	217	510	
4073	34441	A	4114	210	281	
4074	34442	A	4115	1	675	
4075	34443	C	4116	126	434	
4076	34444	A	4117	804	2061	WERREAGGEDEGINIH*YEE EMKKHESNNVGLLENLTNGVT AGNGDNGLIPQRKSRTPENQQF PDNESEEYHSLGDKSKTSFQNS NNNNNKQEQEQQNPTFSNTR KLTKLYKAPIPPSIILSGCPNIND SNWQEIIEHGMQTAGLPTRPLSH GLQQKGAAFRCLGCKCEPFTG SLILQKAKTNTQKWQATYPKS QNEQLVPSVGKSYRCSTPAQP MKTAVGHKPKCATGAELPKAL GAQPLHPCALDVGGQFKGNF GAVGLNGLLGLFHVGSVGLL VGPDGGLISEGVVREDLMCG VWSAGTWSVGTAERCLEKPGA LHVIEGPLDSWDGVPVMPNGPV KSRQSSCLDGPGRCCSEILTGQS HGNKKPARASSKSSQINDRPL AVLTNQYQCEQLASERQPSNS

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4077	34445	A	4118	1	357	GKLMPLGSTRKPQVPVDRKMG HEGVFVWQAGLRARPGSLPFS HGLTLHLHWPLALPV/GATSSP CEAGDLGVPLAAGTWCPWEA *RQEEAGWQAPGRAGPARVG WGGTGLTSAEVIIT
4078	34446	A	4119	1	771	MLISHKQLSPQLLSLTPLSE GK AGWAGECPNPPSKDSPVQIGG/ GPPPGYQKCR*DTASMLTMAP CHGPVCPHPGWPRSGSRVIL PAPPGHHPWP*GPRARNGLGT QGCTGWWQVQETCFPGGWL DRHLVGPAATGARCLPAARGP/ DGALHPAVPTGKLGQPGPGA RHQRTYD*LPRPCGAAGLGSP A*HPISEETENQWGLHGPPQPA WARPDHGC/APILSPSLKRRP GRVTAGGPMPCFSTSSVPTT
4079	34447	A	4120	1	402	MLISHKQLSPQLLSLTPLSE GK AGWAGECPNPPSKDSPVQIGG/ LHQLPKMQIRYSIHADDGVS AAHKRGLRKRRLKTLISLPRQES AFFPHGQGGDPGVVPGSSFLHP LGTTPGQGPRARNGLGPSRAA PPAGRGVAGGSPSGVPAATGA RCLPAARGPVGPYTOQQORAS* KGS LGPGARHQR TYD*LPRPCG AAGLGSPPA*HPISEETENQWG LHGPPQPAWARPDHGRQPLRC HPP*RGSGGPGKAAVSQQIPR AGQEGTH*DPTEWGPDPDQDG GPRESCRGLQGGRGQCLCDWS PNTSEI*YPHA*NGD*KAG/PPM DTKSQLQVSTPKSPASHGEDVA RLEEPEASGD/RSPV/GLPGASLI PIWRPPFSRISVRTFLPSWNL RDCGLGLTSLASSSGRVTA
4080	34448	C	4121	111	218	
4081	34449	A	4122	2	453	WWPVLSPPECLPGRLPSPG*V RGAPWWPEPASQDKSQLSSR GFGKVS LGKGMAFSPLQTAP* KWLGLSPPLSSTENTASRGHTS PSSRNGFDSQPRDSRTGRECQA TQLPAQHSHAEVLHFGGAMSG QLSLVGPQDSKRTARLTDSQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4082	34450	A	4123	1146	1775	KGWLEGAPEA*ERYPGVPPCVV CSLSDAPWVGHPAPSLGVV*EP NPP*SRGESQGTSSICRQSSGD LG*KLESPIHTVIPRHTSQARQG HTAPFPFFQVFS*LLV*LKAVSL APAEAP*PASGLHAPWPVAPRV TCAI/PAKGTTPVAPGAELRPVS PPILLP/PDSRSSAFFPSRKGPASP YEICSPPTS*/EVPS*TYKSMGP GIRLPALPASPRVPSEGPLSEH PEGPPALPPAIPFS/SPSWFKQCS FSIRPGWLLHGAPOQKGW/PQA SWVGKGT*PEKRGSPRGPESHA LNLRVALPGVAV/*EGPACVGV GGPPQPPGAICEATAPPSI/VPL SLPAPFFGTLP/PPTPAASP/PPAL PPLLRRGRPRPCAALALPALSSL FS/PPVFSLLSLQLPADRVVRQVH PVLRAFGPPFRPPKQIPSSSGDL PPPSLPGR/PVL*LEKWLPPAPK ASPPSSVNILLVVVKLNTFRCG PLVKNLVPPSV/PCPCPCSYKYL *ILIYIHTLHMGGQPPSPSSAGNQ SLCYPCGGLVAQPTKRTLVPPTI QLQSVPPPV/KPPCHARPVD SQP PPSLPPPTKHGGAVQA VWPDS FYPVLLSLG
4083	34451	A	4124	146	1701	TFLGYLETAHGPSAQQCPTGLF AFRSLGRGLLLTSLPKQPARSPP REDVPRSTTQEMTRPRHPPRKP AQPGLGARRRGAPV/RGLSKSR ELNSGNTSDSGNSFTPPHPRTR GPCWRISPPPGAESQGDAMLL ARMQMPSLGLMSRTFFHSSST GKARGFQSPCLECAEVKKSSLV PSTARSSPMKGCSRSSSYASTRS SSHSSQSPNPRASPRVRTIITCIL *TRKRPRETKSSAKVT*HYYSK SGKRSPSSRSSRRSPSYSRYS PSSPNSPADIPQNSHPQPSASTD RPHIQSPQFLPTHQGLRNIHVLT PAAPALL*CPPANADTPAQAPQ PPLRY*QPSQTLTAAPSSSLRSP LRQRADPIP*PSGGAGSQI/WK DSQQRERERARRRRRSYSPMR KRRRDSPSHLEARRITSARKRPI PYRYRSPSSSGSLSSSTSSWYSSSS SRASRSYRSRSRSRSRRRSRT RTSSSSSSRSPSGRSRSRSRSR SRSRSRQSRSYSSADSYSTRR

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4084	34452	A	4125	1	1068	MLLLELNAPEHVLETINFQTLT AFCNTFHILRPTKAPGFVYAWL ELISHRIFIARMLAHTPQQKGW PMYAQLLIDLFKYLAPFLRNVE LTKPMQILYKGTLRVLLVLLHD FPEFLCDYHYGFCDVIPNCIQL RNLILSAFPRNMRLPDPFTPNLK VDMLEINIAPRILTNFTGVMPP QFKKDLDSYLKTRSPVTFLSDL RSNLQVSNFPGNRYNLQLINA LVLYVGTQAIHHHNGSTPSM STITHSAHMDIFQNLAVDLDE GRYLFNAIANQLRYPNSHTH YFSCMTLYLFGRRRANSRPFQ EQITRVLLERLIVNRPHPWGLLI TFIELKKNPAFKFWNHEFVHCAP
4085	34453	A	4126	1	984	MQANLEMGAGNVTSMGMEPL AIPHIYCCSEGTNFSNTENHCL RAALSMLLNGTPFAFVIDLAAL ASRREYLKLDKWLTDKIREHGP SVHGLFPSRVLSPALPGAFPG RHNGGSCVAPQSGLPGVHPVEL PWSISKFLRLRSPANFSDVLGSR SKVLLLMCTLK YCGMQLGADA TRVDMLTFLPTLGFIRNNDYTD DTKASELTELSHNLHAYDSVTG VPGDETECSKTVSTWAYTAESL QGYMAAKLLGRNLTVPSTRYLF LNAIANQLRYPNSHTHYFSCTM LYLFAEANTEAIQEQT/RLVRE RI*S*ANAYWHSEKFYQFTCEL
4086	34454	C	4127	1	399	
4087	34455	A	4128	1	868	MANVCNPSTLGGRRGRIITRPE DPGSPVYSVPASYPHPKWLGA QPATVVTGPNVTLRCRAPQP AWRFGLFKPGEIAPLLFRDVSS ELAEFFLEEVTPAQGGIYRCY RRPDWGPVWSQPSDVLELLV TEELPRPSLVALPGPVVPGGAN VSLRCAGRLRNMSFVLYREGV AAPLQYRHSAPWADFLLGA RAPGTYSYCYHTPSAPYVLSQR SEVLVISWEITLAPPTPGGT*S AWGWPGWSSSPWARWSLLTG AVRTALLFPQVPHRATTWPVT SYDWVWLP
4088	34456	A	4129	1	270	
4089	34457	B	4130	39	919	

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4090	34458	A	4131	3	466	GRALCPPRLLAAGRVLPGRRRS PGPGPGVP/GG*R*GGAEP APRGRVLPSSAGSQFSAATPA QNGLPALRGPSRPGIRSKAVR PVPLGRVGVYFRDALRASGQS GRKLCGIGNTLSPTSFSVGKEVP RKHETNQKHEKGILCMEAVKP
4091	34459	A	4132	1	1647	MWRWLYAGARMTVRDKQPLE QMLAGCTHASLVPTQLWRLLV NRSSVSLKAVLLGGAAIPVELT EQARDMGIRCFCGYGLTEFAST VCAKEADGLADVGSPLPGREV KIVNNEVWLRASMAEGYWR NGQLVSLVNDEGWYATDRRRE MHNGKLTIVGRLDNLFFSGGEG IQPEEVERVIAAHPAVLQVFIVP VADKEFCHRPVAVMEYDHEVS DLSEWVKDKLARFQHLVRWLT LPAEPKNGGKIFHVSAKRVGAL TTRMEAAQQHADDKIRQMIN EQRLSEGFENLANRFEHSNRR VDEQNRQSI: NSLLSPLREQLDG FRRQFRTASLMKVAGWDYLM NSLYANSSALVNRVRYKWIA AFEGGFTGIVATLDTRGPVPM AFRVDMDALDLSEEQDVSHRP YRDGFASCNAGMMHACGHDG HTAIGLGLAHTLKQFESGLHGV IKLIFQPAEEVVRVARGRWSMQ VS*MMLIILLPCTLALAYLRALL CAAVIILWQPPNLTTRTSPVPLT QAQNKQTVTMPCWRHTSHSCT ACNRPAQRSSFOS
4092	34460	A	4133	864	1128	TGRSTIRKQRREPRRKAATLRF DRNGCRARCTPPGRKEQRYQQ TADGDKGAEFYRRPEGVEIVA VMEQRDEVIQADKLAGECHKRI DAL
4093	34461	A	4134	618	1102	HSNAAPTARSSFFVQNTPS CGY SRRAWRISSEETDRTSYRNIQ CGNHPPVPARLPAQTGDGDIP PRPRWQSPQAPRKPDP/LIR KNKIPMFRSATTQPLGTGIAK ASSSEVKAIIGARVKMTRSENF GIQSSLNILIMSATSWEPPQP TRLGP

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4094	34462	A	4135	2400	3201	VGGGRNRSPGVACWVEDGNG DAVRDQWALDADWQASQAM RRKQQPEYWQHDAATADADR QMNMPLVLRALVAGRAQEM NGAQGKTLKGVDEASARRG TKTEDVCEEDTRDDAMIAWM PR*PGVLPRADAWANVLNHGV GWKKAQLKSTWMPQVQQ*W RGDKAANSNAVAHTVVLN SGGDATQTAAPFISPLSV/EEV CVTMVIA*FWMWDSGSGGVVL CSSSGRSLTSWSATKVRG/SGH KGRWCSRQGVTCQVRHGGHV APH
4095	34463	A	4136	118	1008	
4096	34464	A	4137	3	1140	KHTYMLSILKPVRTSALPPPAP AQTLCQTLSRVSSRL*DHPSR WGLR/PSTGMSQARACSPGSLG WMQRSSFTPGAGRVRHIPISA GSTRRPACGSRSAAPVPRCRR TR*G/RSSVVERFMTALSLACR ALPGP*AAPGPSITRRFTISAEK DTRL/PREHVPLVCTHAIAVPD RGAAVRPTRRRDAAPPSPLVG DVTLQCPQSQ*RGSNAPDQVRLP CVG*RPSSSLQRSGLSVFSADGS TSGPEPASGRKDAGWPARVLR GTLRGAPEAGADWGPYSPGSP GAAASGAPWLGQPQALQGAG GQLVGSSENGERTGKPRVSVS VAYGEIALPADTSSWRAGAA VLLGLSRSTGGEGPGNMHGG QSQMLTLEVL
4097	34465	A	4138	10	585	PLEMELNLISIEVWGERLGISTG TEKMPTLKHRTW/PVECSKASSL EGDLRLS/L*LEVISAFSADPASA DDSPGCWKKKDDCSMVHLHR QEWQQQCCQ*K*RKQPPGER RNKCGSHPVCGTIVLWQP*QTH/ QISSCPTVGCPPSHSSFSILDGAN AGQEQSQSTTEPEPALFLLPPSRG AFGPFGLLSDLRRQL
4098	34466	A	4139	1	474	
4099	34467	A	4140	458	612	ASCMASVDISVLTTCMWRCETIQ SSSFLCLLTPLWE*SWCHVTRIC PFISLG

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4100	34468	A	4141	1	829	MGRPDLILSSILGLRWLLLPQSS RAGRRAIREASDAEQVTFSGG TVPARTSSGREWRSLGPDMET TSLFCIDTKTTLFVYRYGDHIP LVPEQSGLEPLLIWADPGLFHV RLFHILLTIDDNFCGLDMNAPLG VSDMVRGIPVFTEDRDRMTSVI AYVYKNHSLAFVGTKSGKLLK /VRSSAAP*VWDQTPRSLGQQ GAQRQP/ILRQCVYTFQLN*RC PHSTARRELRTGGFIPTRSHQD GLRSAARCTQGTQ*ASWSCV HVCASVRAMCSYC
4101	34469	A	4142	5	237	NFGAMTRIR/DLPWEINPLSSCS SLCEKDPPTTSSPQTN*PKEHHT NFQSETGDEFYPWTQNFSTGHG LGKTVFPWCL
4102	34470	A	4143	1125	1190	
4103	34471	A	4144	306	573	RNFGAMTRIR/DLPWEINPLSSC SLLREKDPPTTSGPQTNQPKKH LTNFKSGKRPLLTLFNLSHCP TTFPPFFNLSELLISIPFIW
4104	34472	A	4145	1	329	ASHSWQTLQHSGRYSRSSG/SA GSPRDCAARAPTISPGCMAWL NLDSISPSQSKASPLSQLTCPET SYTGCP*SAPHSPPPWPQERC ACKGHCLHHRDGCYGYN
4105	34473	A	4146	2	336	SILTRKCKYGMIEPT/NIPGLGA AGPTGMFFGSAPSPMGGISPAM TPWNQGAATPAYAWSPSVGSG MTPGAAGFSPPKA/PTYSPTSPG YSPTSPTYSLTSPAISPDSDDE
4106	34474	B	4147	1	1260	
4107	34475	A	4148	150	335	SFQQSAPW*ASGQSCASDPAPP ATARGRFGPHQSQAFHSRHSPIP DPLPPCSGGWGHRSRW
4108	34476	B	4149	1	3267	

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4109	34477	A	4150	1528	2973	GKQIFSLIIPGHINCIRTHSTHPD DEDSGPYKHHISPGDTKTVINNW LLIEGHTIGIGDSIADSKTYQDIQ NTIKKAKQDVIEVIEKAHNNEL EPTPGNTLRQTFENQVIAVVGQ QNVEGKRIP*LPPPL*WGAGRR EGVG*CGRFSEHSRSSAAGYRG GRPCC/PSWEDDP/GAPPDPAS AQIPAPTRSGCVRC SARSPGPP AECAAGPSHWYNQSGTSSQKP CWKA*AYPGSGTQSRGQSAR SHP**SEAESGA*SQMESACPRR SAVQRQQ*PDSQTSAAECSLG WAPAHCCVPSR*PLLRPAWPS* *CSECPGKS*NQWSPQCQ*YD PNPQSTVVAEDQEWVNVYYE MPDFDVARISPWLLRVELDRK HMTDRKLTMEQIAEKINAGFG DDLNCIFNDDNAEKLVLRI RIM NSDENKMQEVVMGVLEVSVSHV
4110	34478	A	4151	459	940	HLPGGGVPGREGGSPDQHVAP GAYSGGAGGGSTRGRGSRRRR PGRPRPGPRQPRR GALPGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSLRR PPRGPACATPPPCRPPARRTCTG RCPPSCCLCGSPITWRRPPPTG GALESPKRR
4111	34479	A	4152	264	1386	SSRCQPVCESGHPGYGQSPA/YT TAGRTESGGTGST/GDNHPLWP CI/GGAPCAQNTPHLRVC*RSH ALALDSAGSSPESPH*RASIPH TTLGQKRRSWAGTAHS/PMAPC AAASISTST*LSHHHSPAQSV PSSHTTSPFCPIQKFHCFR/SPQR NTS*VVLCPGG*LRVG*WPSSG HDRSWYHTREPSVGN*HRSHQ RR*RGTAAPAGPSARLQCPARG SRSSHSAPASSRRRPFPGSTPAG LGFP SARFPVGPV VPAALMNR PTRGERRFAYWAPGWFFFPVR RATADCPSP/SW*ESCSKRSTL VCPSRRKSLMVVPKSAKSPVL AK/YGPVGHDHGTEDHVVLGE VQKRPVAPMTMGTPKHKA VHP RAPH
4112	34480	B	4153	52	363	

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4113	34481	A	4154	321	802	HLPGGGVPGREGGSPDQHVP GAVSGGAGGGSTRGRSRRR PGRPRPGRPQRGALPGGEHG LRASARCAARAQQRDPG/TPSC SSWACPTPRRPWAPAASSRLRR PPRGPACATPPPCRPARRTCTG RCPPSCCLCGSPITWRRPPPTG GALESPKRR
4114	34482	A	4155	15	263	CGRFSEHSRSSAAGYRGGRPCC VPSWEDDP/GAPDPAPASAIQAP TRSGCVRC SARSPGPPECAA GPSHWYNQSGTWKCKG
4115	34483	A	4156	3	518	SPSVGSGMTPGAAGFSPSAASD ASGFSFGYSPAWSKPGVPGVP QVPSKPLKSLHPGGVVRHL.SGQ VCFHSSG*VCPLLIHFVGCFT GGAMSPSYSPSPA\VEPRSPGG YTPQSPSYSPSPSYSPSYSP TSPNYSPTSPSYSPSYSPSYSP SYSPSYSPSYSP
4116	34484	B	4157	620	6763	
4117	34485	C	4158	430	870	
4118	34486	A	4159	1	3039	MDSETRRTAKVRLMTVLRLDQ DRVSGVQAHPQFQQAICPLCG VSLTRSGTTFGSPSEIYSLGESR ASSGLPRRDGRLIGEEPPEKKFS RSPKGD/LSSGGQRIDYRVCPVT KFNL*VLSF*PRGQAGGQSPG FSVRRLLVLVWSSGTFV*NGK* QKLL*TLCEVHD*GVQGPASG SPVCSSTAKATEFEKDPSPGFSS SSLPLTPYISFSRVTAASSAPGLG SALTPQTLKRKGRI*AICL*VVE TPKVR
4119	34487	A	4160	1	772	MVARAFLWSQVIRRLGRKGGL SQDGRGCNTALAEGRDPLDT RGHPALCLPRRAPRPAEVRRE GEAEQPEAGQPPGAAPRRARD NGAAAAAAGRLLQSVRPVV CPHPGPQASYGLRYIAKVLKNS IHEKFPDA TEDELLKIVGNLLY YRYMNPAPIVAPDGFDIIDMTA GGQNNSDQRKNLRSTAKVLQH AASNKLFEGENEHLSSMNNYLS ETYQEFRFKNVTFDIIATEDVGI FDVRSKFLGVEMEKVQLNIQ
4120	34488	A	4161	174	444	YHRHDSWRNTRR*VKLDGKGE PKGAEESEATSKYTAALKHEK GVLLDIDDLQTNQNAVNDFSV GPQDEVIVEDITNCYLCEIFKRY EWVT

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4121	34489	A	4162	379	520	GTSHRGASQRRCCPPLSKTGPK TPCGKGAPSA*QGGLDVQGEP GGKIGDSSGECVGGNVACLHK GGGTRADSQVPGGMRGGRMS YGG/HLTAEGPMGRSGPR/GAV PSLYPPGFSRGSCSRQYSGAHM PILTGHVGVWSESLDPPRAGQD RFLGTARP*GTSHRGASQRRCC PPLSKTGPKTPCGKGAPSAFPI AGPTFDHKALM
4122	34490	A	4163	455	798	
4123	34491	A	4164	32	2109	WIGGCPGSPQDATAIMGWTLA PHSSRCHRCCHYRCHRCCLCP AEMTVGRPEGAPGGAEGSRQIF PPESFADTEAGEELSGDGLVLP RASKLDEVLSQEEIDPTSDSTG SIYHTLLDLAQGRWLSVWSLS FSLTQRVMKTSKMRKTWRVS SKTRTGGWCRSSARRL*GVAPQ GAA/DSLNNLPSNIPRQTPPP GSRPPSQHRVSVWASSITVPRP FRMTLREARKKAEWLGSASF EQERQRAQRQGEFEAECHRQF RAQPVPAAHVYLPYQEIMERSE ARRQAGIQKRKELLSSLKPFSF LEKEEQLEAAARQDLAATAE AKISKQKATRRIPKSILEPALGD KLQEAELFRKIRIQMRALDMLQ MASSPIASSNRANQPRTATRT QQEKLGFLLHTNFRFQPRVNPVV PDYEGLYKAFQRAAKRRETQ EATRNKPFLLRTANLRHPQRPC DAATTGRRQDSPQPATPLPRS RSLSGLASLANTLPVHITDATR KRESAVRSALEKKNKADESIQ WLEIHKKSQAMSKSVTLRAK AMDPHKSLSEEVFKAKLKENRN NDRKRAKEYKKEEEMKQRIQ TRPYLFEQVAKDLAKKEAFQW YLDTLKQAGRRKTL*ETRVKA PGLFKRRPKSRIFPGSKKLQNS ASEIQSR/RLEGSLEQPASPRKV LEELSHQSPENLVSLA
4124	34492	A	4165	251	637	

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4125	34493	A	4166	1	1344	PGRTRTSMADVFLSAPIPRGC ADGRDADPTEEHMAQTERNDE EQFECQELL*CHVQVGAPEEEE EEEEDAVLVAEAEAAAGWM LNFLCLSLCRAFREGRSDFRRT RNSAEAIHGLCSLTACQLRTIYI CQFLTRIAAGKTLDAQFENDER ITPLESALMIWGSIEKEHDKLHE EIQNLIKIAIIVCMENGNFKG AEEVFERIFGDPNSHMPFKSKL LMIIISQKDTFHSFF/QHFSYNHM MEKIKSYVNVVLSEKSSFTLM KAAAKVVESKRTRTITSQDKPS GNDVEMETEANLGYKKKC*LT NSLR*LNQVRVQYPY*GSHKNL FLSKLQHGTQQQDLNKKERRV GTPQSTKKKKESRRATESRIPVS KSQPVTPKHKRARKRQAWLWE EDKNLRSQVRKYEGGNWSKIL LHYKFNNRSTVMLKDRWRTM KKLKLISDSED
4126	34494	A	4167	1	1345	IPGSTISCLKGQYPSEFPNMAED VSSAAPSPRGACADGRDADPTEF QMAETERNDEEQFERQELLEC QVQVGAPEEEEEEEEDAGLV AEAEAAAGWMLDFLCLSLCR AFRDGRSEDFRRTNRNSAEAIHIG LSSLTACQLRTIYICQFLTRIAA GKTLDAQFENDERITPLESALMI WGSIEKEHDKLHEEIQNLIKIA IIVCMENGNFKEAEEVFERIFG DPNSHMPFKSKLLMIISQKDTF HSFFQHFSYNHMMMEKIKSYVN YVLSEKSSFTLMKAAAKVVES KRTRTITSQDKPSGNDVEMETE ANLDTKRSHKNLFLSKLQHGT TQQQDLNKKERRVGTQSTKK KKESRRATESRIPVKSQPVTPTE KHKRARKRQAWLWEEDKNLRS QVRKYEGGNWSKILLHYKFNN R/TSVMLKARWRTMKKLKLIS SDSEDWIVFVKL
4127	34495	A	4168	3	378	LTSGSRADQGEQEEGAEGGR ASSSSSSSPRGQPHPHLHGDP AEHRPGHPLCSPDDLTVAYQM PEVPAEDM/SDPSFCARQGGQ RGLDSGPAPWSSSHSPHSRFQ EASHGACAGWRWCRQEEL

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4128	34496	A	4169	1	1044	SGQE VNKEDGQADVQDHHH DEDG VGD LARQPHLH LHLRL CRQCGLLPRL LIPRI.QQPSSLS LAGLGPGLFGDDGLGLQLGG GLACRLGASERGG LQRGGGRG RGRGLGP/GPRARAGPQRVGA RAAWCAQHSCGSPGKAPPPAP A/TGAGGACRASMAMRSVAGR AGLRRPAPSDGVTDRLPSPLGS PFQAP/EAQQA VLGHGPGPLG LRGRPGR*RGATLGPRLT/PRA AAGSRGA AVGGPLRRRPGRGA PAGSPSPGSPA AAGASDIPDLA GRSPEPAPWPKECQWTPGWQ PGRPVPLQLWPWRGLSIGSGM PLGEGLEDGSDPMTPSCLPGT
4129	34497	A	4170	1	732	SLTQAGTVSLGLDAEGQEVFP FSAVLP MVAPNDLVFDGWDISS LNLAEAMRRAKVLWDGLQEQ LWPHMEALRPSPSYPIEFIAA NQSARADNLIPGSRAQQLQIR RDIRDFRSSAGLDKVI VLTAN TERFCEVIPGLNDTAENLLRTIE LGLVSPSTLFAVASI LGGCLCS FNGSPQNTLVPGALELA WQHHR VFVGGDDFKSGQTKVKS VLVD FLIGFRLQRP/VSI VSYNHLGNN
4130	34498	A	4171	1	908	MEKAPPQTQHEGLKSKEHLPE QTDEGKTEYRRVPSLRAVVLFR QRS CIENILRACVGLPPQNHML LEHKMERPGPSLKRVPQVAAT YPMLNKKGPLVWEVSPATLFA VASILEGCAFLNGSPQNTLVPG ALELA WQHRRVFVGGDDFKSGQ TKVKS VLVD FLIGSGLKTMSIV SYNHLG/NN DGENLSAPLQFRS KEV/SRSNNVDDMVA/ SNPML YTPGEEDPHCRMGRNLPE*GSS
4131	34499	A	4172	85	529	ECGARPGSSTRPPARLSPLFCFS AIRAALKTRPAPALACTWRTG* RASLPTTRCAGSLGTCTAEGS EGCSPHPLGTGTG/RQEACPGT APAGSPSCLHPRGRPRPCPPGTL APRMSCPWPRSPPLTRYLPSGE NLQSKLES LNTSEKF
4132	34500	C	4173	215	324	

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4133	34501	A	4174	2	505	YKCEVCDKVFNQ*FLVCHNR CHTGKKPYSCYECGKTFSQTSS FTCYRRLHTGGKPYKSEHNK TFG*NSALVIHKAHTGENPCKC NECGKVFNQKAHLARHRLHT REKPYKCECEKVFSRKSHLER/ HKLKRGGVAL/C*ECPTVYQN TSLRSLSCSYPMSLNG
4134	34502	A	4175	1	6192	
4135	34503	A	4176	2	3389	
4136	34504	A	4177	3	875	GEEAALSCMIHSTDDATRLGA RDTEPLWHVPAQ/ARLSAIAGS SGNKHPSR/QDAAGKDSNPRHS KVGSKPSAGSLRLSSREGEDRTA WTGPRGAVEQEVTGPDLC*GR GQQGLLVGWT**EQKRGQKGP QYSSSHSSNTLSSN/ASSSHSDD RWFDPDPL/EPEQDPLS/KGCM SLAK/APRPAKPHKPPGSMGLC/ GGGREAAGRSHHADR/REVSP APAVAGQSKGYR/PKLYSSGSS TPTGLAGG/SRDPPRPQSTLWH RTWYL/YHTASAAVHRGLCRE LEQADQIPPSWYGRPMGNS
4137	34505	B	4178	108	318	
4138	34506	A	4179	103	540	RRGCESHKTLRRGTWSGLDAR GGGPGPGQVSAGRDGAEVWLS TCDRGHALSGSVEELLFLQN/G ARTER*EGPGEWPRPPPPGLASP ALWRFWAEQVGGSFQNESSPS CRTARGSSRTWGSILQNSSWLF QDLGLHLAEGCFLETP
4139	34507	A	4180	33	896	KITRHTAPGKIRIVPKESQEST PQDQAGPGRATSCSARWSPR SWKSHELFCMEPQVLEEPRA VLQDQAGPGRATSCSARKGR GPEKPVQGLPN/GSVRAHSGGR AAPQSPRGHGPGRG*TAAPLP HLCPLTPVLLQG*GPD*WPLGW ATMRPLPLRAQAPPPPHWML LTSPAPPPGTGKPGQGRGQTSG SCVPATDPHCLSAAPSGKLGPP CDFLEPP*QRTTNWGSSEAGSP KSRCPRGHVPSGGSKGGIFLSL HFGAPQSLFPPGSQPHGLIGAS
4140	34508	B	4181	1	625	

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4141	34509	A	4182	160	1149	FASERMKVEPWRAGPGRRAWS EGAGQAPQKKRARAAGAEPLPA TPALPGGKMVARRTKLA\RGTR RTY\PEPTVYAAIPIKFSEKQQA SHVLYVRAHGVROGKSTW\PQ KRTLFVLNV\PPYCTEESLRLLS TCGLVQSV\ELQEKPD\LAESPKE SRSKFFH\PKVPVGFQVAYVVFQ KPSGVSAAALALKGPLL\VTESH PVKSGIHKWISDYADSV\PDPEA LRVEVDTFMEAYDQKIAEEEE KAKEEEGV\PEEGWVKVTRRG RR\LCSPGLRQ\PCGCWRGRDG SAA\KRAAQLLRLAASREQDGA SSAA\RK\KFEEDKQRIELLRAQR KFRPY
4142	34510	A	4183	2	361	GTMVARRTKLA\RGTRRTGIPS PPC*AA\AIPMCSEKQ\QASHYLY GRAHGIQ\GKSTWPHKRTIFA FNGPPYCSE\QESLSCLQSTCGL VQSVKLKEKLELGWESRSKFFH PKVPV\TEEQ
4143	34511	A	4184	917	1128	
4144	34512	A	4185	1	660	MAWQMMQLLLLLVTAAGSA QPR SARARTDLLNVCMNAKYH KTQ\PSPEDELYGQ/C\SWRKNA/ CSFTSTTQEAHKN/TSHLYGFN WNHCGEMV\PACKRHF\QDTCL YE*PPNLGPW\IRRYAWLPGIQE LAELNFP\GVSAGSNPSSSIQG WVPGILEPEPFFSTKISQVDQSW RKEWVLNV\PLCKEDCEQ\WWE DCRTSYTCKSNHGKGWNWTSG SNKCQVAAA
4145	34513	A	4186	216	781	MDMAWQMMQLLLLLVTA GSAQPRISARA\RTDLLNVCMN AKHHKTQ\PSPEDEAVVWDP/W MCKGSCRKTKSWNI\HRKSKCE VG\LA/WEACSVSAGTGRGPGC GRWV\GAPQGP/CPRKCSSG*PT W/VQRSQNMEEMAV\VNQSWR KERILNV\PLCKEDCERW\WEDC RTSYTCKSNWHKGWNWTSA PSAVCDPLL

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4146	34514	A	4187	3	625	QCRPWKRKNACCSTNTSQEAHK DVSYLRYFNWNHCGKMAPDC KRHFHPTGTPALYE/CAPHNLGA WDPAGWIQSWRKERVNLNVPLC KEDCEQWWECDRTSYTCKSN WHKGWNWTSGFNKCAVGAA CPTFHFYFPTPTVLCNEIWTHS YKVSNSYRSGRGIQMWFDAS PGATPIEEVIAFYVAAMSGAG PWAAPWFLSLALMLLWLS
4147	34515	A	4188	1	268	EQGRH/GSSTPVGPRGPRGAE HAPKHQCGDRAGPQVGMQ RRRDPPRAPAPRPWCQQRRA LSSLGGSHLCDDA*VQPSAGLG KVLKF
4148	34516	A	4189	2	1632	WKRCPLPRAAATFPSGSGAG GARREAGGRAPTPGPASPTAR GHARNSPAPARTAGRTGSAGA WQTPCPAPLFPMSAGLPAACH WNPV*LRALKTG/LEGVLGSA DTQHNRTVDGSLAPNAACVYT PKINGNRHPNTCKMFIVSLDA KGKKWKQPTVHIQQRKRETCG LHPRKCLQYTPS*WSTTTGILPS RTPRISCVQFVKKGLGQAGLLG HPGACLLCTL*PAGVGTFLFP RGC*GVVH*LEHTTCG
4149	34517	A	4190	2	87	
4150	34518	A	4191	3	291	
4151	34519	A	4192	112	286	AWLLWLTSLPWGSLYALALLA NKPAL*SLLLRYTLPPHHQC EKVPRWNEPQPTLFP
4152	34520	A	4193	1	933	
4153	34521	B	4194	1	999	
4154	34522	A	4195	135	1160	VVALVRSTLELFTDDEEEGE YDEVTEEVTEQVYLPAKAKVA QEEEVHPYSPAPHYFEEKEW PDPPDLSFLEDTGKVVAPVTE QHLERLLSVLFQRQFSRLDERD DAVEQLRGVCIRAWEKITSGGE QYPSFSAVKQGPKELYADFIW NLLRQESLKKVISDSAAQDIVL QLLAFGNVNLDCQAALRPIRGK AHLVDYIKACDGIKQDSERF AFTIPVNNLQPAKHFYFTDG SSNGKASYSGSKGQNGQPIWIL SRHLKPYHEPDAKEEIPGG/CPR TPWLQPCRD*C*GGP*/PVSNT R*TQPPTWGQIKKLSQMVEENL RKAGQLVTMTVYWN

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4155	34523	A	4196	502	578	LV*EDCIAERAELVRNESYGIID WSP*GMFSLNCTSQSACHGHT MFSW
4156	34524	A	4197	2	408	
4157	34525	A	4198	3	853	LLKVMSAKIFTKKENSTERL CGDGEKRGPDFRTERS VWLLR LEEA VAMVQQRGSRAPE SRVVA QVLTL LDGASGDREV VVVGAT NRPDALDPALRRPGRFDREVVI GTPTLKQRKEILQVITSKMPISS HVDLGLLAEMTVGYVGADLTA LCREAA MHALLHSEKNQDNPV IDEIDFLEAFKNIQPS/LVFEASL GLMGIKPVDWEEIGGLE DVKPE VKTAH/WSLRQKSGHC/RSCAR LPTGLLATLGSGSGSGRATEAV SGPAG*KRASIGSSQRP RRFPPT
4158	34526	A	4199	266	370	AERINSITVFSETLKRFLQASGK *FHRDIHNSRN
4159	34527	A	4200	1	1780	MGDVNQS VASDFILVGLFSHSG SRQLLFSLVAVMFVIGLLGNTV LLFLIRVDSRLHTPMYFLLSQLS LFDIGCPMVTIPKMASDFLRGE GATSYGGGAAQIFFLTMGVA EGVLLVLMYSYDRYVAVCQPLQ YPVLMRRQVCLLMGSSWVV GVLNASIQTSITLHFPYCASRIV DHFFCEVPALLKLSADTCAEY MALSTSGVLILMLPLSLIATSYG HVLQAVLSMRSEEARHKAVTT CSSHITVVGLFYGA VFMYMV PCAYHSPQQDNVVS LFYSLVTP TLNPLIYSLRNPEERSHRGVKL NECNQCFKVFSTKSNLTQHKRI HTGEKPYDCSQCGKSFSSRSYL TIHKRIHNGEKP YECNHCGKAF SDPSSLRLHLRIHTGEKPYECNQ CFHVFR TSCNLKSHKRIHTGEN HHIECNQCGKAFSTRSSLTGHN IHTGEKPYECHDCGKTFRKSSY LTQHVRTHTEKPYECNECGK SFSSSFLTVHKRIHTGEKPYEC SDCGKAFNNLSAVKKHLRTH TEKPYECNHCGKSFTSNSYLSV HKRIHNRWI*/YYGRNFWRKAL IDLSSLR*FERAHTGYISYLLQH
4160	34528	C	4201	18	182	
4161	34529	A	4202	1	389	
4162	34530	C	4203	114	548	

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4163	34531	A	4204	122	735	LRAQQQH*N*VLT.LHKPACT.LST TS*K*LHKIRK*L.WHLRDRAPFI FTSEMEYFITEGGK/NPQH/QDF VELCCRAYNIIRKHSQ.LLLN.LLE MNSYNGYVGLLHNILQLEREG LATKEELQONFPPLSVSLPFDQS INQISEHRSLIFNGQYPYGSCWF RQAVCKLIQKYAGEWGIATA ELRAEIDLNVLFKFTIQVLSWKV QASLQ
4164	34532	A	4205	139	4496	KMAYSWQTDPNPNSEHEKQYE HQEFLFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPT APKWDSTGHSLNEAHQISLNEF TSKSRELSWHQVSKAPAIGFSPS VLPKPQNTNKECSWGSPIGKHH GADDSRFSILAPSFSTLSDKINLE KELENNHNYHIGFESSIPPTNS SFSSDFMPKEENKRSRSHVNI PSMLLLKGSLOPGMWESTWQK NIESIGCSIQLVFVPQSSNTSLAS FCNKVKK
4165	34533	A	4206	1	3150	MEKPRPLEAPSAWPQDDVQCG VTVMGDGAAVRANKTPWPQD LEQTKWIEIKKSFTWSSQLSL NRGFLTCKDENNNAGLLRVSS YSSREDQLKNIASDSLFLPFGG LCQSPGTGSHCSNQMETQGGGS PGGAVRGDKALGPEKARQCGG MNGSGKYCKFRVLAIQGKPEC LATLMQPDLDGDSPLREMNIV EHLRASFPVEQWYWRGGQRGE AEGARSSKAENNTSLICNFRLD YAPIEKQWDLHFADYFAEDLK
4166	34534	A	4207	1	1203	

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4167	34535	A	4208	1	1470	MLHSRGFLAEVFGILARHNISV DLITTSSEVSVALTLDITGTSTG DTLLTQSLLMELSALCRVEVEE GLALVALIGNDLKACGVGKE VFGVLEPFNIRMICYGASSHNL CFLVPGEDAEQDGTGTSIGGAQ KKKMYANNGAIDRKLLFEATF VTIEKCCDTNQKDDTHALGQ PIRGHDKSLAGSCFYACRSEEG LSQYRAYDSRGQLIAVKDTQG HETRYEYNIAGDLTAVIAPDGS RNGTQYDAWGKAVRTTQGGAL TRSVIEYDAAAGRIVRLTSENGS HTTFRYDVLDRLIQETGDFGRT QRYHHDLTGKLIRSEDEGLVTH WHYDEADRLTHRTVKGETAER WQYDERGWLTDISHISEGHRV AVHYRYDEKGRLTGERQTVHH PQTEALLWQHETRHAYNAQGL ANRCIPDSLPAVEWLTYGSGYL AGMKLGDTPLVEYTRDRDLHRE TLRSFGRYELTTAYTPAGQLQS QHLNLLTYRHANFAL
4168	34536	A	4209	757	907	RRYCRITVRWQSM/WADNRRIA VDAHYPYR*CRS/GRVTEKND/ LIPKGVIRTDDETRHYHYDSQ HRLVHYTRTQYAEPLVESRYL YDPLGRRVAKRVVRRERDLTG WMSLSRKQVVTWYGWDGDRLL TTIQNDRITRIQTIYQPGSFTPLIR VETATAVMDRILKDHQIVVDIP HGEAWLRDDEERPMILIAAGTG FSYARSILLTALARNPNRDITII WGGREEQHLYDLCELEALSLK HPGLQVVPVVEQPEAGWRGRT GTVLTAVLQDHGTAEHDIYIA GRFEMAKIARDLFCSEARNARE RLFGDAFAFI
4169	34537	B	4210	1	3258	

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4170	34538	A	4211	281	1571	CQCPGAACPTTSCRVPVHWA/Y DEADRLT/HRTVNIGETAERWQ YDER/GWLTDISHISEGHRVA/V HYRYDEKGRLTGERQT/VIIHQ TEALLWQHETRH/AYNAQGLA NRCIPDSL/PAVEWLTYSGYL AGMK/LGDT/PAANLDIRIPYAT DPA/GNRLPDPDLHPDSTLSM/W ADNRJARDAHYLYRY/DRHGRL TEKTDLIPEGV/RTDDERTHRY HYDSQ/HRLVHYTRTQYAEPLV E/SRYLYDPLGRRVAKRK/DRTR IQTMYPGSGFTPL/IRVETATGE QAKTQR/RQLADTLQQSDGED GGSVVFPPVLIVQMLADR/LESE SSADRVRSFISLANQSKCVEHA Y*RWQCHLGVCWWSSHQIPAV PLTGSVTRWHCHLASSSEAGSV AWLPHLSEGHNSRTSSPELLRS RMCAWHTLSAQSVHVLVSLYL EILALMNSINSL
4171	34539	A	4212	311	788	
4172	34540	A	4213	29	395	RIFHSVIGVAAHKGGVYKTSVS VHLAQDVAEIT/LLEGNDPQGT VS*YQPGRTLIPLEAALRNIAH LSIPPPKIFAAPILRHYFALFFC GHSLFAPHIELLEAGTVLQLPQ GPWSSPTS
4173	34541	A	4214	1	1033	MKMPEAIATKEKIDKWDLIKIK SFFSTPKETNVRNRHHTEWEDI SAIHLSDKGPISYIYKNLRFTR KKQPHYKVGKGNEQTRILESHP HLLKGLASTPFDSEGVRTERRD IHKDILTQWLLTSYSARKLGLK STGHAGGIHNWRIAGQGLSFEQ MLKEMGTGLVVPGTAEARSC IRAYFYDIHETLCRQEEMALSV VDDHVREKLIWLRQHEDMTI LLSEVSAACLHCEKTLQQDDCR VVLAKQEITRLLETQKQQQF TEVADHIQLDASIPVFTTKDNR VHIGPKMEIRVVTLGIGMGAG KNLLSLF*V*NRVEFHGSPFPTI WFLTWEIVGFLK
4174	34542	B	4215	414	1022	

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4175	34543	A	4216	896	1626	NATTIRYEHQRLVKAQQYLHQ QGITRCNSSTLTSAAPGRVDSP PTSMIVAPALIIRFACFTASISEL CVPPSEKESGVTLRIPITHLMRE LTCRLIRDKSATVTGSHTLVVA RHCCYAAPGGCCLLANWLKPG LFGPIGVLSRRGTSVILPIGGFY QWNPMICPNGVPMQHG*RRG LAQERPLEEWLPVCRDMLNAF FLPDAETEAAMTLIEQQWQAI AEGGLAQYGDVPLSLLRDEL AQRLDQERISQRLAGPVNICTL MPMRSIPFKVVCLLGMNDGVY PRQLAPLGFDLMSQKPKRGDRS RRDDDRYLFLEALISAQQLYI SYIGRSIQDNSERFPSVLVQELI DYIGQSHYLPGEALNCDESEA RVKAHLTCLHTRMPFDPQNYQ PGERQSYAREWLPAASQAGKA HSEFVQPLPFTLPETVPLKRYN DSVRAPTCAESRAIFTSTRNNTL QLFFNANFRPWARGLATNVN DRRASVDHQIRMFHRIYQVRM RATIRKGIRRDVEDPHYSSDAG TYLSPNSRQISNGNWQSHIGRSP SLLL CRTWGLLFTGKLVETRFI WPNRGVIPTGNERYIAHRRFLP MEPDDMPQWRCPHATWLAEA KMFDSLAKAGKYLGAACKLMI GMPDYDNYVEHMRVNHDPQT PMTYEEFFRERQDARYGKGG
4176	34544	A	4217	838	1575	CFFLSPSPSPSPNRSQTTEE TKRQE/ERERKREEEEEKGRR KETKKRRNRQEGQKHRKEEKE GEKQTKQRTETERETKRRRENE QAKAHKGTRKRKEEQKKAKA ARRRTHKRQNP SRGREGTHPK QRQGKEE/VNRQNEEAKQKR EEAGRTRR/EDRGRKDDKKERR QQQTEKKAKPKAEHQERTDT TTKKARQREGRPSERRRRERE/ MSKHDPQNRAEKTNEEKEEGR QHER*TKSSSTGI

SFQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4177	34545	A	4218	1	692	MNALHAELEMTSQFDQELAA KFEADHEMALLMKNKDFDRDRE EQRRLEAQARREHEERIKREAA EQARRDAEAKHKAIEIAAARR EAEEKARAELEAERQRIEAQRA EREKKETEERARREKEEAVAAE RRRQEEAEAAALVEEQKAE EARRAADKEHRRRTVNR/GLRR SDCSGHPRRIRTESSAGDRWRQ SAGRAHQILRQT*THSLTTAS KNGAGLSSNSPTRKRS
4178	34546	A	4219	3	1120	
4179	34547	A	4220	1	831	MVKARKIMETPPQPAWEMRVRI CTVDWSKLNPIPDDFSLIKSEK KYDHPELIVDESRLRVVYAPSR YFASEPKADVSLILRNPKAMDS ARNQALLEGYFSFTA TEDQLEQ AKSWYNQMMD/SPEKGKAFEH GNMPA\QMLLQVPYFLRE\ERE H*IIITPILHMRKQE QSG*/RNL KAAQLSMMQDLQTLMAASY CSELGHVATQFGMLACTRNP NSWDRNSETSGKAE GFIP\QLG DVADPSVRCSSVSL WGHSSPK LLRSVCMANRICVKLQRWT
4180	34548	A	4221	1	1503	
4181	34549	A	4222	1	1113	
4182	34550	B	4223	1	760	
4183	34551	B	4224	1	1755	
4184	34552	C	4225	1	4215	
4185	34553	A	4226	1	3240	
4186	34554	A	4227	1989	2144	
4187	34555	A	4228	1	1203	
4188	34556	A	4229	1	4767	
4189	34557	A	4230	31	512	EYRKSPDIRPIVIQHGEAEITH HFR*QELADKTLIFEITHREMQR FQPVGTGDIREPVVFVFRWLT NPFNILEHGEPEGIRVDAAVPR AVIGGLEDHIGVAVQKLQHKTF RYFPFIQMVKDGVPVEGRPAF VHHLSLFLRIKILAHLTHTNQDF
4190	34558	A	4231	369	918	RPGMSNPWRDLFRGTVDPTND RLSALVEI/YRMMRPGEPPTREA AE/SLFENLFFSEDRYDLSA/VG RMKFNRSLREEIE/GSGILSKD DIIDVMKKL/IDIRNG/KGEVDDI DHLG/NNRIRSVGEMAENQFRV /GLVRCTGTVPFLHQQKCEYH L/PQRPVASTLSRYF*HFRLLNF SMPRANEIKKGMV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4191	34559	A	4232	3	1012	SVVLKIVERVDGYFSPPLFLGA AFGSHVRSRALPDCVLFVRVTI YLCVLAASVARTFSPLLPVSRKK HITPLGGFQLHETHLCLQDCRTI ILRPRLGEFGNKFSQLVDTIDLH INQHGLAHL*KESARGQYSLLL LGMVSLCALILILWRVYRSVT CPLADQTQALHRLLDGDIVSPF PETAGVRELDITIGRLMDAFRSN VHALNRHREQLAAQVKARTAE LQELVIEHRQARAEAEKASQAK SAFLAAMSHEIRTPLYGILGTA QLLADNPALNAQRDDLRITDS GESLLTILNDILDYSAIEAGGK NVSVQSYVARLEPVAASGWHK YPWLN
4192	34560	A	4233	1	502	
4193	34561	A	4234	1	653	
4194	34562	A	4235	2	300	YALATPLPSV/INQWQLALDKG QLPTE/VAGLAPQHPQYAAHME SYWPYSALR/EILQRTGMLDGG PKITL/PGDDTPTDAVVSPSAVT NSHGR*VPTLGGVWGL
4195	34563	C	4236	40	105	
4196	34564	A	4237	355	526	
4197	34565	A	4238	116	949	RPGTGRCSAVQLPVLLLRGPHS SHTVGTHMVLDLSQQLCVYP GNSDESMPAATQARERLLADT AKKKAQIAELQSFVSFRFSANA* KSRQATSRARQIDKIKLEEVKA SSRQNPFIREFQDKKLFNALE VEGLTKGFDNGPLFKTLNLVLA EVGENLPVLGTNGVGKSTL/LK TLVGDLPDPSGTVKWSENARI GYAAQDHEYEFENDLPVFEWM SQWKQEGDDEQAVRSILGRLLF SQGDIKPKAKVLSGGEKGRML FGKLMMQKPNILMDEPPTHP
4198	34566	A	4239	1	319	MVKKMARAPMNLVALANPEPEI LACRHGRKEVRPDAIIC/TPGRS DYPNQSETNVL/CFPANVHRIPQ AASHLRAHQSRIPISLMSISAKIL TYLLANQIQFLVKQH
4199	34567	B	4240	263	1390	
4200	34568	A	4241	1	323	
4201	34569	A	4242	3	1855	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
4202	34570	A	4243	2	964	LLKHGVSLEYIQDKEGLSALDLV MKDRPTHVVFKNTPDPTDVYTW GDNTNFTLGHGSQNSKHHPEL VDLFSRSGIYIKQVVLCKFHVSF LSQKGQVYTWGHGPGGRIGT WEMNRHAWVPRLVGRD*MVII VSPSWPAKDHDTVVLTEGCV YTFGLNIFHQLGIIPPPSSCNVPR QGLHNRQNRPPVPGSAGPTS MEPSKIRPTGLKFSLTTQQSEI DLGCSSLCWDYRREPLRLAYW FIKKDIAKDTDEETRRHGVSLYI QDKFGLSALDLV MKDRPTHVV FKNTGSLQFQSIPSCRESQILSEK QGDLFREEPMFGS
4203	34571	A	4244	1	725	FRVDPVRKHFGLFYAMGIVL MMEGVLSAC*HVCNYSNFQF DTSFMYMAGLCMLKLYQTRH PDINASAYSAYSAFVVMVTV LGVVFGKNDVWFVVFSAIHV LASLALSTQIYYMGRFKIDLGF RRAAMVYFTDCIQQCSRLPYM DRMVLLVVGNLVNWSFALFGL IYRPRDFASYMLGIFCNLLLYL AFYIIMKLRSS*KVLPVPLFCIV ATAGMWACALYFFQNLSSW
4204	34572	A	4245	1	833	MKPVWVATLLWMLLVPRLG AARKGSPEEASFYYGTFLPGFS WGVGSSAYQTGEAWDQDGKG PSIWDVFTHSKGKVLGNETA DVACDGYKKVQEDIIILRELHV NHYRFSLSWPRLLPTGIRAEQV NKKGIEFYSLDIALSSNITPIV TLHHWDLPQLLQVKYGGWQN VSMANYFRDYANLCFEAFGDR VKHWITFSDPRMAEKGYETG HHAPGLKLRGTGLYKAAHHII/ KAHTL*VCFHAADKGPETEEK RRLNWTYSSTWLGFRFHHHGRG
4205	34573	A	4246	1	672	GTQNAVNG/VIIFLSWGDVKS FWIYRGGRKREGPLFAH*Q/FLI YTIHRAVGSINYVIANYKLFPI TPGVDFICTSLIAGILTIKLFLLI NQFEKQIQKGRDITSARIMSRI IKITIIVGLVLLYGEHFGMSLSG LLTFGGIGGLAVGMAGKDILSN FFSGIMLYFDRPFSIGDWIRSPD RNIEGTVAEIGWRITKITTFDNR PLYVPNSLFSSISVENPG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
4206	34574	A	4247	1	347	PLRPVGGQPGPGGAGT/RALRAPPLPSSSELICYGPGQPGRWPRCPQFPSLPPHSS*LLHTGHWPCITLGYCFIPILRAAPPLPCKCASPVL/SC TYPLPAAPSLPVLVHTSIKCFCHLQ
4207	34575	A	4248	43	446	VLPVAVPRPGQ/PPCVPAVPVQAPPPRPSPGVWSQATGSPGPAGAAPSWRIGLPAVPGHGTAGVLGPGPPGQRQPGPGGAGTQLCGPHFLRLNLNVA YGPGQPAL/RNVPLQTAPALTPSPQHLLCPFLSTHLLNASVFIC
4208	34576	A	4249	1	1521	RIPESRLPTIAFVQAPWARSGLLRWEKHAGQQVGVWARGPGVGRGRQAAGGGAALICRGGAGSAVRSACAGPLSLASGAGCR LHPSYSFGFKVGS/PTVPAALSS*STS/RGREHGGVTVPVMTQNPRS'PDGPARVEDCEAIA*GTGWLQQGIGTRPPGTGLGRAR/GAPAVQWNPV/KSCQGP GHPNR LPSHGPPSGEAGRGW/RGLQITPQL/PEVTHRRVLPGDHPATEA/GGFGTG*PGLPGRVPGPGVGTYQAKALTPLGPVGLLAPASCAQLQOSADGPGATGHL*ELAESQRRQPTGIPPGQLAVSGWATVPGVPAAPRPFPAQQA/SVPTPSYWA/GSPGAAAWPESHRR*ACDWAW**VLPVAVPRPGQ/PPCVPA PVQ/PQSHRGPADHGARLY*GLPQAEQLHPGGGLPAVPGHGTAGVLGPGPPGQRQPGPGGAGTQLCGPHILFLCLNLNVA YGPGQPGRWPRCPQFPFLPPLSWNIFVGTQKKKKKKNSQLKKKKK
4209	34577	A	4250	167	582	RSLGLAVTEMVPVVRTMGQKLKQRLRLDVGREICRQYPLFCFLLLLCLSAASLLLN*RRSAEPGRRL/SL/LK VQTPGPCCLTVRRPRSCTGTDQWGERAPQRSGLGEHGGASRPEAQAGGVGLIASFPEASSPELPFSHP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4210	34578	A	4251	402	1465	DLILSHPTAWFTIKYKPKQLGL QELFPQGHSCAVCGKVKCKRH RPSLLLENYQPWLDLKISSKVE\ ESLSKDLELVLENFVYPWYRD VTDDES FVDEL RITL RFFASVLI RRIHKVDIPSIYNQETIKSSNESI *KWIVKARQKVKNTEFLQQA LEEYGP ELHVALRSRRDELHLY RKLTELLFPYILPPKATDCRSLT LLIREILSGSVFLPSLDFLADPDT VNHLLIIFIDDSPAEKATEPASTL VPFLQKFAEPRNKKPSVLKLEL KQIREQQDLLFRFMNFKQEGA VHVL/QFCLTVEEFNDRILRPEL SNG*NAVSS/WKNCRRFIKHTV WMKVLTKDLIPSLVEEIPR
4211	34579	A	4252	1	1232	FPGRFRFLVVRLRGAEEASERQ VYSVTMKLLLLHPAFQSCLLLT LLGLWRTTPEAHASSPGAPAI AASF*DLIHYRGEGDSLTLQQ LKALLNHL DVG VGRGNVSQHV QGHNRNPTTCFSGGDLTAHNF EQLRIGSSLEHFCPTILQQDLS RACTSENQENEENEQTEEGRPS AVEVWGFGLSVSLINLASLLG VLVLPCTEKAFFSRVLTYFIALS IGTLLSNALFQLIPERSYKNKAQ VDSLPTFLAQAGMMLWRVRIR RRVVDPIRESWMLPFTKIPLWG YGLLCVTVISLCSLLGASVVPF MKKTfYKRLLLYFIALAIGTLY SNALFQLIPENRRKWWQPVHN TFGGSTA WHTDKSIEQSIDLFD EVKKESEKETPSLQIGDLGPQES LKTfNNTNSPHH
4212	34580	A	4253	3	924	VGACTAAARPLPIPQLPIHHR GEKSQ LWAHSGSSWGFLAVAA VPPSHLCPLQSRGWKRPP/PLA SAGVLPGCCCCACLVSPLAQ AGVLGPKPAAPLGPGPWVSVAP CSRPGPCGTRSPA/P*GHPAMG R/GVHEPRVGPAPPEKAIITETG AGLAERRGQGLGGSSFRSAEP QGCRLSGPQSPGGDPAHTILRPP SQNGDCAEMHACRLHPAILGT HGTGGLAAQSHAPRALLPSCPS SQQPADGWCSLHLCLPGLLLAP RIHGPSTREGGPGHGTGPPTNP ASSGATRGTRRVRPSPRSPTL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
4213	34581	A	4254	1	318	VADPVGAARAGGQPLAGRVW PRAGGGHSPRVLGAAGPGPHV CTLRLPGTAIRTEPGAPLACAR AWPGSSPAG/PECLPTSC*E*EG QEPSSHVASLPWGPVGGETQ
4214	34582	A	4255	1	718	FFFFFFSLCHLYWVSPTPGPHG KLANMANWAPWPS*GLSKLVG KHSCPAG*LPGHARAQASGAP G/ISPDSSAREA*ECT/PCGP APSTRGECPPSSRPHS/SQQDP GRCSFAPAVPQDAGGQGHWC APATGHSAPRGCPPARAAPTGS ATPAPPPAACASSLSMVSAPS R*TTGIASSGTSIPETKHQGT TAPAGT/GPGGSTGPKA/PGPAP AHPTRLAGTSGHTAPPTCPPAV
4215	34583	A	4256	702	1026	RSGRTQRAAGVSGSALHQVQS WPHLKISADQRAGLLF*EHPFP PSASSGCLDVSISSYPVGSDFIN GMARANGRWKFTFTGLHSGKPL GFSDAFCQHNLILLCWKWTW
4216	34584	A	4257	170	1049	RSGGCSAELVPSSRWPRGSRAG AAAGTETPG*PRVYVPAGNGE AGGPGAAWARRAALPGTAA GPPRPAARPGAAPARGGPAPGA PAQALPR/TPTWPAAR*AQRAP SPPSWGSAQPGHPGDLAAGVG RGAGGGHSRRGRHHVVRSLAD LLQLPGAEGAGDRGHLPGPD/ GERS*AASSFSAAGRAAGTASC CSAGGTPPSPCTILSTSSSLAH VASSS/RRRAEGDTKVS/RGRAE GQDSETGREPGVLHRGSGRTQ RAAGVSGS/RSAPSPVVATTSS LLTSVQGCFSENILSP
4217	34585	A	4258	178	556	QSPQEHFHPECGRRDILCQVRQ EIRWPNPGEVHHILGLEICPVWI LQLHLALRTRAPEHPLQVHRPG GGAV*RGVPPPLRLI.QACDGPE VPAAGRPRPARSSPGQWPP*/PA AVAPPVTERPPTPSAA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 95/040,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
4218	34586	A	4259	5	1044	TGRILDGWHWAKELRLDCPLG DSRRPPFSRVSTEGSPAFLALRL PNVTAGS*EVSMLASTETPLVIT RPSPG/GHDPGAPRGAAASPA GSPAP*QKSPRLSAAAPLLAS DPAPPRAAAPADTESSVQPPA APHAGPWT/PSAPGLDVHSPPP VPSRGPVQSSAEPHNRPSGAT RPRP/PPRGAAASPAGSPAP*QK SPRLSAAAPLLASDPAPPRAA APPADTESSVQPPAAPHAGPWT LERSWAP*RLPTIPVADPLCR APLSHRYP*GDCQRSGLCHTSP GRASHLPGPGAHKRTPHACWL PLECHRRSPHP*THPSG*PGPSP QSFFPEFLGSGP
4219	34587	A	4260	2	576	CLVNSTRRSFQLRLVPVPKFQ PPHMTVR*LFNFGRLTATTFS/ LRKSYAVREAYELQNCPPPPF QNGYMINSDYSVGQSVSFECYP GYILIGHPVLTQHGIRNWNWY PFPRCDAPCGYNVTSQNGTIYS PGFPDEYPIKDCIWLITVPPGH GVYINFTLLHTEAVNDHIAVW YENLSSQNICDCDQOF
4220	34588	A	4261	1	837	MWAGNAWRAALSGVPCGRSA QSVLAQLRGILEGELEGIRGAG TWKSERVITSRQGPPIHVDGVS GGILNLTSVRFIRGTQSIHKNLE AKIARFHQREDAILYPSCCDAN AGLFEVLLRPEDAVLSDELNCA SIHGICLCKAHKYHYCHLDVA YLETQLQEAQKHRLFLVATDG AFSMDGDIVPLQKICRLASRYG ALVFVDECHATGFLGLTGQGT DELLGVMGQVTINSTLGKALG GASGGYTTGPGPLVSL/RAQP YLFNSLPPAVVGCTSKAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met had	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4221	34589	A	4262	1	2142	MIILDAEAKAFDKIQQPFMLKTL NKLGDGTYLKITRAIYDKPTA NIILNGQKLEAFPLK1GTRQGCP LSPLLFNIVLEVLAAQAIHQKEI KGIGLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNTWTQEGEHTLGPV VGWGRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLSNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWNIP CSRGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTASEVTSHIYNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPTT KIHSRWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVILKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELQIYRKK/TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM
4222	34590	A	4263	1	1989	
4223	34591	A	4264	1	1104	
4224	34592	A	4265	1	879	
4225	34593	A	4266	1	1659	
4226	34594	B	4267	1	1500	
4227	34595	B	4268	1	1962	
4228	34596	B	4269	1	1716	
4229	34597	A	4270	1	1152	
4230	34598	A	4271	1	4752	
4231	34599	A	4272	1	2790	
4232	34600	A	4273	1	3477	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
4233	34601	A	4274	1	1007	MLDASCHRTSDSKFFSGVQTG FLTPELAHLVGPCDRDHNSSPA REQNWTENEFDELTEVGFRKW VITNSSELKEHVLTSQKEAKNL EKRAIKQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVSAQNL LKLISKFSKVSGYKINVQKSQA LLYTNNRSQIMSELPTTIAMKR IKYLGILTRDVKDLFKDNYKP LLKEIREDTNKWKNIPCSWLGR INIMKMAILPKAIYRFNAIPKLL *TFFTELEKTTLNFIWNQKRARI AKTILSKKNKAGGITLPDFKLY HKATVTKTAWYWYQNRVIDQ WNRTEASEITPHIYNHLIFDKPE
4234	34602	A	4275	737	2460	RIKYLRIQLTRDVKDLFKENYK SLLNEIKEDTNKWNIPCSWIG RMNIIKMAILPKVIYRFNVIPIK LPMTFFSELEKSTLKFIVNQKR ARIAKTILSQKNKAGGIMLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTEPSEMTPHIYNHLIFD KPDKNKQWGDLSLFNKWCWE NWLAIQRQLKLDPLTPYTKIN SRWIKDLNVRPKTIKLEENLG NTIQDISMGKDFMSKTPKAMA TKAKMDKWDLIKLSFCTAKE TTIRVNRQPTWEKNFAIYSSD KGLISRIYKQLKQIYKKKTNNPI KKWAKDMNRHFSKEDVYAAN RHMKKCSSSLAIREMQIKTIMIY HLTPVTMAIIKSGNNRCWRG CGEMGTLLYCWWDCKLVOPL WKTLLWQFLRDLELGIPFPAIP LLGIYPKDYKSCCYKDTCTPKL ARDDQIHILQHRRKELETRQK QYRAWYEINPFHSVWPVTAGK SPRHQLPVWVHNPTSPYLQL QTRDGEESNENNFSGTILASDFF AEIDKLSILQIHMEMEGTQNSQ NNLDKKKTKMEDLHFSISKLLH SYSIQDNVISA
4235	34603	A	4276	3	355	RQPVHLVHELPPQSWGICLNSS EQHGALQHSSLLH/RMCSEPW SADPQ*R*TCRNL*LPVRGPPRR TDLFSVSSKSTLKEWPLLLMIL AELGSYLILSGRREESYFTSLVL ISIGDC
4236	34604	B	4277	78	791	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4237	34605	A	4278	1	3395	MIISIDTENAFEKIQPFMLKTL NKLIGDGYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTGRQGCPL SPLLFNIVLEVMA RVIRQEKEIK GIQLGKEEVKLSLFVDDMIVYL ENPIVSAQNLLKLISNLSKVSGY KINVQKSQAFSYTNNRQTESQI MNGLPFTTASRKIKYLGILQTR DVKELFKENYKPLLNEKKVDT NKWKNIPCSWIGRINILKMAIL P/KELEKTTLKFIWNQKRACIAK SILSKKNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWN RTEPSEIIPHIYNHLIFDKPDKN KKWGMGSLFNKWCWENWLAI CRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKLEENLGNTIQDI DMGKDFMSKTPKAMATKAKID KWDLTCLRSTAKETTIRVNR QPKWEKIFAIYSSDKGLISRIY KELKRIYK/KKNNPIKKWAKD MNRYF*KEDIYAANRHMKKCS SSLAIEMQIKTTMR/YHLTPVR MAIIKSGNNRWEMNNENTWT QEGEHTLG/HC/WWKARRSR CLTWMAAGKKRMKRLQMT
4238	34606	B	4279	1	2011	

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4239	34607	A	4280	1	2661	MTMNFVADSHITGRNPLASAA AKTGLRPLPRPCGARVWNPPD AGGGGVGSLKSTPLGPLSAAN SPVHQGSVPQTRARGGGTLFQE VVTSRTLAFRNSLSAFTEVTS TVSGRKGGRSTHLAGRRVSGG EGSRKAAAAALAAVAAAPGPV RRCSSQSCFSSSGSSHYARTSP VRVRPRRSLSSRAAGNRAEAT ESAMEKTLTVPLERKKREKEQ FRKLFIGGLSFETTESLRNYE QWGKLTDCCVMDPASKRSRG FGFVTFSSMAEVDAAAMAARPH SIDGRVVEPKRAVAREESGKPG AHVTVKLFFVGKEDTEHHHL RDYFEEYKIDTIEIITDRQSGK KRGGFVTFDDHDPVDKIVLQK YHTINGHNAEVRKALSQEMQ EVQSSRSRGDGYGSGRGFGD GYNQYGGGPGGNGFGSPGYG GGRGGYGGGPGYGNQGGGY GGGYDNYGGGNYGSGNYNDF GNYNQPSNYGPMKSGNFGGS RNMGGPYGGGIWKNTSITERK KSRKLDLIQSKKGSRTKEAPQP PVASLCMHLGHWRLMVSPPGA QLTGKNSHGLSVSSVRKSNVGP RRLCAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPLSRPKPPTQISLVLPKT DGALERMPQQL/HAASS/GAKVP NPSTQTPPVLLAFFYPNLP* N
4240	34608	A	4281	1	908	MRKVKGKNRQSFKCLPPPSGA LQAHGAAPHGSLTLHLHLV PVSSAAMKATGPDNAQSQVSP PGHAPSAEDPTGSRTVSSPCTD RPHPLSWPTWISLALLLKT ALERMPPQLPSLHPSQGTQSIH PDPSTSTFLLFPQPTLKRAAF CPSPSIVNPAVWDTSTPSVAEHH TPIRITLKEPTQLFSQKQYPIQA ALVGLQPIHSHLLASHLLRPTDS PFNTPLPVKKPNGTYRLVQDL RLINQAVLPLVQE/DYSVLLVLP LNVTPGLPPATAFSYPPSPGPVA RARLASRLHSHAA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
4241	34609	A	4282	1	915	MPNYVTFDTDKQLISDTPNNQV PMNRASMAFDKCLTGC RFDD AIVQFDMITYWPF TVVNDAGR KVQVEYERDKLLPIGGVFGS DKDEGNCKSLPWEDCYQCET SQNVQDFLFDVTPLSLDIKTA DGVMAVLKCDATIPTRQTQT TTYSDKPSM/LIAKDKNLLRKFE LTGVPPAHHGAHQIEVTFDINA KGILNV/TLTDDKGHLSKEDI MVQETEKYKADEKQRDKVSS KNSLDPYVFNMKATAEDEKLQ VKINNEHKQILSKCHEINWL DKNQTAEEKEFEHAQQUEKSS
4242	34610	A	4283	1	994	MHQTKKGNQWHFGMKAHIGV DAKSGLTHSLVTRPNEHDLNQ LGNLLHGEQFVSADAGYQGA PQREELAEVDVDW/LIAERPGK VRTLKQHPRKNTAINIEMKA SIRARVEHPFRJIKRQFGVVKAR YKGLLKNDNQLAMLFTLANLF RADQMIHCTRGEGLITTKIPKAP DNGSYCLPSKNDDSEEDPEMS PMVVTKMKEIAEAYLGKTVTN AVLTVPAYFNDSQRQAT/KKDA RTIAGLNGLRISNEPTAAIAYG LNQKVGTERNVLIFDLGGSITPR IRTPETGSDDAIKSILEQAKKEIE SQKGECDCPCRQSLRPPGPAAN
4243	34611	A	4284	3	677	
4244	34612	A	4285	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKQORLLARAEEK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIHKGKARGLRVHRKTCTTV AFTQVN
4245	34613	A	4286	3	432	NSRVDDFVAAQDAKGGKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ/QRLLARAEEKAA KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIADVDPIELV VFLPALCRKMGVPYCIHKGKAR LGLRVHRKTCTTVAF
4246	34614	C	4287	62	217	

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4247	34615	A	4288	2	801	PKGKKAKGKKVAPAPAVVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTRFVKWPRYIRLQR QRILYKRLKVPAINQFTQAL DRQTATQLLKLAKHVRPETKQ EKKQRLARAEEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVAHDVDPIELVVFLPA L\CRKMGVPYCIHKGKARLGR VHRKCTTVAFTQVNSDKG/ ALAKLVEAIRTNNDRYDEIRR HWGGNDLRPK\SVARIAKLEKA KAKELATKLG
4248	34616	B	4289	1	273	
4249	34617	A	4290	1	441	
4250	34618	B	4291	47	482	
4251	34619	A	4292	1	762	
4252	34620	A	4293	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLSHFQWGTLDTCVV MRDPNTKRSRGFGVYATVE EVDAAAMNARPHKVDGRVVEP KRAVSRSDSQRPDYFEQYKGIE VIFIMTDRGSGKKRGFAVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSQGRGS GSGNFGGGRGGGFGGNDNFR GGNFGSGRGFGGSHGGGGYGG SGDGYNGFGNDGSGNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPGYGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF
4253	34621	A	4294	1	1674	
4254	34622	A	4295	1	506	KYHTVNGHNCVVRKALSKQEI ASASCSQGRSGSGNFGGDRG GGFGGNDNFRGGNFGSHGGF GGSCCGGGYGGSGDGYNGFGN DASNFGGGGS/YNEFG/NYNNQ SSHFGPLS/GGNFGGRSS/SPLGG APASTYVKGPNSQRTQNEGWF EG*APWRGDGGARGNKGGGA

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4255	34623	A	4296	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCGWIEEER DESRKSETIFKDLFKVPVLKETI YYKFYGPVPYQIETVYFMAISP PKSKQFDKTKQNNNNKKTHQF VIVFFKTDHLSARGRRRSIVK VSLLPVAVIGLKSFLKPKDQLR KLFI\GG\LSFETT\DESLEEFSSR QWQKRYTDSVVMRDPNTKRSR GVGFVITYATVVEVDAAWMNA RPHKVEWKELLEPKRA\VSRED SQRP\GCPH*LVKKIFVGGIKEDT VEHHRLRDYFEQYGGKIEVIEIMT DARGSGKKRGFAFVTFDDHD\VS VDKIVIQKYHTVNGHN\CEV* KSPVSKSKKMASASSKPKEGRSG FWETFGGGSWEVFGGNDNF GRG\GNFSWSV\AFGGSRG\GG GYG\GSGDG\YNGFGNDG\SNF G\GGGSYNDFG\NYNNQ\SSNF GPMKGG\NFG\GRSSGPY\GGG QYFAKPR\NQGQYGGSS\SN
4256	34624	A	4297	1	920	DPGDTPTNTASAPNCRSGKGRSS SPEHIPPLEKLEDSMQTNPSTNP EPGRLAEWLDPEERQQSLQFGL QEATSIGKGGQYIKGTPHGTK ESEQQPSALDLPSDRAYPNEKE PENQLWRLVIKLIKEAPEKGAY LNVIKAVYDKPTNGEKLRAFPL RTGTHKRCPLSPLLFNILLEVLA RAIRQEKEIKSIQIGKEEVKLSLF ADDIIHYLESPKYSSRKQLQELIKE FSKVSRYEINVHKSVALLYTNS NQAENQIKNSASFTIAAKNKIK YLGYYLTAKADGKYKENYKTL MKEIIDDKNKQKYIP
4257	34625	A	4298	1	1194	
4258	34626	A	4299	3	1834	
4259	34627	A	4300	285	502	
4260	34628	B	4301	77	1306	
4261	34629	A	4302	1	354	
4262	34630	A	4303	1	1182	
4263	34631	B	4304	1	1995	
4264	34632	B	4305	1	1518	

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4265	34633	A	4306	1	918	MCPVGPWTHPPVVISPVSECIVGI DILGSWQNLHIGSLTDITMVHYI DDMMLIGSSEQEVANSLDLLV RHLHARGCKINPTKIQGTSTSV KFLEFQWCGVCQDIPSKWVLE QKALQQVQAQVQAALPLEPYD PADPMVLEVSADGVAVWSL WQAPIARIHGSRNQGVEVEVSP LTNIPSDPLAKFLFPAPSTLCSA GLELLVPEGGTLPGNTTMIPL NWKLRLVPGYFGLLLALSPQA KNGVTVLAVIDPDYQDEITLL FHNGGGEEYARNTGDPRLHLL VLPSPMIKVNGK/LQHPNPGRT
4266	34634	B	4307	1	1599	
4267	34635	B	4308	1	1569	
4268	34636	A	4309	3	422	
4269	34637	A	4310	1	1089	
4270	34638	A	4311	2	549	LKMTAMQRPMEKRMMNREIIL KERLSLTGIDIKILKKRSIMKVE SHRGEQISVSLSALQRIKYLGIQI TRDVKDLFKENYKPLLNKLKE DTNKWRNVPCPRVGRISIVKM AILPK/ILKKKTTLKFIWNQKRA HIAKTILSKKNKAGGITLPDFKL YYKAT/KTAWCWYQNRDTDQ WNRTPKPEI

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4271	34639	A	4312	371	3036	LIAYQPKKVQDQMSQPNSTR VLEVLARAIRQEKEIKGIQLGK/ EEVKLSMFADDITAYLENPIVS APNLLKLISNFSK/VSGYKINVQ KSQAFLYTNKRQTE/QIMSELPF TVASKRIKYLGIKLRRDVKDLF KENYKPLLNEIKEDTNKWKNI CSWIGRINIVKMTILPKVIYRFN AIIKLPMTFFAELEKTTLKFIW NQKRAHIAKTILSQKNKAGGIM LPDFKLYKATVTKTAWYVY QNRDIDQWNRJEPSEIIPHICKH LIFDKPKDNKKWGKDSL FNKW CWENWLAICRKLHLDPFLTPYT KINSRWIKDLNVRHKTIKTL EE NLGNTIQDIGMGKDFMTKTPK AMATKAKIDKWDLIKLSFCT AKETTIRVNRQPTWEKIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHHMKCSSSLAIRETYNDR RIGKLTQTCDETAQPHVCTISR PMLSSPYRSSLTEKWSQDFSKP PYPFLFHKGYNPREQDKEVLT RAIRQEKERKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNPK VVSNFSKVSGYKISVQKSQAFL YTNNRQTESQIMSELPFTIASKR IKYLRQLTRDVKDLFKENCKP LLNEIEEDTNKWKNI PCSWIGRI NIVKMAILPKVIYRFNAIPIKLP MTFTFVLEKTTLKFIWNQKRAH
4272	34640	B	4313	1	1995	
4273	34641	A	4314	3	549	
4274	34642	A	4315	3	614	EAYGQTECTGGCTFTLPGDWT SGQFINILEMCELESPCKSFSAD SARYVLGHVGVPLACNYVKLE DVADMMNYFTVNNEGEVCIKGT NVFKGYLKDPEKTQEALDSDG WLHTGDIGRWLPDIENHNRLIV CTLTNTSWRSHKIIVLKYQKA DDTKTPKETTFQNMNLFLEKE RATAVLIRGGVGETSDLSKKK PAKLLANF
4275	34643	A	4316	1	478	MKLDLHLSPYTKINSRWIKDLN LRPETIKILEDIIRKTLDDIGLGK DFMIKNPKVNATKTKINKWDLI KLKWNCTAKEISSREIREPTEW EKIFANSASDKGLISRIYKELKQ IRSTLQLLFGISELPASLFLGFGA IMSKSKASLNTSTAILRQLIW

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4276	34644	A	4317	1	1125	MCHGIGAQIIPSHQT VQLDITAF LKT VKK NKHKFYPAFIHILARL MNAHPFERMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYYTQGDVLMMP LAIGGPLES PDRDGGPLESTNR DASPESWSCRKSTPRLVAVVS AAKVFI RDKLMERRNRRTGRT EKARIWEVTDRTVRTWIGEA V AAAAADGGGFRVDLARRSIRK DRNARSQNPVHTEGDMNMNIK KIVKQATVLTFTTAFLAGGATQ AFAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYVQPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQVKGVDN SID\SWKNAGR VF
4277	34645	B	4318	1	1374	
4278	34646	A	4319	1	1293	
4279	34647	A	4320	1	1278	
4280	34648	A	4321	1	1254	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGV\N GYYCEES\LFNKA\YGGGTNFF RKESQKLQQSAKKRDAELANG ALGIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWWYL FTDSRGSKMTIDGINSNDIYML GYVSNLTGPYKPLNKTGLVLQ MGLDPNDVTFTYSHFAVPQAK GNNVVITSYMTNRGF FEDKKA TFAPSLMNIKGNKTSVVKNLSIL EQGQLTVN
4281	34649	A	4322	1	726	
4282	34650	A	4323	1	1050	

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4283	34651	A	4324	1	1185	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNISDSWKNAGRKFVSDSD KFDANDPILKDQQTQEWGSA TFTSDGKIRLFYTDYSGKH YKGQS LTTAQVNVSKSDDTL KINGVED HKTIFDGDGKTYQ NVQQFIDEG NYTSGDNITL RDPHYVEDKGH KYLVFEANT GTENG YQGEESLF NKAYY GGGTNFFRKESQKLQQ SAKKRDAELANGALGHI ELNND YTLKKVMKPLITS N/TVPQAKG NNVVITSY MTNRGFFEDKKATF APSLMNIKGNKTSV VKNLSILE QGQLTVN
4284	34652	B	4325	1	867	
4285	34653	A	4326	1	495	
4286	34654	A	4327	3	1394	GDMNMNIKKIVKQATVLTFTT A/LLAGGATQAFAKENNQKAY KETYGVSHTIRHDMLQIPKQQ QNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNAADGTVAEY NNGYHVVFALAGSPKDADDT SIYMFYQKVGDNISDSWKNAGR FVKDSDFDANDPILKDQQTQ EWSGSATFTSDGKIRLFYTD YSGKH YGKQSLTTAQVNV SKSDDTLKI NGVEDHKTIF DGDGKTYQNVQ QFIDEGNY TGDPLEAETA VINH KKRKNS PRIVQSNDLTEAAYSLSR DQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKE VVFYR PEEDAGDEKGYES FPWFIKRAH SPSRGLYS VHNPYLIPFIFGLQN RFT QFRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKID WIIERYQLPQSYQRTPD FRRRLQV CVNEING
4287	34655	B	4328	9	1004	
4288	34656	A	4329	1	768	
4289	34657	A	4330	1	1308	
4290	34658	B	4331	58	753	
4291	34659	B	4332	1	409	
4292	34660	B	4333	1	921	
4293	34661	A	4334	1	1026	
4294	34662	B	4335	1	945	

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4295	34663	A	4336	1	528	MNMNIKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKADDDTSIYMFY/Q KDQTQEWSGSATFTSDGKIRLF YTDYSGKHGKQSLDTA\Q*NV VKSG
4296	34664	A	4337	1	1701	
4297	34665	B	4338	97	1449	
4298	34666	A	4339	1	1581	
4299	34667	B	4340	1	1539	
4300	34668	A	4341	87	1078	SLPNLDNAAICSSSSPTRTR*SL SEGATQ\AFAKEKYPHKHTKKR SGVFHITRHDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKALDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKADDDTSIYMFY QKVGDNIDSIDSWKNAGRVFKDS DKFDANDPILKDDQTEWSSGA TFTSDGKIRLFYTDYSGKHGK QSLTTAQVNVSKSDDTL KINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYRGPLESPSTHQAEFNPTS CVSSGLTLQGFPAPAWLALAH VHPLKHKSGGNSRLSAAIWGIK RKPAR
4301	34669	A	4342	1	1344	
4302	34670	A	4343	1	1713	
4303	34671	A	4344	3	1918	
4304	34672	A	4345	254	1118	RPPAFAKK*PKAYKET/YGVSHI TRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWP LQNADGTVAEYNGYHVVFALA GSPKADDDTSIYMFYQKVGDN SIDSWKNAGRVFKDSKFDAN DPILKDDQTEWSSSATFTSDGK IRLFYTDYSGKHGKQSLTTAQ VNVSKSDDTL KINGVEDHKTIF DGDGKTYQNVQQFIDEGNYTS GDNHTLRDPHYVGGTSEWPGV FSVSCVFFGQQEGV/HG*DEFLD FSYWFQGG*ICLYQKAS*QNTT SYKRYTGS

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4305	34673	A	4346	1	1952	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDS WKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTGSLNSSKTEKY QVPHIDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDS WKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKH YGKQS LTTAQVNVSKSDDTLKINGVED HKTFIDGDKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL VFQDHTGTEEHPQPQERP RTQSFTSAFAERRECIPNPADT KLSKIKTLRLATSYIA YLMDLL AKDDQNGEAEAFKAEIKKTDV KEEKRKKE LASKCLDLEQLGAS VEPTGNLRTKITKEKPRHTGPPE VVVPGCCPHSRSA YKSDKYAH TLTVTASQHAPPPPTHMEGFEL FHL PDLCSPSQDAQTGRTQMK PDHSPRPSHRVPQAKGNNVVIT SYM TNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTV
4306	34674	A	4347	1	1029	
4307	34675	A	4348	276	1248	CVWLGRGYYPKAYKET YGV SHITRHDMLQIPKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNIDS WKNAGR VFKDS DKF DANDPILKDQTQEWSGSATF TS DGKIRLFYTDYSGKH YGKQSLT TAQQLQLVQFQEVDTDFDFPE EDKKEFEFEECKEFFSTGPARPP TKEKVKRRVLIEPGMPLNHIEY CNHEIMGKNVY YKHRWVAEH YFLLMQYDELQKICYNEFVPSV IFLRYKSPGEAAGTCHLKQRRW VMPEAAAPVGTGSRYP LTGQL
4308	34676	A	4349	1	242	MNSIQIPKQQQNEKYQVPQFDQ STIKYIESPKELDVWDSWPLQN ADGTVAEYNGYHVAFALAG/S PKDADDTSIYMFYQKI
4309	34677	B	4350	1	2198	

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4310	34678	A	4351	1	2796	
4311	34679	A	4352	2047	3531	
4312	34680	A	4353	1	3336	
4313	34681	A	4354	1	1409	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDLSIARVGVGMARG NAITLPVCGRDVKFTLEVLRGD SVEKTSRVWSGNFRDQELLTE DALDDLIPSFLLTGQQTAFGR RVSGVIEIADGSRRRKAAALTE SDYRVLVGELDDEQMAALSRL GGATQAFAKENNQK\AYKET GVSHITRIIDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNIDSWKNAGRVFKDSD KFDANDPILKDQTQEWGSGATF TSDGKIRLFYTDYSGKHGKQS LTTAQVNVSKSDDTLKINGVED HKTFDGDGKTYQNVQQFIDGY LLEPDGGALQNFQRYTGIQHVH RIGMAERMWCDNRERHTYSS SGGNRLPNPGPDRSVRHFPDPR FLCPSCATVTPLHELIANKYLSG KIGAKKLRKLLIKHVD
4314	34682	A	4355	1	2316	
4315	34683	A	4356	93	924	AQTDAAEKSVSIAQLFQACLSIF SSGDV/AGGATQAFAKENNQK AYKETYGVSHTIRHDMQLQIPKQ QQNEKYQVPQFDQSTIKNIESA KGLDVWDSWPLQNADGTVAE YNGYHVVFALAGSPKDAADTS IYMFYQKVGDNIDSWKNAGR VFKDSDFDANDPILKDQTQE WGSATFTSDGKIRLFYTDYSG KHYGKQLTTAQVNVSKSNDT LKINGVGKYKTIFDGDGKTYQT VQQFIDEKNYTSGGHHTLKDP SYNPLDLSGNSGYQSQET

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4316	34684	A	4357	1	3118	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNISDSWKNAGR VFKDSD KFDANDPILKDQTQEWGSA TFTSDGKIRLFYTDYSGKH YKQSLTTAQVNVSKSDDTL KINGVEDHKTIFDGDGKTY QNVQQFIDEGNYTSGDNHT LARDPHYVENKGGHKYLG FETNTGTENG YQGEESL FNKAYYGGGTNFFRKESQ KLQQSAAKRRDAELANGAL GIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKM NGKWYLFDTDSRGSKMT IDGINSNDIYMLGSD ESPNDFGNRHLHKERLA VYRWHAFCSGNTMPIV LVDWSDIREQKRLMVL RASVALHGRSVTLYEKAF PLSEQCSKKAHQDLADL ASILPSNTTPLIVSDAG FKVPWYKSV EKLGWY WLSRVRGKVQYADLGA ENWKPISNLHDMSSSHS KTLGYKRLTKSNPISCO JILLYKSRSGRKNQR STRTHCHHPSPKIYSA SAKEPWVLA TNLPVEIRTPKQLV NIYSKRMQIEETFRDL KSPAYGLGLRHSRTSS SERFDMILLIALMLQ LTCWLAGVHAQKQ
4317	34685	A	4358	1	1326	
4318	34686	A	4359	2140	4390	
4319	34687	B	4360	1	7271	
4320	34688	A	4361	1	1729	
4321	34689	A	4362	5118	5687	
4322	34690	B	4363	1	4726	
4323	34691	B	4364	1	3688	
4324	34692	A	4365	1	1401	
4325	34693	A	4366	1	1932	
4326	34694	A	4367	1	1407	
4327	34695	A	4368	1	1491	
4328	34696	B	4369	1	855	

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4329	34697	A	4370	137	1014	ASEGKQMLRDFVTTRSAKELL KRALNMARNNQYQLQKHAK L*RPMSL*RCIN*QPGRD/TN KKENFRPISLMNIDAKILNKILA NRIQQHIKKLIHNDQVGFIPGM QGWFNIHKSINIIHHIKRTNDKN HMIISIDA EAKAFNKIQQPFMLKT LNKLGIDGTYLKIIRAIYDRPTA NVILNGQKLEAFPFGTGRQGC PLSPLLFNIVLKVLAIRIQETEI KGIQLAKEEVKLSLFADDMIVY LENPIISAQNLKLIISFSK/VSG YKINVQKSQAFLYTINRQTESQI
4330	34698	A	4371	3	1234	
4331	34699	A	4372	1	2850	MGMGPAKPGMGGNLLVCWLQ RPWEKRSIWA EYVRSRYSHS WLPLSRKGCDFSGTCRQTL TQPLRQWGLEGIKKPNSWIISEE SVSNGGPPLIPRQTASGVDLQ QTPTDLQLRVLTVRRTKNQK GIASTSTKRTSTPKPHLYVTIHK DQSYIKPQRWGKNIAEKLKILKI RVALS LQRNAAPHQQWNKAG RRMSLMSSQKKASEVIESQMN EIKGEEKFREKRVKRNEQSLQEI WDYVVRPDLRLIGVDP
4332	34700	B	4373	16	701	
4333	34701	B	4374	1	3743	
4334	34702	A	4375	227	686	KVMLAEYPVFAQLTLTLPPSSA SWEPSRGPGRGIRGSCPEWLA SGPGKAAAPGAGVPPPAASFDP PPRLRAPALAVSRGLRRELPSG LDWTHCLRTLPSLIVQILQAAA LLGLPPAYS DQLQRAGQLHFYS GLIKISLVLTTLRSFWGTTE
4335	34703	A	4376	216	644	VTYSKEKEGCEVADSVAKTAL EKDGAPRTGDP RPNLGADPPRS LVSSAGPQAVRPVKPARQFPQP PPRYSQGPAAAGEEGRGMPP GAGRRLPGPPLPGPEASHSGQL PLM/PPGPGPRLGSQEPVSLSR LQTQARMPGPRP

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4336	34704	A	4377	18	1023	QIQHSPLVSLPSLPQPLVAEE EPPVA/PWPRRLPATSTSH/PSH PLTEPVPTSGRGCLWTKRQ QKMCRTITYTSVGRK/CTFPIDS GALRLSDGEMRALQITGPQOST VEGHTHLQSL/PHHDRVATPG TEPLRAAGNRRIYPGP/VT SQ VQPQLLCGYGNASRTPAALTPG PAPPTQASLPNGICPHLQMG PTSPC/PPEGHPSSSLYISLSPPP PSAPALRLPPPLP/SAPTAPAL/P/ PAAPSAPALRLRLPCCSFRPR PAAPSAPAPRLPPLLVCSEFRPC PAAPSAPAGLLLPPLLCCSGLSP RLCCPHSSCSDPPRLQRKADSS
4337	34705	B	4378	1	984	
4338	34706	A	4379	332	847	VKLLQDKEICILCQKTVYPME CLVADKQNFHKSCFRCHHCNS KLSLGNYASLHGQIYCKPHFKP TFQNPKGNYDEGFGHKAHKD RWNVQKPKADSVDIPNEEPN MCKNIAENTLVPGRNEHLDA GNSEGQRNDRKLGERGKLKV IWPPSEKIPKTLPFEEELKMSK
4339	34707	A	4380	305	505	GNLERMLNLGMVKKQKLPAM KTQVLMML*AINVPAKPLFPQSG GAVRTTHGGKSLKETGATSD TE
4340	34708	A	4381	56	260	IVKTQSIDG/MGNLRITEKGLKL EGDS/EFLQPLYAKEIQSRPGLG TQEQSCQTLSSCSSRQGOQHAE
4341	34709	A	4382	137	920	
4342	34710	A	4383	532	1680	LLTTRTSFRSENHRHVGLLVM TDNTRDKEYFGDESKRENEKT VEKSIGEKQATLTTHANIITIRH CVKPEPDFSDHLNLLGRADIT GEEMAAQRSSVEKLANGNIAL VDSLRSRSLLEGSDPHKRLSG AQDIKTTVVEVIADVVEIARELE LEVEPEDVTEFLQAHEKTLTDV ELFLINEQIKWFLEMKSTPRED AVIIAETITKVEYDINLVTKQK QGMRLTLPILKEVLLVWKCHQ TALHATEKPFKGRINPCGKIHT CLNLRNCGQLIREEEEDKEE EEQYEEKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEDE DEEEDKEKEEEDNKEEEEEED KEKEEEDKEEKEDEEEDK

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4343	34711	A	4384	3	495	EDTGTFRIYVESAGAVKKARGF LEFVEDFIQVSKNLIGKVGKNG KVIQEIVDKSDMPVVRIGEDSE NKLPRDEKDDRRSRHQDRSR CPGGRCSRVSRRGRGGPRGG KSSISSVPKDPDSNPYSVLN/T ESDQTADTDASKSHHSTNRHTR SRRRRRTDEDAVL
4344	34712	A	4385	1	550	TESERKDELSDWSLAGEDDRDS RHQRDSRRRRPGGRGSRVSGGR GRGGPRGGKSSISSVLKDPDSN PYSLLDNTESDQTADTDASESH HSTNRRRRSRRRRRTDEDAVLM DGMTNESDTASVNEGLAKDV IEEHGPSEKAINGPTSASGDDIS KLQRTPGERKRLIP*KKENTQE AAVLNGVS
4345	34713	A	4386	1	2063	MAELTVEVRGSGAFYKGF DVHEDSLTVVFENNWPQERQV PFNEVRLPPPPDIKKEISEGDEV EVSRRANDQPCGWWLAKVR MMKGEFYVIEYAACDATYNEI VTFERLRPNQNKTVKKNTFFK CTVDVPEDLREACANENAHKD FKKAVGACRIFYHPETTQLML SASEATVKRVNLSMDHLRSIR TKLMLMSRNEEATKHLECTQ LAAAFHEEFVREDLMLAIGT HGSNIQQARKVPGVTAIELDED TGTFRIYGESADAVKKARGFLE FVEDFIQVPRNLVGKVGKNGK VQEIIVDKSGVVRVRIEEDNEN KLPRDEGMPVFPVFGTKESIGN VQVLLLEYHIAYLKEVEQLRME RLQIDEQLRQIGMGFRPSSTRGP EKEKGYATDESTVSSVQGSRSY SGRGRGRRGPNYTSGYGTNSEL SNPSETESERKDELSDWSLAGE DDRRSRHQDRSRRRPGGRGSR VSGGRGRRGPRGGKSSISSVQY RSNIHNCSTLKRIFLASDMNIVL KDPDSNPYSLLDNTESDQTADT DASEHHSNRRRRSRRRRRTDE DAVLMDGMTESDTASVNEGL DDSEKKPQRRNRSRRRRFRGQ AEVDRQPAIDFIYKEVEKVVSL WQAKDVIEHGPSEKAINGPTS ASGDDISKLQRTPGEEKINTLKE

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4346	34714	A	4387	1	1882	CGSNMADVTVVEVRGNGAFYK GFIKDVHEDSLTVVFENNWQPE RQVPFNEVRLPPPPDIKKEISEG DEVEVYSRANDQEPGCGWLA KVRMMKGFEYVIEYAACDATY NEIVTFERLPRVNQNKTVKKNT FFKCTVDVPEDLREACANENA HKDFKKA V GACRIFYHPETTQL MILSASEATVKRVNLSMDHLR SIRTKLMLMSRNEEATKHLECT KQLAAAFHEEFVVREDLMGLA IGTHGSNIQARKVPGVTAIEL DEDTGTFRIGESADAVKKAR GFLEFVEDFIQVPRNLVGKVIG KNGKVIQEI VDKSGVVRVRIEG DNEKNLPREDGMVPFVFGTK ESIGNVQVLL EYHIA YLKEVEQ LRMERLQIDEQLRQIGRSYSG RGRGRRGPNYTSGYGTNSELN PSETESERKDELSWSLAGEDN RDSRHQRDSRRRPGGRGRSVSG GRGRGGPRGGKSSISSVLKDPD SNPYSLLDNTESDQTADTDASE SHHSTNRRRR/SIRRRRTDIEDA VLMNGMTESDTASVNGELVT VADYISRAESQSRQRLPRETL AKNKKEMAKDVIEEHGPSEKAI NGPTSASGDDISKLRTPGEEKI NTLKEENTQEA AVLNGVS
4347	34715	A	4388	2	421	PRVRSDTDEDDSEAEHFESFIHP TAMMFTSTINLLQTLCLSGVH AEIMQSEATKLCGLLAKSSPNR LVYREQHRSWCTLGFVQSIALT LQVCGALSSLQWITLLMKVVE GHAPFTATSLQRQILA VHL LQA VLP S WDK
4348	34716	A	4389	269	417	DLNCKVGSCFEVYSS*KQGIN*1 KLGD SKT*P*LSGPTSEN LKNSS LAE
4349	34717	A	4390	1	516	
4350	34718	C	4391	1	1527	

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4351	34719	A	4392	200	1267	TFSKASRGGNPHSMTKAPSDFR KARQTGIPGCSQLGSRYSLEPE QSALRLVCIQKLQESSSTTCEDFF CPLCGRAWAVSTPLTDSPSPGH QPAVK*LGLVPFSDTHHPLPFQ VLSTDDTSSSSSCSSSCASSSSP /SLLLLLLFLLLLLLLMLLLKL FLLLLLFL/RPPASPPLLPAL PPL/HCSSSSPASPPAPPPAPPP APPPSPPPAPPPAPSSAPLPPA PASPPFSCSSSSCSCSSSSSFSSC SSLSSSAQAEGSLRAPRESSPSL DPSAPQRVKVPQAGSGIIRA GGALENRPRGKKPWLHFRPGL RSRLPARSLRSRPAPTRWLRSS GRFTGAATATATART
4352	34720	A	4393	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAQSGQCSRN ARHQAQKARSMPLQDQHLALAIL LELAVQRTLSQMLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLQTQFSIICSKDTTPPSEGN MHLLSGPLSPSEFLRESFTVQ NCRNNEEVLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRSMHAFVGVQYLEVR LYALSDAEDGRGTL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTAPASKSR/CSIIRWALG DHSQAFLLQAIADNNIQDHNKVT HQEQGRSYKEVCTPVIERLRFL SNELRPAVGNDSLHSEFKLLSSL PRWRIAQKIIRERRKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPPIAKSPKTITSEN LGPSLGSIPQARFLLMMLSLT LQHSANNLDDLNSGTALALQT ALRLIGPSCDNVEEDMNASQ GVSATVLEATRKETAPVHLVPS GPELAATMKIGTRVMRGVDW KWGDQDGPPLGRVIGELGE DGWIRVQWGTGSTNSYRMKG EGKYDLKLAELPAAQPSAEDS DTEDDASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQRWVAVSLPHALVKSQGTVP

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4353	34721	A	4394	266	1110	WARGGCARNALASGNAIQGGK CNPGLFPPSPNRLVYREQHRWS CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQLCPE/HTSCPVLKDFCKSVI TDVACSSLISTLLVFWGGGLLHT HKEASESWREAKSTSYVAAAR ENEEDAKAEPPTGKIPSDLVRL IHYQENSMGETAPMIQIISHWV PPTTHGIYGSTIQDEIRVGVSYP GHTDARGFQLLLVSGDFSIPYW SLSSAYTSVNSSFVESLQSNLLK GILLPATIMTDPRTTGHQ
4354	34722	A	4395	1	734	MVQLSGKRILNSPYLELRCHQN MDHLGWVVKSLNRSEVSWVP GLEFPWGPKEPREVIAGPLLRN NGQSLESSLEGSHVGVYFSAH WCPPCRSLTRVLVESYRKIKEA GQNFEEIIFVSADRSEESFKQYFS EMPWLA VPYTDEARRSLNRL YGIQAHFLTANAEDFDTTVQV NKIILITYRQENSLSSLKGTGET EAQGRQLQGSFNSVRGHDPRH AIPLSVNRWNPSKSSPSAVWS
4355	34723	A	4396	195	1071	LHEFDSSRDLTSLGGGARTHRR LGGPSDAPRGLPAPPPAPVVRPG /PRSPGFSAGTAR/DAPRPSVQM RAQRPARGSTKDLIETCCAAGQ QWAIDNDECLIPESGTENDVC RTAQRHCCVSYLQEKSCMAGV LGAKEGETCGAEDNDSGISLY KASLTCGLQGRCLNPQQASMG LFSYDVQSSKKINRSIQEKLGG HGVCAATPGGGMNRNCGRLRRS GQRRGGTDRCEAVLTGLFTRA LIREQMGDPHPLDHTGQLAKPL EVEKTPARWKYLDTNGEKEEP ELRTQCPSLYED
4356	34724	A	4397	1	520	MMGEKAEKPDTEKKKPKAKK ADAGGKRNCRYSRSAMYSRKT TSRKKYSAASKVEKKKKFLA TVTKPVGVGDKNSGTQVVKLHK MPRYYPTEDEVPLKLLSHG/KKK PFSQHR/RRVVFLKQLV/SGTGP LVLNQVPLRRTHQKFVIATSTKI GSSNVKIAKRLTGAYFKKVKWK PKHQE
4357	34725	C	4398	67	243	

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4358	34726	A	4399	1	333	QRSCIENILRAC/VGLPPQNHML LEHKMDAKRVGPVAATYPMML NKKGPVPAATNGCTGDANGHL QEEPPMPTT*GPGH TVSRLFLPA APHDP TLKAPTNNNSAATQPSKN KKK
4359	34727	A	4400	587	1013	GAASAGRGPGRAPGLWGRGP AAAGASLVPTD HVHLSYNHLG NNDGENLSAP/SQFRSKEVSKS NVVDD/MVQSNPVLYTPGEPPD HATRCWPHPSAGPSAADRAVP ARPA GAPATEPHAPGTQNGAP GPSLKR VGPVAATYPI
4360	34728	A	4401	2	334	
4361	34729	B	4402	257	975	
4362	34730	A	4403	30	365	EEAETVLVGQLKQLSSCLAVH KYRPETKQEKKQRL LARA EKK AAGKGDVPTKRPPVLRAGVNT VTTLVENKKAQLVCRKMGVP YCIK GKARLGR LVHRKTCTTV AFTQVN
4363	34731	C	4404	62	217	
4364	34732	A	4405	2	69	
4365	34733	A	4406	1	951	GTRPKMPKGK KAKGKKVAPAP AVVKKQEGFRKKW*IPWFEKR PKNFGIGQDIQPKRPPPLL*K WPRQYQACSGQRAILYKRILKV PPAMKPVSPRALD/RQTATQLA *AVAHKVQTORQKQEKKQRL\ LARADEEGCLAKGDVPNERDP PVPSSQEFNPVSPPLVKEQEKLK LVVNWHTD VDPHPSLVCLPC/ LCAPAVS*KMGGPFTCIHQKRA RLWDR LVPQERPCTTCPPFTQV N/SEDKVRL LAKAGLEAIQGPY N*PDTMEIRPSLGVGNVLGPKS VARIAKARNRHKAKETATHTG LNVTL SFLYYKNN

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4366	34734	A	4407	1	1392	MPDVSEEQKESVCTGSMRMREE ESSRKGVRTAGAKSSSSDRVP RLNQEEVESLNRPITGAIEVAIIN SLPTKKSPAPDGFATAEFYQRIRI QQPIIRIQQPIKKLIQHDKVGFI GMQGWFNICKSINVIQHNRTK EKNHMIISIDAEPDKIQQCFM LKTNLKLGIDGTYLKIRAIYHK PTANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEVLARAIQRE KEIKGIQLGKEEVKLSLFADDM IYILENPTVSAQNLLKLSNFSK VSGYKINVQKSQAFLYTNNRQ TFQSIMSELPFTIASKRIKHLGIQ LTRDVKDLFKENYKPLLNEIKE DTKKWKNIPCSWAGRISIMKM AIPKVIYRFNAIPKLPMTFFTE LEKTTLKFIHQKRAHIAKSILS QKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQCTRTQP SEITPHIYNILIF
4367	34735	A	4408	1	1947	MALRLRLSHDVSGALLANGES TGNSGSGSGSSPGGATSGSSQ TSISGDVVEACCSVLMSVCA VPYKVVYAALQCMLLVLTEDPS SHFTRMRRRLM/AYADEVEIAE AIQLGVEDTLDGQDQSF/CRHL FPTTIWKPQRTVP/LECTIHLEKT GKGLCATKLSASSEDISERLASI SVGPSSSTTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHHSQML FPALSTPSSSTPSVPAGTATDVS KHRLQGFIQCRIPASPTQKRF SLQFHRCNPENKDSDKLSPVFT QSRPLPSSNIHRPKPSRPTPGNTS KQGDPSKNSMTLDLNSSSKCD DSFGCSSNS/CCYTSDETVFT PVEEKCRDLVNTLNSSIEDLLE ASMPSSDVTTVFKSEVAVLSPE KAENDDTYKDDVNHQKCKE KMEAEELAAIAMAAMSASQD ALPIVPQLQVENGEDIIIIQQDM TFRHIIPPIQWIYKKESANLLID STGQRLRIADFGAAARLASKGT GAGEFQGQLLGTIAFMAPEVLR GQQYGRSCDVWSVGCAIEMA CAKPPWNAEKHSNHLALIFKLL LDFANTACDGDKESEVEDVET DSGNPDELKKEIMIGLQYQAEI PPYLGEDGNEKDSPPQKKMT GVQNAKEVLST

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4368	34736	A	4409	1	4485	
4369	34737	A	4410	2	927	IDHMIGHKASLNKFKKIEIISSTL SGHNGIKLEINSKRDLQNHANT RKVLNNLLNEHWVKNEIKMEI LKFFELNDHNDTTYQNLWDTA KATFLLRGKFTALNAYIKKTER AQTDILRSHVKELEKQEQTQPK PSRRKEITKIREELNEMETNKK KIQKINETKSRRFEQINKIDRSLA RLAKKRREKIQITSIRNKTGDTT TDTTEIQKIIQGYEHLIAHKLE NLEEMDKFLEYNPPSLNQEEL DTLNRITTSNKIEMVIKKLPTKK KSPGPNGTAEFYQTFFK/EELVP ILSILVHKTEKEGTLT
4370	34738	A	4411	405	517	
4371	34739	A	4412	1	1197	MEISELNAKLSRSEKEKQNEIHK LQLEKLQHFQEEKNKEIALRN TIRDLEQRLSVGKDSHLKRENE QLKISADLIKEKLKSHEQEYKN NIAKLVSSEMIKEEGYKKEISK LYQDMQRKGRIKVTCEWTCSE RKTEGREPGVPVREPTGRSQSAE NEGSKTLAEINTKGTQSPAERIN KIDRLAARLTNRREKVQISSIR NKTGDIRTDTTEKQKFMQGYH EHLMYHKLLENLKEMDKFLEIY SPRLKREDIETLSRPITSDIEM KNLKIPPKLPKLINKFSKVSRYK INVHKLVALLYANSQTDNDQIK NSTHTIVAKKLYLGIYLTQDM KDLHKENSK/PLLKEIIDDTIKW KHIPCSWMSTTNIVKMTILPKTI YKFNAIIKIPPSFFAERKKQS
4372	34740	A	4413	1	190	MIQRKRASIGAPCAWVRKKEE EEEEEEEEEEEEEEEEEEEEK KKKKKKKERTTWLWGNPLT
4373	34741	A	4414	303	429	
4374	34742	A	4415	123	252	
4375	34743	A	4416	1	156	
4376	34744	A	4417	3	351	EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEE/KEEEEEEEEEEEEEEEE LGRLHGGSGKVRGLGFTENQQ GSTNRQHQREDNRKSKQKKIN NTKPEATESLIYNGITITAPA
4377	34745	A	4418	1	192	
4378	34746	A	4419	3	259	
4379	34747	A	4420	1	279	
4380	34748	B	4421	1	708	
4381	34749	A	4422	3	269	

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4382	34750	A	4423	1	322	MAGKQGRSEGAASWRLSSVLQ LNSQYFLQGAQQCTFLAATAW KKRKKEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKKKKKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKENPFSCF
4383	34751	B	4424	327	674	
4384	34752	A	4425	494	960	TRFYDHALHLHRRKGSTTVRSP PPLYFIGESKASALLAISLRWSG RSQPRSSVNQIRKAWGFRPKKG TEE/DERSGCPSDALESDDPMA YIHFTAEGEVTFKSILFVPTSAP RGLFDEYGSKKSDYIKLYVRRV FITDDFHDMPKYLNFVKGVV
4385	34753	A	4426	1	2539	VGGPRGWRCEDPNPVGVGGGGG SCDRRLGLETFRPHAMRALWVL GLCCVLLTFGSVRADDEVVD GTVEEDLGKREGSRTDDEVV QREEEAIQLDGLNASQIRELRE KSEKFAFQAEVNRMMKLIINSL YKNKEIFLRELISNASDALDKIR LISLTDENALSGNEELTVKIKCD KEKNLLHVTDTGVGMTREELV KNLGTIAKSGTSEFLNKMTEAQ EDGQSTSELIGQFGVGFYSAFL VADKVVITSKHNNDTQHIWES DSNEFSVIADPRGNTLGRGTTIT LVLKEEASDYLELDTIKNLVKK YSQFINFPIYVWSSKTETVEEPM EEEEAAKEEKEESDDEAAVEEE EEEEKPKTKKVEKTVWDWEL MNDIKPIWQRPSEVEEEDYKA FYKFSKESDDPMAYIHFTAEG EVTFK/SILFVPTSAPRG/LFDY GSKK/SDYIKLYV/RR/VFITD/DF HDMMPKYLNFVKGVVSDDDL PLNVSRETLLQHKLLKLVIRKKL VP*NRWDMIKK/SLDDKYNDT FWKEFGYQHSSLVVIEGPLRIR TRLAKLLR/FQSSHHPTDNTSLD QYVERMKEKQDKIYFMAGSSK KEAESSPFVERLLKKGYEVYIL TEPVDEYCIQALPEFDGKRFQN VAKGVKFDSEKTKESREAVE KEFEPLLNWMKDKALKDKIEK AVVSQRLTESPCALVASQYGV

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4386	34754	A	4427	2	622	PARAALGILTSHQSGFLKTSTSK ITSTAWKNKIDITMQSTKQYAC LHDLTNKGIGEEIDNEHPWTKP VSSENFSTSPYVWMLDAEDLA DIEDTVEWRIIRNVESLCVMET ASNFSCSVTSGCFSKDIVGLRTS\ ACWQQHCASPAFAYCGHSHFCC TGTA LR TMSSLPRESSAMW*KKKP ARTRLPRGKD LIYFGSEKSDQE TGTL L LPVSS
4387	34755	A	4428	2	1421	QHCSQKDTAELLRGLSLWNHA EERQKFFKYSVDEKSDKEAEVS EHSTGITHLPPEVMLSIFSYLNP QELCRCQSVSMKWSQLTKTGS LWKHLYPVHWARGDWYSGPA TEL\DT\EPDDEWVKNRKDESR AFHEWDEDADIDEESESAEESI AISIAQMEKRLLHGLIH\NLPY VGTSVKTLVLA YSSAVSSKMV RQILELCPNLEHLDLTQTDISDS AFDSWSWLGCCQSLRHLDLSG CEKITDVALEKISRALGNSGHL HQSGFLKTSSTSKITSTAWKNKD ITMQSTKQYACLHDLTNKGIGE EIDNEHPWTKPVSSSENFSTSPYV WMLDAEDLADIEDTVEWRHR NVESLCVMETASNFSCSTSGCF NHRPWSQNEYEQ LNYAKQLKE RLEAFTRDFLPHMKEEEEVFQP MLMEYFTYEELDKIKKKVIAQ HCSQKDTAELLRGLSLWNHAE ERQKFFKYSVDEKSDKEAEVS
4388	34756	B	4429	70	348	
4389	34757	A	4430	2	371	
4390	34758	A	4431	1	907	MGHRINIVCKIDAPCARQTRTF HPVVKTVEDCGRYPVSVIEFGKY EIQTWYSSPYQEYARNLAKEG KMGEREMSFVQQLPQMSGRCS LFRELSSCTYLLNTQPP/AVSIH FLAVWIILLVDGNMSKICYQNL CLLAKLFLDHKTLYYDVPEPLF YVLTKNDEKGCHLVGYFSKWT VLQGGWQVQGI AHFSRALT YLI CFSFPQEKLCQQKY NVSCIMIM PQHQRQGGFRFLIDFISFRLTIG ASFTQLRKQSMNSTEIPLLGD NGKSSPTFWQSLTSSPNAHFS LEAQLSILGHLFQSP

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4391	34759	A	4432	1	3468	MGKKQNRKTGNSKNQASPPP KERSSSPATEQSWMENDFDEL EEGFRLSNYSLEPEDIQTKGKE VENFEKNLEECITRITNKRNFKP TKIKRDKEGHYIMVKGSIQQUE LTIILNIYAPTGA PRFIQVLSDR QRDLDFHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHKSSTEYRFFSAPH HTYSKIDHLLGSKAFLSKCKRT EIITNYLSDHSAIKLELRKLNLTQ NRSTTWKLNN
4392	34760	A	4433	3	1900	FNKCMTLKFRLNKFSRINKIDTP LARLIKKKREKNRIDTIKNDKG DITSNPTIEQSTIREYYKHLVTN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTGSEIMAIINSLPT KKSPGPDGFTAKFYQRYKEELV PFLKLFQSIKEGILPNSFYEAS IILIPKGRDTTKNENFRPISLMN IDAKILNKILANRIQQHKKLIH HDQVGFIPGMQGWFNIRKSINV IQHISRTKDKNHMISIDA EKAF DKIQQPFMLKTLNKLGIKYLGI QLTRDVKDLFKERS/YEPLLNEI KEDTNKWKNPCSWVGRINIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRALIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITLHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLD PFLTPYTKINSRWIKDL NVRPKTIKLEENLGITIQDIGM GKDYMSKTPKAMATKAKIDK WDLIKLKSFACTETIRVNRQ PTKWEKIFATYSSDKGLISRIYN ELKQIYKKKTNNPIKKWVKDM NRHFSKEDIYAAKHKMKCSP SLAIREMQIKTMYRHLTPVRM AIIKKS GNN
4393	34761	A	4434	2	1932	

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4394	34762	A	4435	1	2571	MKAEIKMFFETNENKDTTYQN LWNTFKAMCRGKFIALNAHKR KQERSNTDTLTSQKELKKQEQ THSKPSRRQEITKIRAEMKEIET QKTLQKIKESRTWFEKINKIDR LLARLTKKRKNQIDAINKDK GDITTDPTIEIQTIREYYKHLYA NKLLENLEMDKFLDITYLPRLN QEEVESLNRPTGSEIEAIIINSLP T/KKCPGPDGFTAEFYRRKRGU LPNSFYEASIIIPKPGTDTTKKE NFRPISLMNIDVKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINIIQHINRAKDKNH MIISIDAEKAADFQIQCFMLKTL NKLGDGTYLKIIIRAIYDKPTAN IILNGQKLEVFPLKTGTQRGGCPL SPLLFNIVLEVLAIRAIQKEIK GIQLGNEEVKLSLFADDMIVYL ENPIISAPNLLKLINNSFKGSAY KIKVQKSQAFLYTNNRQTESQI MSELPTFIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIMKMAILPK VIYRFNAILIKLPMFTFFTELEKST LKFIWNQKRARIKSIKSNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNGTEPSEIM PHIYNYLIFDKPEKNQWGWKDS LFNKWCWENWLAICRKLKLD FLTPYTINKSRWIKDLHVRPKTI KTLLENLNTIQDIGMGKDFMSK

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4395	34763	A	4436	1	1965	MTLESEQTFVYAVTATQTGAK EGTRMSKSNVAGQQGDSGEKA LQKTYQKILREKESALEAKYQA MERAATFEHNRDKVKRQFKIF RETKENEIQDLLRAKRELESKL QRLQAQGIQVDFPDGESDSDNC TDVTAAGTQCEYWTGGALGSE PSIGSMIQLQQSFRGPEFAHSSID VEGPFANVNRDDWDIAVASLL QVTPLFSLWSNTVRCYLIYT DETQPEMDLFLKDYSPKLKRM CETMGYFFHAVYFPIDVENQYL TVRKWEIEKSSLVILFIHLTLPRI KYLGIQLTRDVKDLFKENYKPL LNEIKEDTNKWKNILCSWTGR NNVMKMATLPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR AHIAKTILSEKNKAGGIMLPDF KLYFKATVTKAAWYWCQNRD IDQWNRTEASEITPHIYNHLIFD KPDKNKKWGKDSLFWKWCWE NWLAIKRLKLDPFLLPYTKIN SRWKDLNVRPKTKITLEENLG NAIQDIGMGKDFMTKTPKAMA TKAKIDKWDLIKLSFCMAKET PIGVNRQLTEWEKIFAIYPSDKG LISRIYKELQTYKKKTNNPIEK LAKEMNRHLSKEDIYAANRHK KKCSSLVIREMQIKTT/MRYHL TPVRMAIIKKSGNNRCWRGCG
4396	34764	A	4437	300	476	PDLSLWLPITFFPSQLW*IQQL CVLELLFSRSIFVAFSVPFEFES WPALLGWGSSPG

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4397	34765	A	4438	413	1689	OKLYKPERIKYLGILQTRDVKD LFKENY/KLNEIKEDTNKRKNIP CSWVGRINILKMAILQKVIYRF NAIPIELPITFFTKLEKTTLRFIW NKKRVHIAKSIPSKKNKAGGIM LPDFKLYYKATTTKAWYLYQ NRDIDQWNRTEALGITPHIYNH LIFDKPDKNKQKGDLSFNKW CWENWLVICRKLKDAFLTPY TKINSRWIKDLNIRPKTIKTLLE NLGNTIQIGMGKDFMTKTPK AMATKAKIDKRDLIKLSFCTA KETNIRVNRQPIEWKIFAIYRS DKGLISRIYKELKQIYKKKTNN SIKKWAKDMNRHFSKEDIYAA NRHEKKWSPSLVTREMQIKTIM RYHLTPVRIMTIKMSGNNRCW RGYGEIGMLLHCWWECKLVQ ALWKTVWRFLKDLEIIPFPDV IPLGLIYPKDYT
4398	34766	A	4439	3	2404	
4399	34767	A	4440	1	1572	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKMSMA RELHDTCTSFNSRFDQVEERS AIEDQTNEINNGENGTKLENTL QDIIQENFPNLAQANIQIEIRR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKVLEVLARAI SQEKEIKCTQLGKEEVKLSLFA DDMIVCLENPVVSDHNVKLKLS NFSKVSVYKINVQKSHAFLYTN NRQTESQIMSELPFTITTKRIKY LGIQLTRAVKDFFEKQYKPLL EIKKDTNKWKNIPSCIGRINIM KMAIVPKVIYGFNAIPKLPRTF FTELEKTTLKFIWKKKGAKTILS IKNKAGGIMLPDFKLYYKATVT KIAWYQYQNRINQNRNRTETS EITSHIYNHL/IFDKPDKNKKWG KDSLFNKWCWENWL
4400	34768	B	4441	1	1558	

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4401	34769	A	4442	837	4329	TWKGTTDRSTRQKVNKDTQEL NSALHQADLIDYRTLHPKST YTFE/LAPHHTYSKIDHIVGSKA LLSKCKRTEIITNLYSDHSAIKL ELRIKNFTQSRSTTWKLNLL NDYVWHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGK FIALNAHKRKQERSKIDTLTSQ KELEKQEQTHSKASRRQETKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
4402	34770	A	4443	1	816	MRRDYPVKAFTSRKREQHVQK VPSKKSQRQVQRTERRFLETPD LLYQKEKDLLLISSSKKQPRPGI ERHYMMTQGSIHQEDVAILK/V YTSNKRASKYIQQ/TLEIKGKI/ AHPQIVGDFNTPTSTIDRTIRQQI SIEFYDTIKOWDLTDCRTGHPI TEYIFCSGAHLTFTKINHIQGP RILKRFRKRIEIECVLVKGCQA KNRKKEEDLQTY/WMLNIYGP YRSGSYAAIHRQETICSGQLSQ ALRDRFAMNAKLLLSLAHLW VIKLDPM
4403	34771	A	4444	87	307	
4404	34772	A	4445	1	534	MEESRGAKPPALLPGDATLPP GSLGARHPPEP/RPVGP/PPHQ TCPGPSACSSRPPEPRSSPGSPA RAPPAPPPAAPRCEPPLWLL LRVPCPGRSQWSWMTT*/I/SERP VQKRARSQGPRLPCLPLSPP TAPDRATAVATPPVLGPMSSW SPRRAGGPTRPCTALQALSIPA
4405	34773	A	4446	164	660	YPSGRRLREPADVADWDGME ESRGAKPPALLPGDATLPP/AP SGQLGTRPSPPSSRPSPHQTC PSACSSRRPEPRSSPGSPARAPP APPPAAPAPRA/SPRRPLAPRS ASVPAFSAAPPQWPEVGPSPCA LRRAMPRGPGPPPEPLVAEPG EDAAPTAGR
4406	34774	A	4447	1	417	

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4407	34775	A	4448	1	1802	MSYPADDYSEAAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIVEIKNFQYFHKTVS DLIDQKVVELQASRVSSDVIDQ KVVEIQDIYENSWTKLTERFFK NTPWPEAAEAIAPQVGNDVFLI LYKELYRHIYAKVSGGPSLEQ RFESYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSLVNLVHLSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLRLHSL GDYYQAIKVLNIELNKKSMYS RVPECQVTITYYVGFAYLMMR RYQDAIRVFANILLYIQRTKSM FQRTTYKYEMINKQNEQMHAL LAIALTMYPMRIDESIHLQREK YGDKMLRMQKGDPOVVEELF SYSCPKFLSPVVPNYDNPVHPN YHKE\PFLO\QLKGVF**SSSQ AQLS/TPIRSFLKLYT/TMP/VAK LAGFPGPSQSQEF/RIPGFFVFKQ QDERTSVVWTVRFSPAGW*NF SQASEVDFYIDKDMIHADTK VA\RRYGDFFIRQ\HKF/EELNR TLKEGWGQRPWMIFHTHFREP GFECIGQGSVFC

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4408	34776	A	4449	1	1722	MNIKAKILNKILANRIQQHIKKL IHHDHVSFIPRMQGWFIHHPIN VIHHINRTNDKNNHIIIDAEGA FDKIQHPFTLKTNLKDDMTVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPTIASKRIKYLGLQTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINVVKMAILP KVYIRFNAIPKLPMTFFTELEK TTLKFIWNQKRARIKSIISQK NKAGGITLPDFKLYYKATVTKT AWYWYQNRDIDQWNRTEIPSEI MPHIYNHLTFDKPDKNKQWGK DSLFNKWCWENWLAIJRKLKL DPFLTPYTKINSRWIKDLNVRP KTIKTEENLGNTVQDIGMCKD FMTKTPKAMATKAKIDKWDLI KLKSFCTSKETIIRVNRQTEWE KMAFIYPSDEGLISRICKE/LFKQ IYKKKNHPKWKADMNRRHS KEDIYVANKHMKSSSLVIRE MQIKTTMRHHLTPVRMTIHKKS GNNRFWRGCGETGMILLHCWW ECKLVQPL*KIVW*FLKDLSEI PSDSAIPLGIIHPKAYKSFYY
4409	34777	A	4450	1050	1147	PGEWHGQGSFRCWR*PLPQRC GHLLSCRWRT
4410	34778	A	4451	1	614	MEELVDEGLVKALGVSNFSHF QIEKLLNKPLKYKPVTNQNSL GTMQNRAGFPRDEDCLLQVE CHPYLTQEKLIQYCHSKGITVT AYSPLGSPDRPAWKPEDPSLLE DPKIKEIAAKHKKTAAQVLIRF HIQRNVVIVPKSVTPARIVENIQN TEHYKCYGLCVGPNLKKNLYP VDRM/WKNSCGQFVL*ISSHLE DYPFNAEY
4411	34779	A	4452	2	240	WMELESLSHFQIEKLLN/KPGL KYKPVNTQVNSIQFGSILEEGI VNMGGDSSMHVSAPEPPVGQ DVEAEDSDTDDPDPV
4412	34780	A	4453	1	1019	
4413	34781	A	4454	1	2028	

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4414	34782	A	4455	3	1045	DFTSENFSAAWYLIENHSNTSF EQLKMAVTNLKRQANKKSEGS LAYVKGGLSTFLEAQDALSAIH QKLEADGTEKVEGSMITQKLEN VLNRASNTADTLFQ/EKVLGRK DKADSTRNALNVLQRFKFLFN LPLNIERNIQKGDYDVVINDYE KAKSLFGKTEVQVF/KKYYAE VIEPRVEALRELLADKLLTPTST LHDQKRYIRYLSDLHASGDPA WQCIGAQHKWILQLMHSCKEG YVKDLKKGDFSSNVFQSGSAL RRVPDTPVRVLDSQFSRSALRSV PDTVQVLDQFSGSALRRVPDT VRVLDGQFSRSALRSVPDTPVRV LDKCHCSPAkvVMNAVITFTG
4415	34783	A	4456	1	440	MQRNLARAFSPGIKKIKMMCL GNSEKDWPKFRGVGEDAGLLA ARECGALLVIRHLINAVRAIVP NKSNNIILVLQHFDCVNDK/TV QAFMEGSASEVLKEWTVTGKK KLLQGEELARLPFITGGSGSC YSSSTLAVEECRVLA
4416	34784	A	4457	1	276	MEDEMEGLTEAGFRRWVTTNS AELKEHVLVTQCKEAKNLDKRL EELLSRITSLERDISDQME/RELC EAYTSINSQINQAEERISEFEDH LAEI
4417	34785	A	4458	3	361	EMVHRKKKAVHRTATADDDK LQFSLKKLEVNNVSGIEEVNMF TNQGTVIHFNAEMPANSFTITG HAETKQLMEMLPSILNQLGAH CLTSLRRLAEALPKQSVNGKAP LATGEDDDDEVPA
4418	34786	A	4459	1	475	EDSGGGGKFPGARQGGTGQR RRRKAMRRTGAPAQADSRGRG RARGGCPGGEATLSQPPRGGT RGQEPQMKETIMNQEKTRHTC RAQVIRIGGKGTARRKKKV VH RGAAS/ADDKKLQFSLKK/LGV NNISGIEEVNMF/FTNIQGTSGST FNNP*KFGQISWPANTFHHLQ HAEDKGS*QEMLAQHLKPSLG ADSLTSLRRLAEALPKQSV DVGK APLATGEDDDDEV/VDLV/ENF* *RLPRNEANLNSQLLKIKP
4419	34787	A	4460	57	820	
4420	34788	A	4461	1	1527	

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4421	34789	A	4462	8	327	LIWQLTFTKTIKS/CEEYGVKIVST KAILDKNTNQCKGMCKGIRTL KSCLCYLINGSSIVEVQKRLAY AGTLEPSLVHQVYSELSYYKLP GTQVVRHAEVLRMQDSSE
4422	34790	A	4463	2	573	WMEGREKWRGRRKDGRRKEGR KEGRKERREREKGRERK/GKE RKGGKRGKGRKGRKGRER KGTEGKGTEGKGKRGKGEKG GKERKGRKGRKGRKGEKG KEQKGKGRKGRKGRKGRKGRK ERKGRKGRKGRKGRKGRKGRK GKGRERKKGEGGKEGRKERR KEGRKGGKFSNNGMVMEEMQ
4423	34791	B	4464	1	1344	
4424	34792	A	4465	3	373	
4425	34793	A	4466	1	3864	MQWEEAEKDPSGSCVFQRPVP ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHPOP CESRPPVPPEYEVTVLRSGQTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLKGFSDN
4426	34794	A	4467	3	415	
4427	34795	A	4468	396	676	LCFFPYAERPDLQFLC*DLCARSP YLLQAQKYLQEF*AIPHLDDQT EPPDPSVSFYLLDCTLNCTAQH KTC*KKSIGL*EQNQQTLSIPY SHT
4428	34796	A	4469	1	858	MEWEDNPLELGRVAKLLSD HSQTPGLIQMFLFLSLRKSPL VCLSYLFNFRFTLESEVQHLG AITLTAWPKIFLGIREAKSPRS ENTRLATILEAGHRHLGTSVSK DHPVTFWRPRRDQLQSDLKQIKI DLGKFSNPDGYIDVLQELGQS FDLTWRDIMLLNQTLPNERS ATTAAAREFGDLWYISQVVAAV AGLVSEAVKIIQGLTVWT/SHD VNGILTAKGDLWLSDNHLLKY QALLLEGVPLRLRTCATLPAT FLPDNEEKIEHNCQQVIAQTYA
4429	34797	A	4470	918	1939	

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4430	34798	A	4471	3	2693	PQVCLTIESQEVNCLLDAGAAF SVLLSCPGQLSSRSVTIRGVLGQ PVTRYFFQPLSCDWGALPFSHA FLIMPESLTPLLEREILVKAGAIL HLNIGEGTPICRLLFEEGISPEV WATEGQYGGAKNAHFVQVKL KDSTSPYQRYPLRPEAQORL QKIVKDLKAQGLVKPYSSPCNT PILGVQKPKRQWRLVQDLRIIN EAVFPLYPAIPSPYLLSQIPEEA EWFTVLDLKDAFFCIPVHPDSQ FLFAFEDPSNPTSLTWTVLPO GFRDSPHLFGQALAQDLSQFSY LDPVLQCMDDLLAARSETLC HQATQALLNFLTTCGYKVKP KAQLCSQQVKCLGLKLSKVTR ALSEERIQPILAYPPYKTLKQLR GFLGITGFCRIWIPRYGKIARPL YTLIKETQKANTHLVRWTPEAE AAFHALKKALMQAPVLSLLTG QDFSSYVTKNKQTKKKK*IA LRVLALV*GTSLQPVAYLSKKT DVAAGWPHCLWVMAAIAVLI SKAVKMIQ*RDLTWVWTHSDVN GILTAKGDLWSDNHLKYQA LLEGPMLRLCTCAALNLDLFL PHNEEKIEHNQQVIAQTYATR GDHLEVPLTDPNPNLYTDGRSF VEKGLQKVGYA VVSDNGILES NPLTPGTSQAQLAELIALTWALE LGEGRVNIYDTSKYAYLVLIH AHAVIWREREFLTSEGTPIKHQ
4431	34799	C	4472	11	1639	
4432	34800	A	4473	95	2539	
4433	34801	A	4474	345	768	PRGARSTRCLPVERR/CDGLQD CGDGSDEAGCPDLACGRRLGSF YGSFASPDLFGAARGPSDIHCT WLVDTQDSRRVLLQLELRLGY DDYVQVYEGLGERGDRLLQTL SYRSNHRPVSLEAAQGRLTVA YHARARSHPLMNE
4434	34802	A	4475	47	563	RLRFVFTGAFHALSFLSFVV LCCTYLKGLKVARFHCKRIDV/ MHHADARAAGGPAPQCAGTLS IEEQKRRQRATKKISTFIGTFL VCFAPYVITRLVELFSTVPIGSH WGVLSKCLAYSKAASDPFVYS LLRHQYRKSCKEILNRLHRRSI HSSGLTGDSHSQNLVPSE

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4435	34803	A	4476	1	332	ERGRQEMSAKLRPPAEPCCVPA RISP*RPS*RQ*MERRCPPWRCS PMP/CFREHALQVRCGPTSA DCGRDPLFSHPKPLPHVPVDIG WVATAGAQRSSPVFSSLFVW
4436	34804	A	4477	297	943	TGSWGGGGADQLRPALTALM PPDNRFGENTPAAPANGHCAP EPDITLVQDHSSELPIGAAATMA HEIGHSLGLSHDPDGGCCVEAAA ESGGCVMAAAT/GVRGHPFPRV FS/SCSRQLRAFFRKGCGACLS NAPD/TRTPGAAALCGNGFVEA GEECYCVS/GQECRDLCFAHN CSLRPGAQCAHGDCVRLVR/ CMEGSGSHQLPRLVPGGDSAEI LM
4437	34805	A	4478	1	836	MGPLTRFDVKIEFSLEEWQCLD TAPGNLYRDMLENYRNLVFL VMCSHFAQDVWPEHSIKDSFQ KVILRTYGYGHENLQLRKDH KSVDAKVVYKGGYNGLNQCLT TTDSKIFQCDKYVKVFHKFPNV NRNKIRHTGKKPFCKNRKGSF CMLSQTLQHKKIHTREYSYKCE ECGKAFNWSSTLTKHKIHTGE KPYKCEECGKAFNRSSNLTKH KIIHTGEKPYKCEECGKAFNRS STLTKHKRIHTEKPYKCEECG KAFNQFSILNKHKRIHMGR
4438	34806	A	4479	1	588	MLGKVQQEQETIAKDLVVTKY KMGCGT/DIANRVLRLSVEASS SGGQDYILKEGDLVKIDLGVH VDGFIANVTHTFVVDVAQGTQ VTGRKGDVIKAAQLCVEAALC LVKPGNQNIQVREAWSKVALS FNCMPIEGMLSHQLKQHVIDGE KNIQNPTDQKKDHEKAEFEV HEVYAADVLYSSGEGKAKDAG
4439	34807	A	4480	85	561	LSHCLPLQTTEVGGFGNLLGY WIACSGCVLSTGMLSHQLKQH VIDGEKTIQNPTDQKKDHEK AEFEVHEVYADVLYSSGEGK VRRVPELAKRGD*ECSPDQMLL KLLFQAKDAGQRTTIYKRDPSK QYGLKMKTSRAFFSEVERRFD AMPFLRY

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4440	34808	A	4481	1	1408	GTSAPQPARSALLALACLPA LARAFAARPLEDRGSDHSLW LGRETEAAAAQKRGCSGGS KMSGDEQQEQITVD/DSLVT KYKMGGDIANRVLRLSEASS GVSVLSLCEKGDAMIMETGK FKKEKEMKKGIAPTSIS/VN VCHFSP/L*KSDQYILKEGDLV KIDLVGHVVDGFIANVAHTFV DVAQGTQVTGRKADVIKAAH L\CAEAALRLVKPGNQNTQVT EAWNKVAHSFNCTP\EGMLSH SLKQHVIDGEKP*FQNPTDKQK RAHEKADFEVHDVYAVEGLV KPQERARPKDAGQRTTIYKRDP SKQYGLKMKTSRAFFSEVERRF DAMPFTLRAFEDEKKARMGV VECAKHEL/VWQPFNVLYSGRE GDFVCPVLNFTVL\MPNGPML ITSGPFEPDLYKSQMEVQ\DAEL KALLQSSASRKTQKKKKKKAS KTAENATSGETLEENEAGD
4441	34809	A	4482	3	190	
4442	34810	B	4483	1	588	
4443	34811	A	4484	1	1312	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLANIGQKED FEEARKKALKGAKKVFIEDVS REFVEEFIWPAIQSSALYEDRYL LGTFFARPCIAKQVEIAQREG AKYVSHGATGKGNQVRFELS CYS LAP\QIKVIAPWRMPFYNR FKGRNDLMEYAK\QHGIPVTP KNPWSMDENLMHISYEAGILE NPNQAPPGLYTKTQDPAKAP NTPDILEIEFKKGVPVEGGPTF KDG\TTHQTFL\ELFMYLNEVA GKHGVPYLTWENRFHWELK SRGILRRPQAG\TILYHAHLDIE AFTMGGDRAQIPNQGLGFEFVE LGVYRFSGTAPCELVGPCLRQ SPQERVEGKSAGVPSLKGPRCT SLQPEVPHCSLYNEIELVKHGT CQGDYE\PN*LPPGIQTSLKA EGNYHRLPRAKVTAQIRPRVQ
4444	34812	B	4485	47	482	

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4445	34813	A	4486	2328	3435	KTTTLEDNLGNTIQDIGPKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKRNVKHDESLRS HYE*WGMLTDCVVMRDPNTK RSRGC GFV TYATVEEVDAA'TN ARPHKVDGKVVEPKRTVSRED SQRPGAHLTVKKIFVGGIKEDT GGFAFVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQGRSGRGGGFGGNENFG CGGNFSGHGGFGGSHDGGGGYG GSGDGYNGFGNDGGYPGGPG YSGGSRGYGSGGQCGNQDSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNQY SNFGPMKGGNF/GRRRSGP*GD GGQYFAKPPNHSGYGSSSSSS
4446	34814	A	4487	1	762	
4447	34815	A	4488	3	333	
4448	34816	A	4489	1	1676	MRDPNTKRSRGFGV TYATVE EVDAA MNTTPHKVDGRVVEPK RAVSREDSQRPGAHLTVKKIFV GGIKEDTEEHLRDYFEQYVKI EVIEIMTDRSGGKKRGFAFVTF DDHDSVDKIVIQKYHTVKGHN CEVRKALPKQEMASASSSQRG RRGSGNFGGRGDGFGGNDNF GRGNGFSGRGGFGGSCGGGY GSGDGYNGFGNDGSNF*G/GG SYNDSGNYNQSSKFEPMKGG NFGGRSSGPYGGGQYFAKPQ NQAARCVAAARWLFRTAERLVF LQKFPPWAVVEVTVVIVAAPA AATATTRDGGGCSRNCNPEVF PELLGCPNRRGPPGVREKQQQ TNSKSTRRQEITKTIAELKEIET KTLQKINESRSWFYEKINKVDR LLDRLIKKKREKSQIDA KNDIG DIVTDP AEIQT TIKEYYKRLYAN ELENLEEMDKFLATYSLHSLNQ EEVESLNKPVTSSEVAVTNSL PTKSPGPDGFTVLLEVLA PAIR QEKEIKHIPGREEVKLSLFADD VIVYLENPIVSAQNLLKLSNFS

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4449	34817	A	4490	1	1445	MKCLKFINHKEILEASERKQAE SLDFPFKKLRWHLCGEWIEER DESRKSETIFKDLFKVPVLKETI YYKFYGGPPVYQIETVYFMALSP PKSKQFDKTKQNNNNKKTQF VIVFFKTDEHLSARGRRRSIVK VSLLPVAVIGLKSFLKPKDQLR KLFVIGGLSFETTDESLRSHFEQ WGTLDTCVVMRDPTNKRSGF GFVTYATVVEEVDAAAMNAPH KVDIGRVVVEPKRAVSREDSQRP GAHI/TLVKKIFVGGIKEDTEEI HLRDDYFEEIILNSMEKIEVIEI MTDRGSGKKRGFAFVTFDDH DSVDKIVIQKYHT/VGNHNC VRKALSKQEDG*VLHPAQRGA RSGSGKLLVVGRGRWFSVGM NFGVRGGNFSWSVAFGGTRGA GGGYGVQWGMAYNGFGNDGA SNFGGGGSYNDFGYNYNQISS NFGPMKGGNFG/GRSSGPYVG GGQYFAKPRINQGGYGGSSSA
4450	34818	A	4491	134	612	TVLNSMSVLAISTLLKITGELL QSFQDGLLWNLVIGIRIDGLSP KVRKVLQLRLRQIFN/GTFVK LIKVTVNMLRTVEPYIAWGPVN LKSVNELIYKHGYGKISKRIA LTDNVLIARSLGKYGIICMEDLI YEIYTVGKRFRKEANNFLWPFKL
4451	34819	A	4492	1	1983	
4452	34820	A	4493	1	1527	
4453	34821	B	4494	1	2211	
4454	34822	A	4495	1	2478	
4455	34823	A	4496	2	1544	
4456	34824	B	4497	1	2151	
4457	34825	A	4498	1	744	
4458	34826	B	4499	1	2172	

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4459	34827	A	4500	1	2535	MKSGHPEKEQDNDSDVQETREIT IRGLLCTALMRHSTGAIAIYLGVL LSGSASLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETIIVLPSNVIN FSQAEKPEPTNQGQDSLKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIYVLGLDICRPFFVSRVSEE GRMGQRGEEDANSLDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAFAFDKIQQHF MLKTL SKLGDGTYLKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPSPLLFNIVLEVLAIRIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPVSDQNLKLSNFS KVSQYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRKIYLG QLTRDVKDLFKENYKPLLNEIK EDTNKWKNI PCSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKF1WYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNLYFFDNPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPF LTPYTKINSRWIKDL NIRPKTIKTL EENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLKSFCGTGKETTRVNRQPT
4460	34828	B	4501	1	1785	
4461	34829	A	4502	1	1415	
4462	34830	B	4503	1	3262	
4463	34831	A	4504	1	278	

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4464	34832	A	4505	3	2528	ENKDDTTYQNLWDAFKAIVCRG KFIALNAHKRKQEKSKIDTLTSL QLKELEKQEQTHSKASRRQEIT KIRAELEKIDTQKTLQKINESRS WFFERINKIDRPLARLIKKKREK NQDITKKNCKGDITDPTETIQT IREYYKHLVANKLENLEEMDK FLNTYTLPRLNQEEVESLNRPT GAEIVAIHSSLP/T/K/KSPGPDGFT AEFYQRYKEE/LEKEGILPNSFY EASIIIPKPGRDATKKENFRPIS LMNIDAKILNKILAKRIQQHIKK LIHHDQVGFIPGMQGWFNIRKSI INVIQHINRTKDKNHMIIIDAEK KAFDKIQQRFLKTLNKLGDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTQGCPLSPLLFNIV LEVLAIRAEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLSINFSKVSQYKINVQKS QAFLYTNNQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLEKIKDDTNKWNIPCS WVGRINIVKMAILPKLPMTFTT ELEKVTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNR EPSEIMPPYNYLIFDKPEKNKQ WGKDSLNFNKCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTEENLGITIQDIGL GKDFMSKTPKAMATAKIDK
4465	34833	B	4506	1	5401	
4466	34834	A	4507	1	5271	MNIDAKILNKILPNQIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRAKDKNHMIIIDAEK SFDKIQQPFMLKTLNKLGDG TYFKIIRAIYDKPTANIILNGQKLE VFTLKTGTQGCPLSPLLFNIVL EVLAIRAEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKQISNFSKISQYKINVQKSQA FLYTNNRQTESQIMSEIPFTIAL KRIKYLGIQLTRDVKDLFKENY
4467	34835	B	4508	924	3423	
4468	34836	A	4509	525	673	RDSWGTCPSVSGAGKVDWPPSS *HHR*HQWCCGMPHQLSTKE NISIKDHLTEKKRKGAV*RII

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4469	34837	A	4510	25	1766	GTCQFAAMNVVFAVKQYISKM IEDSGPGMKVLLMDKETTGI MVYVTSQSEILQKEVYLFERID NREIMKHLKAICFLRPTEKENV YIIQELRRPKYTIYFIYFSNVISK SDVEVIGLKLIEQEVVAEVQEF YGDYIAVNPFLFSI.NILGCCQG RNWDPAQLSRTTQGLTALLLSL KKCPMIRYQLSSEAAKRLAECV KQVITKEYELFEFRRTTEVPPLLL ILDRLDDAITPLLNQWTYQAM VHELLGINNNRIDLSRVPGISKD LREVVLSAENDEFYANNMYLN FAEIGSNIKNL.MEDFQKKPKPE QQKLESIGSMKA\FVENYPQFK KMSGTVSKHVTVVGELSRLVS ERNLLEVSEVEQELACQNDHSS ALQNIKRLLQNPKVTEFDAARL VMLYALHYERHSSNSLPGLM MDLRNKGVSSEYKRLVSAVVE YGGKRVGSDLFSPKDAVAITK QFLKGLKGVGNYVTQLQPPFL HETLDHLIKGRLKENL.YPYLGP STLDRPQDIIVFVIGGATYEEA LTVYNLNRITPGVRIVLGGTTV HNTKSFLEEVLASGLHSRSKES
4470	34838	A	4511	1	1335	MAPVTMMGYRSGMKGILADV QLQVGPWPWLHLVVIAPVPEC ITGIGIFSSWGSPDVGPPLYDIR AIMWGLAPAEWTWILGNNHR RFLAQLKPRVIMQDFSNVISKS DVKSLAEADEQEVVAEVQQVI TKEYELFEFRRTTEVPPLLLILDR CDDAITPLLNQWTYQAMVHEL LGINNNRIDLSRVPGISKDLREV VSSAEIDEFYANNMYLNFAEIG SNIKNL.MEDFQKKPKPEQQKL ESIADMKAFVENYPQFKKMSG TVSKHVTVVGELSRLVVSERN LAGRFSEVEARNWACQNDHS SALQNIKRLLQNPKVTEFDAAR LVMLYALHYERHSSNSLPGL MMDLRNKGVSFWRKYSKARVL AVVEYGGKRVGSDLFSPKDLA VAITKQFLKGLKQGEIVNCVLA AANVYIKQLPLSIQPSASLNGCI SLEKKPLVSTQRN
4471	34839	A	4512	1	816	
4472	34840	A	4513	26	257	
4473	34841	A	4514	56	236	

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4474	34842	A	4515	170	373	HSPRGSTASF/CEVSETKNPPID IPATREAEGLRSRLAVYSTRDS PCVACSGSYTQAQGLGRKFQ DP
4475	34843	A	4516	262	358	
4476	34844	A	4517	2298	2556	NHKNPRRKPRQYHSGHRHGG LHD*NTKSNGTKSNGKSNQ* QWDLINLKSFCTAKETTIRVNR QPTWEKIFTIYPSDKGLISRI
4477	34845	A	4518	801	944	DQEPINSRHILATQMGSPITKQ SNPGV**KECGFSCSPRVRYL VS
4478	34846	B	4519	85	660	
4479	34847	A	4520	693	827	
4480	34848	A	4521	272	339	
4481	34849	C	4522	532	2754	
4482	34850	B	4523	1	519	
4483	34851	B	4524	266	935	
4484	34852	A	4525	1	1584	
4485	34853	A	4526	1	723	GALPNGDRGRRKSRFALYKRP KANGVKPSTVHVISTPQASKAI SCKGGHSISYTL.SRNQTVVVEY THDKD.TDMFQVGRSTESPIDFV VTD.TISGSQNTDEAQITQSTISR FACRIVCDRNEPYTARIFAAGF DSSKNIFLGEKAAKWKNP.DGH MDGLTTNGVL.VMHPRGGFTEE SQPGVWREISVCGDVYTLRETR SAQQRGKLG.LQTGDMAENT/T VHALPSNCMVWRRS.QTRQOIS
4486	34854	A	4527	1	335	
4487	34855	A	4528	328	871	DCGGGRARTAI.FAGAAARAADN KKCAGARRALGRARGCSATAR PRRRRRRPRGLAPPRPARPPPG GMSYKPN.LAAHMPAAALNAA GSVHSPSTSMATSSQYRQLLSD YGPPLSGYTQGTGNSQVPQSKY AELLAIIEELGKEIRPTYAGSKSS MERL.VKRGIIHARGL.VRECLAE TERNARS
4488	34856	A	4529	1	653	MAGPAESSPQGAHPNSPFALQH HSSLTVKPLHRQNVIIHQVAG QENRRGHQAGSSTSPQPLEALK RPNLRAPFHSQSRRLIP.PAGNP TPGAAAPADPSTQRRDRWGCA LPMPRV.AAGSAHHQAGPTAA AQHRTPVALFSPPLSL.VYGGQQ RKESETPIVPTPPARARGWTET GVEHV.PAYNRTRAPEKCDI/SV PSPHSSFDAETSHPRHISPCPG

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4489	34857	A	4530	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQQRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVIAHDVDPIELV VFLPALCRKMGVPYCIKGKAR LGRVLVHRKTCTTVAFT
4490	34858	A	4531	1	2073	MKPCAHSWNAELSRNIHRHSFN LVMVAASQVAVSQLLGSYEILL LVSIELMFCFGLGYFFIPMQEW PNTYGERVFDVDESSVFKWNH KCLHKTEAERDYTEKKRLKLCG HKPGNAVGGQKLEEARNRFFT RAPGGSAAALPTLRFQPSDTRF LLASRTILTFETKNPSELAERLR SVCNGQSNAYARLLEYRLNAL RGLWNAQRQLALEEQHERESS GDEETLALLKRGQLLQQPEQAP FTSRMGLLLVFLIQSQSRDTPS LCNITAIEVLLNCLRDCQPLSLT KEPADCLNGIETLLCSWLEETS DTGRHIFPHKQKENAAAALVAL ACARGFVYCRNEEPEPGWVAF GSGSLLHRPVSFDNPKHSLFQVI DQNTLQVCQVPMANHLPIG STMSTVHLSDDGTIFYFIWSPA SLNEKTPKGHSVFMDFELVTL KGKKAKGKKVAPAPAVVKKQ EAKKVVNSLFEKRLDIQPKRELT YFVKW/PRYVRLQQQRILYKQ LKVPAINQFTQALNCQTVTQL LKLAKHYRPETKQKKQRLLA QAEKKAAGKGGVPTKRPPALR AGVNTITTLVENKKAQLVIAH DVDSIELVFLPALCKMGVPY CIKGKARLGRVLVHRKTCTTVA FTQVNLEDKGALEKLEVGIRTN DNDRYDEICCHWGGNIGPKS VACIAKLEKAKELATKLG
4491	34859	A	4532	1	2565	
4492	34860	A	4533	1	644	MPKGKKAKÉKKVAPAPAVVK KQEAKKVVNPLFEKRPNFNGT GQDIQPKRDLTHFVKWPCYIRL QQQRTILYKWLKVPPEINQFTQ APDSQTATLLKLAH/KYRPET NQEKKQRLLARAKKAAGKG DIP/TSKPPVLRAGVNTITTLVE NKKKAQLVIAHDVDPIKLVFL PVLCHK/MGVPYCIKGKARLG HLVHRKTCTTVTFTQVNSDK

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4493	34861	A	4534	1	931	KSIQKGLKMCSSSLPPSKMP KGKKAKGKKVAPAPAVVKKQ EAKKVVNPLFEKRPKNFGIGQ DIQPKRDFTRFVKWPRLSGC MRKRAILYKAG*KLPPAINQF HPGPWDPANKLLQLL*AWAHK YRPMETKAKRKKQRL/LARA/E KKAAGKGDVPNERDPPV/LRA/ GVNTVTHLWWRNKKAPAWVV IATRRWIPFEL/VVFLPALCREK WGSFYCIKGKARLGR/LVHRR PCTVTGFFTR*NSKDKRLLA* AGLEAIRTQFTIDQIRWSGRH/ WGGNVLGPKSVARIRQASKR QRLKELATKLG
4494	34862	A	4535	3	227	
4495	34863	A	4536	1	338	
4496	34864	A	4537	1	352	
4497	34865	A	4538	2	368	
4498	34866	A	4539	3	468	
4499	34867	A	4540	2	790	PRGRNRRRKTQERRMTLNESP EKIGKWIECYGHPASKLVEIYI HTVFVEDKLSICRSFNKKADGS WRMTVDYCKLNQVVTAIAAAI PDVVSLLQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELDGCFSLPRDTTLVHYI DDIMLIGSSVQEVENKDLLLVK DKLLHLAPPTTKEEVQHMVGL FGFWRQHPIHLGVHLQPIYRV RKAA/SFEWGPQEKAQQVQ AAVGGKQSENNLGHQKSPGLW
4500	34868	B	4541	179	1219	
4501	34869	A	4542	1706	2517	THLLVPGMQPLTWQMPSPFLS ISPTRSNLPSAAIPVIAQWA/HE QSGHGGRDGGYTWAQQHGLA FTNTDLATVNAKIGFAYPVCDA SAKTTIRGLLECLIRCDGPHSIA SDQARIHRSRNQEVVEVAPLT ITPSDPLAKFLLSVPTLRSAGL EVLVPGEGMLPPGNTRTIPLNW KLRLPPGHFGLLLTSLQEAKNG VTVLAVGIDLDYQDEISLLHN GGKKEYARNTGDPGLGRLLVLP CPVIKINGKLQPNPGGTTNGS DPSGMKV

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4502	34870	A	4543	3	367	DLWPFTRVTVH/WGKANDQTF QGLLDGTGSELTLPYGPKRHCC PPVKVRVYGGQTDGWSRMTV GYHKLNQVVTPIAAVDPDVVS LLEQINTTPAIKVVVHSSIPSSN GSGVYVIRLEQVLKAQ
4503	34871	A	4544	2	541	
4504	34872	B	4545	1	681	
4505	34873	A	4546	2	1091	PRGRNRRRTFQERRMTLNESP EKIGKWIECYGHPPASKLVEIYI HTVFVEDKLSICIRSFNKKADGS WRMTVDYCKLNQVVTAAIAAI PDVVSLEQINTSPDTWYAAID LANALFSIPVHKGYINSLALCH NVIWRELD CFSLPDITL VHYI DDIMLIGSIKFLGVQWCGACRD IPSKDPADPMVLEVSADRDV WSIWQALIDESQQRPLGFWSKS LPSSADNYSFERQLLAYWAL VETERSTMGHQVTMLPELPVM NWVLSDPSSHK/ANGLAGWSG TGKKHDWKIGDKIWRGGMW MDLSEWSK/DVKIFVSHVSAH QRVTSAAEEFNQVDRMTRSM DTTQPLYPPTPVIAQWAHE
4506	34874	A	4547	1	1236	
4507	34875	A	4548	1	1467	GEKGNQDQTFERKLLDTGSELM PLRVVPIPTSLFNSPIWPVQKTD GSGRMRVDYHKLNQVMTPTA AAVDPVVSLEFINTFLGTWYA AIDLANALFSIPVCKAHQKQFA FSWQGGQYTFVLPRYINCLA LCHNLIQRDLDHFLLPQGITLV HYIDSGPFK*PEAASFEGPEQ EKALQQVQAQAAALSIGPYD PADPMVLEVSADGDVWWSL WQAPKGESQWRPLGFWSKALP SSTDNYSSTDVQLYTDSWAVA SSLAG*SGTWKHKHWKIGDKEI WGRGMWMDLSEWSKTGKIFV SHVNAHQLVTSAEEDFNQVD RMTRSDTTQPLSPATPVVAAQ WAHEQSGHGRNEGYAWTQQ HGLPLTKADLTATAECPIQCC QRPTLRPRYGTTSQGDQATC WQVDYIEPLPSWKQRFLITGI NTHSGYGFAYPNCASAKTTH GLIACLIHCHGIPHSIASLYRER GTHFTDKEVQQWAHAH

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4508	34876	A	4549	2	1602	NLSPILPQDLWPFTRVTVHWGK GNDQTFQGLQDTGSELMIPGD PKRHCSPPVKVGSYGGVINGV LAQVRLTVGTGPRTHPVVIS VPECIIDIILNSWQNPHIDSLTG RVKAIMVGKAKWKPFPELLPIK IVNQKQYRIPGGIAEISATIKDL KDAGVVIPTLPFNSPFWPVKKT DGSWRMKVYCKLNQVVTPII AAVPDV/VVSLLEQINTSPGTW YAAIDLNAIFSI PVHKAHQKQ FAFSWQGHQNTFTVTILLHIH KVGHAQQHSIIKWKWYIHDGA RAGSEGTSKI.NEEVPQMPMVT TSAALPSLPRPAPMASWGVLV DQLTEEEKTRAWFTDGSARYA GTTQKWTAAALQPLSRTSLKG SGEGKSSQWAEQLQAVHLVVHF SWKDKWPDVRLYIDSWAVAN GLAGWSGTWKKIIDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI

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4509	34877	A	4550	1	1891	MLSSTQNAGGSYQVRVGA.LDT QEWWKGEVSPRTLNV.DGRAL VSVANTHGTDRPAYTLNPQSR DQRSGVITLGYKRPLEREDLFE LKESDSFCTACPIFEKQWRKEV LRNQERQKVKALNKLDEALCP GIII.TQSTDNANLFQKQPHRHT QTSGRWQIIIFCEHSSDFGWNG YGYAVALLVVVFLQTLILQQY QRFNMLTSAKVKTAVNGLIYK KLGWSGKVS.WLILHDVGHGIM EGYIAWGGSDVRITWEKKST EMRTRPAQKMALLLSNVSRQK FSTGEIINLMSATHGLDSKPQSP LVCPSFNPNGRISPLARAGLAD HYRVTHLQILKLYAWEPSYKN KIIKIRDQELFEQKSARYLTVFS MLTLTCIPFLT.KISLGRLEDFLN TEELLPQSIETNYTGDHAIGFTD ASFSWDKTGMPVLKESIRIRIEQ VLNQSLSFETVDYPGSVAYVSQ QAWIQNCILQENILFGSIMKKKEF YEQVLEACALLPDLEQLPKGD QTEIGERAVNISGGQQRHVSLA RAVYSGADVLLDDPLSAIDV HVGKQLFEKVIGSLGLLKNRTH ILVTHNLTLPLQMNLIIVVMKSG RIAQMGIYQELLCKTKNLTNFT KSSVNNKKVGEWEESGRGS
4510	34878	A	4551	2	542	LTSAKVKTAVNGLIYKKVSLAT LCVYFLLDERJILAPKVFTSMS LFNILRIPLFELPSVISAVVQTKI SLGRLEDFLNTEELLPQSIETNY TGDHAIGFTDASFSWDKTGMP VLNRGSEAYVSQAWIQNCIL QENILFGSIMKKKEFYEQVLEAC ALLPDLEQLPKGDQTEIGERV
4511	34879	A	4552	1	667	IETNYTGDHAIGFTDASFSWDK TGMPVLKESVAYVSQAWIQ NCILQENILFGSIMKKKEFYEQVL EACALLPDLEQLPKGDQTEIGE R/GKETAVNISGGQQRHVSLAR AVYSGADVLLDDPLSAIDVH VGKQLFEKVIGSLGLLKNRTSH SVCHYTLLAVPHLLEVLQTLGN FIQSLGFNYHEYANNSNAYIVN LDLFPFGQTCVYKLLSPIRCLIC
4512	34880	A	4553	201	336	QQTPGKAVHAPFIADQSLT*EL VSVFPQQLFPYRR*DSHSGKS
4513	34881	A	4554	3	515	

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4514	34882	A	4555	1	852	MPCTTSGLDKVPSTSKKALTRY GYGSLTLDFSGSIIPCKMCLSPS TRIVRPSQPRGTEDPDETDTEF VNSDESFLLEGTASPPVAVASP PRPMLPSAFPPLSEDINPVLPEA TVLASPEVVAKQTHVDSPRKPL STFLFASRPVTKLSRQTPGGE VDSVTCEEKTDGPWRKTVDYC KLNQVVTPIAALVPDMVSLLV QINTSSDTSYAAIDLAKAFFSIP VYKAHQKQFIFSWQAQYVTF VLPQGYIISPALCHNLIR/DLD HFLLPQDITLVHYIDDRL
4515	34883	B	4556	288	327	
4516	34884	A	4557	51	598	LFGGCHTSGGLAVRVPMPRG SRSRTRMAPSASRAPLK*ELE PRQAQVAQPPAAAPSAVGS AAAPRQPG/LFMAQMATTAG VAIVGCCGGHTLGHGVTGGLS VGGKLI*ALRRP*HQFNQGSF RGTAQAKHSKQPALPLLWRIKT SFREVVPPEPRVTIQGFCGFP RLLETVPDL
4517	34885	A	4558	1	10434	MTVIRSGIAYILHLKSYDVNIQT GSNACNQPTHNGDCSHFCFPV PNFQVCGCPYGMRLASNHLT CEGDPTNEPPTQCGLFSFPCK NGRCVPNNYLCGDVDDCHDNS DEQLCGTLNNTCSSAFTCGHG ECIPAHWRCDKRNDKVDGSD HNCPTHAPASCLDTQYTCDNH QCISKNWVCDTDNDCGDGSD KNCILNCTASQFKCASGDKCIG VTNRCDGVFDCSDNSDEAGCP TRPPGMCHSDEFQCCQEDG
4518	34886	A	4559	24	849	ATGRCCCGLAPGFLCWVLYP GGRGSA/CEPHVLRGTGSPLORE QRTNGRTDLSSLNPNLNFDSPP RCKHKNQLAITLRKIRKLATS LFSSTIFRISGTSV/IISAPGAGLPL PALFPTRCQPKFSRSIDPTGKAV QTADIRLSARATLWLGGSIEESP VLCSTLRLRLRPPLTW/TS RPTQPTCAQTQTNSVSGIAAPS AIRVIYPESVVLNAVIVLPGDPE VSGLPRAFKRFSVEVRLDCGT FKLLLVYCTHPGDKKVNTCKT GALVAF
4519	34887	C	4560	192	449	
4520	34888	A	4561	1	786	
4521	34889	A	4562	3	14073	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4522	34890	B	4563	58	1282	
4523	34891	B	4564	1	684	
4524	34892	A	4565	1	1356	MGRKYTLKWEFEEGFTEKKEL KKVTS EGYITPVEIYDYRQYCY ALQRPIATTQIDVDVRDGHTRRL AKLEKQEQTTHSKASRRQEIIKIR AEPKEIETQKTLQKINESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDKGDITNPTEIQTITIRE YYKHL YANKLENLEEMDKFLH TYILPRLNQEEVESLNRPI TGSEI EAIINSI.PTKKSPGPDGFTADFY QMLEVLARAIMQEKEIKGIQL GKEEVKLSLFADYMI VYLENAI ISAQNLKKL/SNFSK VSGYKINV QKSQAFLYINN RQTESQIMSER PFTIASKRKYLGIQLTRDVKNL FKENYKPLLNEIKEDTNKWKKI PCSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRACITKSILSQKNKAGGI MLPEFKLY/YQGSSTQTAWYW
4525	34893	A	4566	1	1102	MANCDINRKDEKGGKEKKDRS KSKSLMDTLKRQLSAKQKPKG KAGKPSGSSADETFSSSSAPIV FKAVRAQRPIR/STLSRSHCSP MPWPLRPTNSEETCIKMEIPSP LNGVRKDFHDLQSETACQEQE NSLKSSASQNGDLYLR LDEHVP VVI GLLPQDIQYTVPLDEGMC PLEGSSSYCLDSSSTMEVSVPVS QVGGRSFPEDSQADQNLVVA PEIFVDQSMNGLLTGTTGVM LQ SPRVGPHHVPLSPLLPMQNN QIQRNFSGLTGTEAHMAESMLC HLNFDNFNSAPGARVYVVSQSS GPMVVTSLTEELKR/LAKQGWL WPPLKSVRRCVLARRSLYTKQL NQEEGT E LNLGSSCLLC
4526	34894	A	4567	364	661	PFHFTCFCKVYFADPGSAARS VPGSPSAVCAQCILCTGHCAVC PGLGEHHSSGRITMKTKLHSH KLKPCYLLC*SKN*KTQGGSPK S*NVNKKYLVTLI
4527	34895	A	4568	53	470	CISIIILPGPSAKT LSPVLSLSPY TASFQPTFVRFTSHQT T YLSLGS VPYAQLKCSAGQQRGELLCCR GVWGSWISVSHFETIATLP AAC LEDGE\DFNLGGILDSSKYL*SIQ KTNTHRIVDGVVSETNIH\DLV

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4528	34896	A	4569	1	1635	MGWTCILFLVAAATGAHFLV QLVQSGAEVKKPGASVKVSCK ASGYTFYCYLHWREPVSFIGG RCILLTLGLGDCLWGEAWTQ GDVLQPSDRASFLAMGVNTTG QQVGDLSGDFPNSVGKACKCR EFHTLPLAHTSSTTHETFPGMS HIALQLSQGSSLLQCLEAQQTG QRQELTVSANEQPESRGHGCVL LCETQSEKGSVRAQAQTSLKGS QKRLGGARTLCTGLSPGQRKQ ERSKIDTLTSQLKELEKQEQYTS KASRRQETKIRAELEIETQKT LQKINESRSWFFEKIYKIDRPLA RLIKKKREKNQIDAKNGKGD TTDPTEIQTTLRQYYKHL YANK LENLEGMCKFLDAYTLRLNQ EEVESLNRPTGPETIAIN/STPT KKSPGPDRETAEFYQ/RSDVLA RAIRQKKEIKQLGKEEVKLSL FADDMIVYLEIPIISAQNLLKLS NFSKVSQYKISVQKSAFLYTN NRQTESQIMSELPTIASRIKY LGIQLTKVDKDLFKDNCKPLLN EIKEDTNK WKNIPCS
4529	34897	B	4570	1	429	
4530	34898	A	4571	1	897	MDLNYTLEQMDLTDIYRTFHPT TTEYTFYSTGHGTFKTDVIG HKMSLDKFKKIEMISNTVSDHS GIKLEINSERNLENHANTWKLN NLLNECWVKNMKMEIKKLF ELNDNDTTYHNLWDRAKVVI RGKCIALNTYIKKSERAQTDNL RIKKNHMIISIDAEKAFDKIQH PFMIKTLKISIRGTYLNLIKDIY DKPTANIMLNGEKLKAFTLRTG TRMNQGCPLPSLLFN/VLEVL ARAIQKEIKGIQIGKEEVKVS LFADYVIVYFENPTDSSRKLEL IKEFSSFWIQD
4531	34899	A	4572	1	1461	
4532	34900	A	4573	49	365	
4533	34901	A	4574	45	534	VCHLEPGERCPSRGCRVGV QTEKMQTAGALFISPALIRCT RGLIRPVSAFLNSPVNSKQPS YSNFPQVARREFQTSVVSRI DTAAKFIGVAGSATVGVADSGA GIGAVFGSLIIVYARKLSLKQQL LFYAILGPAALSEGMI/GLFCLMV AFLILFAM

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4534	34902	A	4575	98	624	DWYSRSHPKELWEGSKKKSIN HSACSLQAHGGPISTSLNPHSKP RGRVSPPPGKRQQECRAPGRS PELAGPPANVQETSQKNACAS RLSEPPGEGPEPAAHPPQPIIRGS SSGPCSRGGYRQPLFFGPAASG VPASGSVRSRIPGAPQGVAlAR RGPQGSPPAPRFFPATERQS
4535	34903	B	4576	1	604	
4536	34904	A	4577	3	331	LAPAPSAAWRTGLKALTSPST WMLCASEHHVSGSCVGDHLLA GCRQEKTLPCQRVCVFCRRRR ARSLQAQCGLSLTPALELLPVPF LKLCPGPPRRRRICRILPGAGL
4537	34905	A	4578	1	871	
4538	34906	A	4579	3	510	GPSPRVDDFVAAAAA AVAPVV LYACPRHSPIPPWSIRGRRVVVT GFGPFGHEHTVNANWIAVQELE KLGGLGDSVDLHVYEIPVEYQTV QRLIPALWEKHSPQLVVHVGV SGMATTVTLEKCGHNKGYKGL DNCRCFPGSQCCVEDGPEISDSI IDMDAVCKRVTTLGQCI
4539	34907	A	4580	1	285	MAPGALPALGEEEGPGASGLSA ELGHLASAGSRAFRETSDVSALD TPFPAGTFRLEFKLRQTESGR RKDWKPKCKVQPERRKQKCL TCVKLEC
4540	34908	B	4581	1	228	
4541	34909	A	4582	1	697	MGLERPVDYVMWLPALWNS AVVSAPVGEWALAGTGNQGL QDIQGMHCPEEGISQIHGRDHR NAKDSHTGVWCSCITGLIITIIIR PKCRFSIDRSDSDYLPSTSSCRRD PGGAEPQCDRPRVEQLCSVLAN RSGPLAKCHWYESPVSYTQVC VSDLCQYGTGNRMLCTMLEAY VQLCALRCALPARVASQPGMQ LRVACPANSYYDSCGPPFPATC ASLNSSAPCTLQCTVSCFCLEGF ALEAGSSVPHACCGCHLQGRY I/APGPWPSATGMRAPCPTRRC VSLTSASMARATACCAPCWPR TSNSAPCAARCLPAWRASLGCS YVWRVQPTATMTPVGHPSRPP VLASTPPRPAPSSAQ
4542	34910	B	4583	1	208	
4543	34911	A	4584	2	230	

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4544	34912	A	4585	106	669	GCGCVLLPGGVGAPGHSPGEP VPPRDARQLRTCLAGTLHLST SCGHPTGAWRGALGSQWNGH NPVQDHLQEAQPWFLEFDRG* RCFWRMATSFPRYPITWDDY*R LPCCRCLPQCKKPAETTGCLPIS GEKTHGGVGDLLGEAPARLRQ WASQRQPATDLP*ASRGRPA* GKDTHRACVAGEAAQDA
4545	34913	A	4586	2	597	TPKGGIRLGLAKLGCPTAWINP YGRGMPLAHSVLSSGARVLVV DPDLRESLEEILPKLQAEINRCF YLSHTSPTPGVGALGAALDAAP SHPVPADLRAGITWRSALFIYT SGTTGLPKPAILTHERVLQMSK MLALSATADDVVVYTEVLP.Y HVMGLVVGILGCLDLGTSLAS YGLRVYFYLWSVLGSPRRTLCL
4546	34914	A	4587	9	573	EEEEERKKKKKKKKEEEEEEEE GGMGEEKKKKEEEEEEEEE KEREKER\EKERKKKKEERKEK ERERKKKERKKKEKERERKEG EGERERKSTECTSSSYI\IKKLVV KQPQAAPSGEIPEEGIAVLGGDS SMPVIVPEDLPVGQDVEVEDSD INDPDSLILVSSQAGGGGVITAY CNLEHLGSSDPPT
4547	34915	A	4588	1	297	
4548	34916	A	4589	114	752	DGSAAPRATSDSFITYVCVSEF PVDDFMELGRSIPDTQL/DAVIE SQKANQCAVLIYT/SGTTGIPKG VMLSHDNITWIAGAVTKDFK/P TDKHETVVSYLPLSHI/AAQMM DIWVPKIGAL/IYFAQADALKV RLSKDLGSDFILLGSPVGLRPST KRLPVLSKLGHTYRRVVVVEE SSGPHITISNQNNYRLQGPMMK LKRHFVAQYKKQIDHMYH
4549	34917	A	4590	1	837	MVTQKLPNAQENLKHAEQAA GCCPGRSHIFQHVGPAGESLR GEGCSTHPEAQGAQERCEQWK KDQHWCLASHTDVTQQWGRH IVQEGGTHRGPSAVLSLRTALD EG/ARGGCSHPITAQLPLQLRHL PRPPAPAR/PSAPPAATSPPTP PPAPAR/SSAPPAATSPPTASSG ACAALPQLPLQLRHLPRPPAP AR/SSAPPAAMSPPARPPAPAR RLRRSTACATLRPGERGSAAA QPGARSETSFCRLG/AAAAVL PAFISSQALACPVVGV

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4550	34918	A	4591	3	377	
4551	34919	B	4592	1	1632	
4552	34920	A	4593	1	1224	MDGTNRFYLYVWETERQQDV EHVARCILCYDKCRPDPECPAG TPGPQEVVDVLVFFVVDSSYGV DADVYRGSLSLADAALEDLEV AEQPGASHRGARVALVTHHTP NFGRGFHLTTYGNRKQMRH VREASARPLQGTAPPGHALEW TLENVLLAAPRPRKAQVLFAlV ASETSSWDREKLWLSLEAKC KGITLFVLALGPGVGTHELAE AELVSAPSEQHLLRLQGVSEPE VNYAQGFTRAFNLNLKSEQSPG TGAPWVVEWGEGETPEGIWACR WTNQYPPPELTEECGGLHRGD TVLQLVTPVNRPFMYAAKENS LKRKTKANFHLEVELEDESIFR AYYEGTLYEVSALPLQRSNELL QKWSLFHGSNGRRVSGSHPEV ALQGGGTGLPAVLVWQLWRQ
4553	34921	A	4594	266	556	HKVQQICYRLRLVSQILFSINQT LAERQIVFTFVYDPDTERDRETR NLADLKQIKIDLKGFSDNPDGY IDILRGLRQSFDLTWADIMLLL NQTLPAN
4554	34922	B	4595	1	735	
4555	34923	A	4596	70	624	PTAMVEEGIAAGGVMDVNTAV QEVLTALIHDLGLARGIREAAK ALDKYVYQSQCGLQPDQKL ATQGGKGMGVHGVKRSKSM ASVLPGNLRKRRAHLCVLAS NCDEPMYVKLVEALCAEHQIN LIKVDNKKLGEWVGLCKIDR EGKPRKVVGCSCVVVDYKGE SQAQDVIEEYFKCKK
4556	34924	A	4597	145	682	SWRNRTVSNGSVSASSVHLCF AECKALCGERILTDGSDVSRPTI AAGGVTDVNTALQEVILKTALI HDGLARIGISRTWPKALDKRQ AHLCVLASNCDEPMYVKLAV EALCAEHQINLIKVDNQET* EKWVGLCKNDREGKPRE*WL VGS*CSSLRTIGKESQAQDVIEE YFKCKK
4557	34925	A	4598	252	590	RSLDLVWQLSGGLAGSAKPK PCTPVKQSTVMSFSPHKEQYFL MDGKKK/YDKSEKEYSILEKH LNLAKKKESHQENSSGPSVS TKLINLFSKRLLCFLPAQLTPY SFCS

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4558	34926	A	4599	1	1662	
4559	34927	A	4600	4430	4904	LIKGRCLGRPSFAYSRSNI*A *S*/P/EGTSAQLAELLALTALALE LGNGKRINVTDSKYAYLILHD HAAIWKERAFLTSGGTPIKYHK EIMELLHTVQKPKEVAVLHCQS HQKESSPLEDTTTAGPLLHPYP AGSSPERSSPSSQQLGLDGLFRGII
4560	34928	A	4601	1	2630	MEQANHPVRLINVVCKDTLKKI VQQETSCPLTHVHYAEAITGR TAPEDKGSLLDQKPTDPTGCP WQVPAHVITLTETWVCLTIEGQ EIDFLDDTGVPKPNGQWRLVQ DLIPIKEAVIPLYPVVPNPYTLIS QIPEKAEWFMALDLKDAFFCIS LHSDSQFLFAFEDPTNHTSKITR TVLPQGFDRDSPPLFGQALAQDL GHFSSPGTLVFQYVDDLILATSS EASCCQATLDLLFLANQGV VPNLWGKLPNNTTRKSWSYCT QCKNPRRWQSYTAKAIKKQLA EAGPVTAILLLIFGPCIFNLLIK FVSSRIEAIMLQMVLMQEPQMS STNNFYQGPLDRCTDPLSGLES SPRCSEAPCLMSQWTGDIYDL LLPPIPHQTTLCDLQNLKGIFSR YHRKWYGEIALLTPTANVCG HSQVPHACSIYHDPVTWNPQ LLPKSLYGVTKWGDKEHFEWG SQQQRAFYELKVKKLMSAPALG LPDLTKLFTLHVSDREKKMAV RVLTQTMGPWLGVPAYLSKQL DGVSKSWPPCLRALAATALLA REVDKLTGLQNLNIKAPHAVV TLMNTKGHHWLMNARITRYQS LLCDKPHITIEVCNTLNPTLLLL VSESPVEHNCVEVLDSVYSSRP NLRDHPWTSVDWELYVDGSSF INPQGESVWGIIQGRPIKLWG KRRKVSARDLAIIGGSVEAPKL
4561	34929	A	4602	1	506	FLALTSRFLFVLLNEETRSHLEK SLCWWKSPHIKMDLLQWISQK AQSDGSTLQQGSLEFFSCLYEIQ EEEFIQALSHFQVIVVSNIAASK MEHVMVSSSFLKRCRASAQVLHL YGATYSADGEDRARCAGAHT LLVQLPERTVLLDAYSEHLAAA LCTNPNLIELSLYR
4562	34930	A	4603	3	381	
4563	34931	A	4604	3	483	
4564	34932	A	4605	3	410	

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4565	34933	A	4606	2	249	SADAPMFDGMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLPLAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
4566	34934	A	4607	2	481	LAPLVKEIHDNFGMGEGLMTT GHAITATHKTAADGPSGLWRD GRGAHQNIIPASTGAAKAVGK VMPELNGKLTGVAFRVPTANV SVVDLTCRRQKPAKYDDIGKV VRQAPEGPLKGILGYTEHQVVS SDFNSDTHSSTFDAGAGIALND HFATLSPPPH
4567	34935	B	4608	79	278	
4568	34936	A	4609	2	1201	PSTACRNSARACSTVSRIFFCVA SRATSLRTPMGKVKVGVNGFG RIGRLVTRAFAFNSGKVDIVAIN DPFIDLNYMVYMFQYDSTHGK FHGTVKAENGKLVINGNPITIFQ ER/YPSKINWG/DAGA EYVLEST GAFTTMENAGAHLQGGAKRVI ISAPSA/DAPMFVGMGVNHEKY DNSLKIISNAISCTTNCLAPLA KVIHDNFGVVEGLMTTVHAI ATQKTVDGPSGLWALMGPR GFFQEHQSLPFTGGC/ARVVGQ GSSPELERGKLTWAWAFRCQ LPKRVNGWDLTCRLUEKPCPK YD*HQGRVVKAGRRKGPLQGA ILGLQLSNPGSGPSGLSTSDNPL LPFDDAWGLAFALQRTFCSKL IFLGIDNGILGYSNQGGWDLHG PPWPTWAFQGS
4569	34937	A	4610	61	226	WRIMPTKKVMITMGRRTQRRM LES/SQQFWPCHLH*KLVPSCLQ LGCLVFHFRER
4570	34938	A	4611	153	495	QHAAECKAHAGLPGLPLPARK LASRHGAPRWQSGVGPQGGKV ENYGRRLVPGTRIHPQSLSHKP AKKIDVARVTFDLYKLNPDQFI GCLNMKATFYDYSLSYDLHC CGAKRIMK
4571	34939	A	4612	1	643	
4572	34940	A	4613	286	698	ESDNNLTQGTISI*QGTIRHPQSLF PLSPAKKI*CGPVLTLTCYKLN PQGLSLGCLNIEGRFFMDYVIPF PIDLALLLGAKRIMKGTLHWA LFSMQTTGPRA/VFTSCYLQQL LDATEDGHPPKKGKASSLIPTCL KILQ
4573	34941	A	4614	59	294	
4574	34942	A	4615	1	2253	

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4575	34943	A	4616	2	197	LARSGMGFYRRGLLGEVKG RV EGNRMWHVVRTSPNHRYTFT LKTHPSVVPGSIAFSLPQ/RPWS
4576	34944	A	4617	302	441	
4577	34945	A	4618	944	1257	RLPFSRPSRVGPTPQAPRLLCNG WRQLPTTFFTELEKTTLKFIVN QKRALIAKT/LKPKNKAGGITL PDFKLYYKATVTKTARFLLYK VSQIDNTDLDFPVKIKFE
4578	34946	A	4619	1	1370	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSM NVIQHINRTKDKNHMISIDAEEK AFDKIQQPFMLNTLNKLGIDGM YLKIIIRAIYDKPTANIILNGQKL EAFPSKHGTRQGCPPLSPLLFNIV LEVLAIRAIRQEIKGIQLGKEE VKLSLFADDMIYLENPIVSAQN LLKLIGNFSKVSEYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SIRIKYLG1*LTRGVKDLFRENY KPLLNNKIKEDTNKWNIPCSWV GRN/NIMKMAILPKVIYRFNAIP IKLPMTFFTELEK/TTLKFIVNQ KRARIAKSILRQKNKAGGITLP DFKLYYKATVTKGAWFQHHK HTLIKEPLLDVFSFNPDPDHGK KQDKQPQTKNIANASADSKNT QQMNGFVTGAATSFIPKDRITAS SLCGCTGRRRQSVAKYLRI RPHI NVPSFTYYK
4579	34947	A	4620	2	671	WHQNLALTRASGSFHS/WEEG KGGADMSHEICVANLQVYVRS TDFDRTLMSAEANLAGLFPNE VQHFNPNISWQPIPVHTVPITED RLLKFPLGPCPRYEQLQNETRQ TPEYQNRSIQNAQFLNMVANET GLTNVTLETIWNVYDITLSCEAP SPPWGRKPPLERLWPRPRELTC PLRYTVQTHGLLPPWASPQT V QRLSQLKDFSLFLFGIHEQVQ KARLQG

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4580	34948	A	4621	1	1923	DSVAFEDVAVNFTQEEWALLG PCQKNLYEDVMQETIRNLDCG HETEFVEYENLRDPMNMLPH TDGPHKCKICGKGFDCPSLKS HERHTHTGEKLYECKQCGKALS HSSSRFRHMTMHTGDGPHKCK ICGKAFVYPSVFQRHEKHTAE KPYKCKQCGKAYRISSSLRRHE THTTGEKPYKCKCGKAFIDFYS FQNHKTTHAGEKPYECKECGK AFSCFQYLSQHRRHTTGEKPYE CNTCKAFSHFGNLKVHERIHS GEKPYECKECGKAFSWLTCFLR HERIHMREKPYECKQCGKAF HSRFLQGHRIHTGFKPYECKE CRKAFSWLTCLLQHERIHTREK PYEGKQCGKAFTHSRFLQGHE RTHAKKLCECLSTVSARKSVD LIASVPLFLNLFSTPKTLRNC SYRRHERMHTGEKPYECKQCS KALPDSSSYIRHERIHTGKPY TCKQCGKAFSVSSSLRRHET HSAEKPYECKQCGKTFHHLG SFOIHMKRHTGDRPHKCKICG KGFDRPTLVRYHERISTGEK PHECKQCGKAFDHLGSGFOR HMIRHTRDGHKCKICGKG FDCSSTLQSHERTHTGEK KLYECKQCGKALSHSSSF RRHMTMHTGDGPHKCKICGK
4581	34949	A	4622	1	256	MKGGSFKYAWALYKQKAECE RGVTIDTSLWKFETSKCYVT IKDFIKNIITGTSQQGQTAS VAFCILSSCPASWKNQVSH RLGG
4582	34950	A	4623	173	717	SINAVASTRRRTIEKFEKEA EAMGKGSFKYAWVLDKLKA ERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMITG TSQADCAVLIV AAGVGEFEA ISICQNGIQTREHALLAYTL GKVQQLICRVNKMDDSTEP PYSQKRYEIVKEVSTYIK KIGYNPDTRAFVPIISGLN GDHMLEPKC
4583	34951	A	4624	3	525	GCPSPGPHRCVAGHGAPGAVC RHVPTAWPGYSRCSPPGPRGV EAVGHQRHRAPEHSTPAADR HRRGLPGSKSDSAMEPSPPAP QAQPPKVPKPRTVFGGLSGPA TTQRPGLSPALGGPGVSRSP EPSPRPPPLPTSSEQS SALNTVEMMPNSIYFGLDSR GQAQAQDK

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4584	34952	A	4625	2	448	RRAHACARRRRKKEMLGVNVLTSHSSQERMKLTFFKKAVNFA DAAAAQGPLLPA MVNPTMFFH IAVDGEPLGCVSF EVRGLESKK *LLI*SIKLC*QIGLFADKVPKT AENFHALSTGEKGFYKGSFCFHIIPGFTCQSGDFTRTPA
4585	34953	A	4626	1	751	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQCLLFLRILPL FADKVPKTAGV*FFFKQKIFRA LSTGIEKGFYKGFPAFHRIPG FMCQGW*LSHRHNGTGWQVH LMGRNFEDNFILKAYGVLGS LSMAKCLDPTKIGSPVFPSC TA KTVEWL/DGQALWCFGK/VKKG LNIVEAMERFVGSRNKGKTSKKI TIADCGQLE
4586	34954	A	4627	3	615	PECIIGIDILSSGQNP HIGSLTGR VRAIMVGAKRRKPLELPLPRKI LNQKQYRIAGGIEEISATJKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPIISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGP AIFCR* LLSF*ETALGLLGF GGN*TFDY
4587	34955	A	4628	3	354	DSWA/VANGLA/GWS/GTWKK HDWKINDNEIWGK/SMWIDL S EWSKTVKIFVSHESAHHIT*KSS AEEDFNNQVDRMIHVSVDTRPL SPATPVIAQWTHEQSGHGGRD GGYTWAQQHGL

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4588	34956	A	4629	281	1529	VRVLSPEKELKLVKNTHTKLL SYPTVGAAVTQLQNLTAMGVI GSHGARGQVVALNRQQRGDL QPFTRVTVHWGKG/NMQIFGGL LDTGSELTLPDGPDKHHCPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHGSLTGRVRAIMVGKA KWKPLELPLPRKIVNQKQYHIL GGTVEISATIKDLKDTAEAVTPIT SPFNSPIWPVQKTDGWSRMTV DYCKLNQVVTPIAAAVPDVVS LLEQINTSPGTWFEWSPKIKAL QQVQAAVQAALPFGPYDPADP MVLEVSVADRDAIWSLWNAAI GESQRRPLGFWSKALLSSADNY SPFERQLASYWALVETERLTV GHQVTLRPELPIMNWVLSDPSS HKVSGAQQRSIIKLLKWIHDW
4589	34957	A	4630	453	719	ARGSKHTGLIAQWAHEQSGHG GRAGGYAWAQHQHGLPLTKAD LPVAMATAECPIQQRPTLSPR YGTIPW/WAWDAPGGRGCWRL QKAGE
4590	34958	C	4631	122	325	
4591	34959	A	4632	1	346	MAGEKVEKPDTEKKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF QIITYSSYTQKVQLPKSTLKQRQ GPCPQAL
4592	34960	A	4633	115	905	EAFQTLHFCCGLRQGTKRMA GEKVEKPDTEKKKPEAKKVDA IGGKVKKGNIKA/KKPKKG/RPH ICSRNPVLCSEGFGRYSRSVAMY SRKAIYQEGSTFSPLKSKVEKK KKEKVLATVTKPVGGDKNGGT RVVKLRKMPRYYPTEVDPRKL LSHGKKV/PFSQ/HVRKLRASITP GTILHILTGRHRGKRVVFLKQL AKLAYLLC/LGPLVLNRVPLRR THQKFCHLPLSTKIDISNVKIPK HLTDAYFKKKKLRKPRHQEGEI
4593	34961	A	4634	2	350	FVALAAVLCRQCLPRAWVCCR AGQSGSRHYRAAICAEKKPLT IEEVAP/DPVGPHEVRVDVHFC GVNFGDILICRDQYQERPHLPFT PGPVADSRKGLPIRSCCPPYNL WHCDFCS

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4594	34962	A	4635	1	556	MGLKLNTHMDQTRGSLSGDTL EGSPSKRAKILKRGGFRGILGG VGQERRTGQRPALPCHDLRR AEVVPDHRRGGRPVGPPIEDL WQIPEKVSLEAAVLPITYGTE SFALEHRARTQPGFIVLVTAAA GATGLAVMWQIQSSGQGNIAA AGSDEKCKLAMEKGAQSSVN YSQGLKDSATDQ
4595	34963	A	4636	1	142	
4596	34964	A	4637	2	368	
4597	34965	A	4638	2	504	HKVGHAQHHSFITWKWYTRD WSRAGPEGTVGPYDQLTEEEK TRAWFTDGSARYAGTIRRWTA AALQPLSRTSLKESGEGKSSQW AEVRAVHLVVHFTWKEK*PDV RLYTDSWAVANGLAGWSGTW KKHDWKIDDNEIWGRGMWIDL SEWSKTVKIFVSHESAHHIT
4598	34966	A	4639	182	840	RTAVKGNLPTTPVLSQWAHEQ SGHGGRDSGYTWAQQHGLLIT KADLAMTTAECLISQQQRPLS LQYSSIPWGNQPATWVQIDYIR PLPSWKGSQSDSRNRNQGV KVKVAPLTITPSDTTAKFLLHV PAALHSAGVDVLVPEGGMPLP GGTTTIPLNWKRLPPGHFGLLI PLSQAKKRVTVLAVGVIDLDC QDEISLLLYNRDAKELYRYTAH
4599	34967	A	4640	3	283	SRVSCSPPLSPPPPLSPPPPLSPP PLLSPPPPLSPPPSPPPVSLPPP PPVFSFPSSCP/PPFPPLLPPLPPP PPLSPPPPPPPVSPSPPI
4600	34968	A	4641	1	531	MGSSHCTQPGMLAAAVGQAVP GTDTGADS VLSASCCQHAIH CAQAIRAKGHLQAHTLPSAPT QPFPSCARQCCKSGDGLGGRLEY NNHEIRSGKHIGVCISFANNRLF VVSIPKSKTKEQILEEFKVTGS YVWLGLSDFDKWPV/GQCCQ SFHGRLRATPARRAERRDARSE AL

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4601	34969	A	4642	115	2405	ATAEGSGSGVKGKRGAGIRKAE RRRTEASGGGGGRRRRSWRR AGAEGVSEADARGGKGKREG KGGSRGGARAHREARRRVEL DRVCCQRRELPPFYNSSSTRAG HREQRARVSRNPISDRISPPQP NGEISGNMATEHVNGNGTEEP MDTTSAVIHSENFQTL DAGLP QKVAEKLDEIYVAGLVAHSDL DERAIEALKEFNEDGALAVLQQ FKDSDL SHVQNKSAFLCGVMK TYRQREKQGTKVADSSKGPDE AKIKALLERTGYTL DVTTGQRK YGGPPDSVYSGQQPSVGT EIF VGKIPRDLFEDEL VPLFEKAGPI WDLRLMMDPLTGLNRYAFV TFCTKEAAQEAVKLYNNHEIRS GKHIGVCISVANNRL FVGSIPK SKTKEQILEEFKVT EGLTDVIL YHQPD KKKNRGFCFLEYEDH KTAAQARRRFN*VGKVQGF GNVGTVEWADPIEDPDEVMA KVKVLFVRNLANTVT EILEK AFSQF\GKLERVKKLDYAFIHF DERDGA VKAMEEMNGKDLEG ENIEIVFAKFPDQKRKERKAQR QAAKNQMYDDYYYYY GPPHMP PPTRGRGRGGRGGYGYPPDYY GYEDYYDYGYDYHNYRGGY EDPYGYEDFQVGARGRGGRG ARGAAPSRGRGAAPPRGRAGY SQRGGPGSARGVRGARGGAQQ
4602	34970	A	4643	2	369	
4603	34971	A	4644	1	1002	MNAGCGQTHDCAYRQKRPE VNEEGRL EQRNRKRQDEWGPR DKPASSGYKAGTLDVENWNRA GEGLKHAHQGLKVDSSAFCT CSLIRTVLMPLSPYY SAGQQA SKNLKESVVPPTAS IENKKQER EDKNWPILPPPVAETSVP PPSVA GIETPIQRILRSAAIAGEPSGPCA FPISVRPDSNNPQQFIHEHTPLEF KLLNELKTSVVNIGVQSPFTLG LPESAFGAMRLLPFDVKHWAR TCLSASAYLTWNLNGQEMCTD QVRQNRRAAGHG DIAEDMLLGN GP/YFRPGTSGTKRAWATIPEE GVPVQSFLPFMEGSEQEPSAQFL ARLREAV
4604	34972	B	4645	1	575	

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4605	34973	A	4646	1	776	VVLNRNLSMSGTIFSMANISML GSLVIIQYITQEIPDPSRVPLVA SWKTYPLFFGTAFSFSIGVDL PLENEMKNARHFPPILTGMP VTTLDIGMAALGYLRFGDVDTK GSIILSLPICWYLIHLSGEGPSQ SFSERETAKQVIVPRSEVNVPRR PVSEHSGRGEQLCGLSCLRYQS VKLLYIAGILCTYALQFYVPAEI IIPFAISRVSSTRWALPLDSLRLV MVCLTSAPMTRSTPFCKYSTRG RRRWLEIPV
4606	34974	A	4647	1	1294	MKGDFMSKTPKAMATKTKIDK WDLIKRKSFACTAKETIIVNRQP TEWEKIFATYSSHKELISRIYTE LKQIYKKKTNNPINKWAKDMN RHFSKEDIYASKKHKMKCSSSL AIREMQIKTTMYHLTPVRMEII KKSNNRQPIVGPCDNSVILLY KILANRIQQHIKKLIHHDQVGF PGMQGWENTCKSINVQIHINRT KDKNHMIIISIDAFAFDKIQQPF MLKTLNKLIGDGMYLKIIIAIDY RPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLAIRIQ EKEIKGSQLGKEEVNLSLFADN MIVYLENPIISAQNLPKLINNF KVSVCINQVQKPAFLYTNNR QTESQIMSLEPFTIASRIKYLVI QLTRDVKDLFKENYKPLLEI/ K/EDTNKWNIPCSWVGRINIV KMAILSK
4607	34975	A	4648	2	711	WNRPRPCIAKTL/SQKNKAGGI TLPDFKVYCKSTVKTAWYWY QNRHIDRWSRTETSEITHIYNH QIVDKPHKNQWGWKDLLFSKW CWENWVAICRKLKLNLFTRY TKINSRWIKLHEKLTIKTLEE NLGNTIQDIGIGKDFMTKMPKA IATKAKIDKWDI.KLSFACTAK ETIIRVKNQPTWENISAIYPSD RSLISRIYKELKNYKRLDAVA HTCNPITLKGQGRWIT
4608	34976	A	4649	1	576	
4609	34977	A	4650	1	771	

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4610	34978	A	4651	1	887	FPEDSEPISISHGNYTKQYPVFV GHKPGRNNTTQRHRLDIQMIMIM NGTLYIAARDHIYTVDIDTSHTF EIYCSKKTAWEILDRPMVATCR MKGKHKDEICHNFIKVLKKK DDALFVCGTNAFNPSCRNYKM DTLEPFGEFSGMARCPYDAK HANVALFADGKLYSATVTDLF AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDIYIFF FREIAVEYNTMGKLLGLHHELL RRTQDYGHKAGCPESCLLSVRR CPPPQSKAHRESVEELIKGCR HAGFCAACGHIT
4611	34979	A	4652	1	2890	MVLLKVDPLWGSRLVLLKA DPYPGTQAHAEHRHGRALAGGL GVGEQSQSLDLLRMSHTYGA FLPRAAVSSWCASVRIRKIKKSP LLDGAPLLYEPDTWLGKWS WTLVFTHPFSAALTHSALTARS DTGSLTSPDGKLYSATVTDLF AIDAVIYRSLGESPTLRTVKHDS KWLKEPYFVQAVDYGDIYIFF FREIAVEYNTMGKVVFPRVAQ VCKNDMGGSQRVLEKQWTSFL KARLNCSPGDSHFYFNI
4612	34980	A	4653	1	480	MEGVVEEKVPVAVPETLKKKQ GNFAELKIKPKMAFVLRIGVS GVSPKVRKVLQLRLHQIFSGT FVKLN/KASVNMLRIVEPYIAW GYPNLKS VNELIYKRGYGKINK KRIALTDNTLIVPSLGKYGILCM EDLIHEIYTVGKHFKANNLLW PFKLSSP
4613	34981	A	4654	3	279	
4614	34982	B	4655	119	177	
4615	34983	A	4656	157	359	HQRCRK**TKLEG*TCRKIEVN TDYIKP**EFWMIYISYILTSI CSSICNENILQLENREKSRNT

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4616	34984	A	4657	65	900	GLAAPPILQKESPHCLWILFTSP VALSTRPPCVISSAALCPRRHG FLPPRLLAPLAAAFPCPRCFLP LPRLFAAPVDFCPRRCGLPL PPRVFAVSCPRRRGLLPPLFAF SAAAFCGFLAPSPWLF AAFGTR CRGFLGLLVPA A A A A F P R R L R F FLPRLFSPA A A V T F C H P C F L P P P PRLSVPA A A S F C R R G F Q Q E I R T V EIRGSGTRVGLQHQTGHLPRGP SSLP A E L H A * A R V S P L E A S P P S C TR/WMQQPEDLGPALTLGRICG VGACWEL
4617	34985	A	4658	927	1157	ARRSTAPVDCK*LQP*AQAAL WVLVWDHEAARQPEGVVQPA PGLWPSSRRWRKFQAPGSSGV CHPGALQACPEELS
4618	34986	A	4659	1	563	MKLVA V F D K Q D L H H G D D I S A SSMHTQSPERFTASELGTNNV SAFSVYQAASEIEVTSVLIHAS SQKGLSSQHILGFGAPQAGGGSF RHLAPQRKEVLEEYFKYDPEH KLIFRFVRTLTKAMRLTAFAIE ITHGGRDVERATGLVNNKIHRQG CGDSFCNIGGNAPYPVCCGKE YVSSSKHQNGIAI
4619	34987	A	4660	1	681	MGKYAEALRSQQKAVLMSVR VMGIEHPNTIQENMHLALHCFT SRQLSLALSLQLGAHYLM/LLV LGE/DHPEVA/LLDNIRRVLHRV MEYDLSLCFLONALAVSTKYQ GPKALKVALGHHLITSVYESKA EFVSALQHQKEGLAAH/TSLGE DQEKTKESSEYLKCLTQLAVAL RRAMHEIYRNGSSNNIPPLNFT APSMASVLEQFKGINGILFIPLS QKDLESLEAEVAQ
4620	34988	A	4661	2	443	VWQSGGDSITSKTNITVCNVCY LYTCIDSSFNQYHSILIVRARQD IWL P V A L H R P W E S S P F I H V I N N I LQKILKRSTQFIFTLIAIIMGLIA VTVIAATAGVALRQSIQTVHFV DKWQKNSTRMWS/QRIDQKL ANQINDLRQTVIW
4621	34989	A	4662	2	377	FAFTWTDPDTHQAQQITWALL PQGFADSPHYFSQAQISSSSITY LGIILHENTRALPADHV* LISQT PISSTKQQLLSFLGMVRYFCLWI PSFTILT K P L Y * F T K A N L A D P T D PKSFPHSSFRSL

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4622	34990	A	4663	1	1095	MAKAVLSKKNK TGSTTLPDFKI YYKDIVTEEPGIELRHITSSTKF SKGLPSRESFSEKQNKTTTHLH PGEINSFIAHTKPA WRS LHTDA HEI WCRDSDQVNSPGRSIPCPA LCSMRKIHLRPLVLRPASPRNIS PILNPLHLIAALLPNKPPFRPPL VSPDLNPQVKDISTPSWATDHV HLTVSLKPYHPYPAQCQYPIQ HALKGLKPVITRLLQHGLKPI NSPYNSHILPVLKPKPYRLVV QDLRLINIHVLLPIHPMVPNPYT LLSSIPASTTHYSVLDLKHAFET IPLHPSSQLFAFTWTDPTHQA QQIT*AVQPQSFTDSPHYLNQA QISSSVTYLGIILIKAHVLSLPIV
4623	34991	A	4664	655	2417	KKRESMNIDAKILNKILANRIQ QHKKLIHHDQVGFI PRQGW NICKSINVIQHINRAKDKNIHMI SIDAEKAFDKIQFLMLKTLNK LGIDGTYFKIIRAIYDKPTANIL NGKKLEAFPLKTGTGRQCPLSP LLFNIVLEVLARAIQEKEIGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDANKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRAHITKAILSQKNKA RGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTPQSEITP HIYNYLIFDKPDKNKQWGKGS LFNKWCWENWLAICRKLKLD FLTPYTKINSRWIKDLNVRPKT TKTLEENLGITIDIGMGDMFM SKTPKAMATKDKIDKWDLIK KSFCTAKETIRVNRQPTKWEK VFSQPTHLTG*YPESTMNSNKF TRKKQTTPSKSGRRWNEQTLLK RGHLCSQKTHEKMLTITGHQR NANQNHNEIPSHTC

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4624	34992	A	4665	1	234	MQNQEKFGELISEWAPYGRPRP QIAVGDHHISVYDGEVNW RMS SLQASAAAGKDYANRGTEWGEE PSQMLRII ELLSGEMCVSRNRG QPLANSERRSEALSPVTPKKLIP ADGHKSDPGRTWMKLETHLSK LTQEQT KHHMFSLISG*FAEN DGFQLHPCPSGSLWPSAGISF FGVTGLRASDLLSLARGCPRF LDTHISPLSSS
4625	34993	B	4666	1	2553	
4626	34994	A	4667	33	272	
4627	34995	A	4668	1	3045	
4628	34996	A	4669	1	334	
4629	34997	A	4670	159	245	FPIVASPWLLC*LMSFAGTWVK LETHLSKLSHGQKTKHRMFSLI DTVVVGSDDFLLRPVGCASS LNAHTSVNIKLELT
4630	34998	A	4671	122	359	TANLKNRGRKFL*PIHLTKG*YPE STKNVKNKFRKKQTPSKSGQK I*INTSQQKTFMQPTGT*KNH HHWSSECKSKP
4631	34999	A	4672	2	66	RLVYADTCFSTIKLKAEDASTS ENMRCLVFCACDSLRLMIVSSF IRVPTKDMYSSFFMAA*YLLQY HQVKSRRRCFYE
4632	35000	A	4673	519	899	SALVCHTC SNWQVHLGDSVFY RSEEQPLEPLPFSYLSLFPGLHP DPVSSGSQQPS*MPHTDASVTS SHGLGGLAGRNSCIYPCCAPAL CADYLGWSPDLFLLSFQHKG NVGVGLAHSPPQFQQN
4633	35001	A	4674	1	278	
4634	35002	A	4675	158	592	GYYWRPSFQSLRENNECQRKS NSVNAGCLNCDHCVLGIYQQH *QNYFSFDIHYFLSETGRKVS I/VYFTIGETEALSGKVVPYWQQ AAGQGCTLHLLLPQTRLFPKGK RRQPGLLREF
4635	35003	A	4676	302	721	
4636	35004	B	4677	1	871	
4637	35005	B	4678	1	559	

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4638	35006	A	4679	3	2386	RVATMAPHRPAPALLCALSLAL CALSLPVRRAATASRGASQAGAP QGRVPEARPNMIVVEHPEFLK AGKEPGLQIWRVEKFDLVPVPT NL YGDFFTGDAYVILKTVQLRN GNLQYDLHYWLGNECSQDESG AAAIFTVQLDDYLNGRAVQHR EVQGFELAPFLGYFKSGV\K\Y KKGGVASGFKHV\PNVEVVQ RLFQVKGRRVVRATEVPVSW SFNNGDCFILDLGN\N\HQWC GS\NSNRYERLKATQVSKGIRY NERSGRA\RVHVSEEGTEPEA\M LQVLGPRIVALPAGTEDTAKED AAN\RLKALKYKVSNGAGTM\ YVSLWAD\NEFTQGA\K\SED CFILDHGKDGKIFVWK\GKHAN TEERKAALKTASGFHSPRWY PKQIQVSVPFLEGG\ETPLFKQV FKNWRDPDQTDGLGLSYLSSHI ANVERVPFDAATLHTSTAMAA QHGMDDDGTKQKQIWRIEGSN KVPVDPATYQFYGGDSVILY NYRHGGRQGGIYNWQGAQST QDEVAASAILTAQLDEELGGTP VQSRVVQKKEPAHMLSLFGGK PMIHYKGGTSREGGQTAPASTR LFQVRANSAGATRAVEVLPAK GALNSNDAFVLKTPSAAYLVV GTGASEAEKGAQELLRLVLA QPQVVAEGSEPDGFWEALGGK AA YRTSPRLKDKKMDAHPRL
4639	35007	A	4680	1894	2161	MFGLPNARAATSTAPFASHSLC LCFRILLLLGPGINLANPRNHLV LHQKFSILGRHFSLATTEPCISL ALAPSKRWECNSSS*RYENN
4640	35008	A	4681	1	1803	
4641	35009	A	4682	1	501	MTFQCVVNTHYLTYP RPQRF YL VVVRPSCASWIMFVLIDRGY VFSYFPQSYGGFGSRILSKPIEV QVGGRSVVAQMWSNKGQYS DLASLGICISRY SAGSVYYPSY HHQH\NPVQVQKLQKELQRYL TR\KIGFEAVMRIRCTKAKPTRH RHYGELEISITIRAIGK
4642	35010	A	4683	350	623	

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4643	35011	A	4684	1	3252	PPGPERSRLGLGVSLHQRSCP K CIAVFTRVSEPRIQFPASRILPSS NTSKDFDPVSGQSNYGGSQGS GQTLNRPPVASNPVTPSLHSGP APRMPLPASQNPATTPMPSSSF LPEANLPPPLNWQYNYPSTASQ TNHCPRASSQPTVSGNTSLTTN HQYVSSGYPSLQNSFIKSGPSVP PLVNPPLPTTFQPGAPHGPPAG GPPPVRALTPLTSSYRDVPQPLF NSAVNQEGITSTNTNNGSMVVH SSYDEIEGGG
4644	35012	B	4685	51	236	
4645	35013	A	4686	1004	1405	
4646	35014	A	4687	1	771	
4647	35015	A	4688	1	405	SENVDDVSVMVG/TPANKALL DTTGFWHD/DFNNA/TPNDICVA IRSE/AADAGIAQAIMQQLAEA/ LKQQA/LDRNLNVMMFSDNVT LE/DEIQLK/TRAREKGLLV/MG PDCGTSMIAGTPLAFA/NVMPE GNIGVIGASGTGFRR
4648	35016	B	4689	1	1656	
4649	35017	A	4690	1657	2259	LPQPQPATPWPSAPTPrFASPA A AMATLWSGTCRIRLWSGSSRA TRTAPAALIFPITALGSGQGAW TTRCAAGTCGRAASCSSMTSA/ AQIFSPCHCPNQDWLAVGMES S NVEILHVKGPEKYQLHLHESCV LSLKFAPCGRWFVSTGKDNLL NAWRTPYGASIFQSKESSSVLS CDISRNKYYVTGSGDKKATVY EVVY

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4650	35018	A	4691	62	1371	QNQSTISVMLRSAMTTTMAAD LITAI/MGQRKQHIDTGFWHDD FNNATPNDICVAIRSEAADAGI AQAIMQQLEELKQLAQSGS SQALTQVRRWDSACQKLPDAN LALISVAGEYAAELANQALDR NLNVMMFSDNVLTLEDEIQKKT RAREKGLLVMGPDCTSMIAG TPLAFANVMPEGNIGVIGASGT GIQELCSQIALAGEGITHAIGLG GRDLSREVGGISALTALEMLSA DEKSEVLAFVSKPPAEAVRLKI VNAMKATGKPTVALFLGYTPA VARDEN/VWFGSSSLDEA/SLAG CFSVRARSPLTRIDGMMILGMF GGCFAASLWANNVKLRMPRSR IRIMQAIIGGHAGFGARLAMGC NLAAFFTGIQFSLHAWFFANP LLIGQTTLEDPHEIDYLDKEFPL YQLVECVVSLNYSYHWECTEI
4651	35019	A	4692	1	1125	MEAEVDKLELMFQKAESDLDY IQYRLYEIKTNHPDSASEKNPV TLCLKELSVKSYQYTLYARFKP VAVEQKETKSRICAGMTKTMN VIQKLQKQTDLDLSPLTKEEKT AAEQFKSHSFGMWPCCLKYRQ NKKKKKKLSQNRSTTWKLNLL LLNDYWIQNEKMAEIKMFFET NENKDTTYQNLDWTFKAVCRG KFIALNAHKKRQERSKIDTLAL QLKELEEQEQTHSKASRRQEIT KIRAEKKEIETQKNLQKINESRS CFFEEKINKMDRLLARLIKKKRE KNQIDAIKNDKGGITNDPTEIQT TIREYYKHYANKLENLEEMD KFLDTYNLPRLNQEEVESLNRPI TGSEIEARINSLPTKKSPGPDGF
4652	35020	A	4693	2	421	GRVGGRVGKIRT*LN*IETKKY KR*NETKSWFFEKIKMDRPLAR LTKKRRIEQITSLRNETGNIITD TTEIHKIIQG*SSSSSSSSSSSSSS SS/SSSSSSSSSSSSSDTFKRPI GIKIEMVF*KLPTKKSRISL

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4653	35021	A	4694	1	654	MEYYAAIKNNTFMSFAATWM KLEAIILSKLTKEQKTKRHMFSL VSTLELGALTALVRCGRWRRQ CDDEAMACVTQGRPLARLTKK RREKIQTSLRNETGDITDTTEI QKIIQGYDEHTYAHKVENLEG MDKLLLEKYNPPRLNQEELGTL NRPITSYEMEMIIKKL/PNEKSP GPDGFTAIFYQTFFKEELVPILLA LFHKTEKEGILPNSFYEAISIL
4654	35022	A	4695	1	786	MPPSLAYKKNRPQQADTQVA/T MSRGVHWRRKKMQAAGRPEDY KRSTQAEHTDRHQHTSRVHQL LLMRIFEMGWKKPSPFQESIP ALSGRDILARAKNGTGKSSAHD IPLLKRLDLKKDTIQTIVIVPTG GPALQVSQICQVSKHMGVVK VVMTTGGTNSGDDVLRLLDDTV HNVIAAPGRILNLIKKGVAKLE ETYL RHIGRPGHFGHFGLA INLI TYGDHFNKLGIEQLGKEIKPIP SNIDKSLHVAEFHSAVENEKP
4655	35023	B	4696	1	501	
4656	35024	A	4697	2	573	YSACFFLFSIAMGILLTVPPSFWI PTSFS AFLGFFSSFSLLVLHQPD FSFVLGLWRIISLLVLKIVEGSS NQGMQMASRSWEWPPSSSRKM ATSVRTLPPEP/GPSGCRAPSAFPF RKEAGADPSGCPGGRQVPLVAI GRGGALEPQRWELRAPGSAGR LPREGGRTPGAQSPAGAQSPA GKQSPGAQSPLH
4657	35025	A	4698	2	346	PPINISVPHC*PFGG/EPLEILIPAP ERSSHVLVSQSPPVTHSSAVHQ VGASLNCGDQKPPNPFSGSKIFF LIYHLMTGQVGRGSSVLCHPNT GIOKEGGTVNEIPAIIEKRKKHA
4658	35026	B	4699	1	468	
4659	35027	A	4700	2	284	ETGEFTQLKELNIQGCNWLTL PELGNLYLTGGKKVCKVENS WVTPIAGQFQLDVSCVSECVCS ETYEYLYGQHMQANP/EPKPKH NNHKSGKD
4660	35028	A	4701	5	189	
4661	35029	A	4702	38	190	

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4662	35030	A	4703	2	882	WPSVSSG/PSSAVSFSSFDPGVA SCTSSASGIQRPMASEVPCASG IPIKIGHRGVDSSGETTYRKTT SSALKCAIQLCITHTVGSLDPTP ERHVLIEPLIELSSSGADGSLH VSIHDEFIITVQHKQAEFLQKL IPGYHIDLNQNSWTLTPKFYGL CCVKAGGKNTQIAVMKNLLLR LNSEGERILLCIGITDILQSYRFV KKLEHSWKALVCDGDTVSVHR PGFYTERFQCFMONTAFKKIPA RTLTTNPAGKDVEQQLSSLLM GMRSGTATVEDSLVVS YKTKH
4663	35031	A	4704	2	410	
4664	35032	A	4705	2	728	
4665	35033	A	4706	1	1208	MKMEKVNTSWLLPPSSISVLIR RGAGSMVLLQLSQRQYIFYEYDS SDRLLAVTMPVARHSMSTHTS IGYIRNIYNPPESNASVIFDYSD DGRILKTSFLGTGRQVFYKYGK LSKLEIVYDSTAVTFGYDETT GVLKMYNLQSGGFSCITIRYRKI GPLVDKQIYRFSEEGMVNARFD YTYHDNSFRJASIKPVISETPLPV DLRYRYDEISGKVEHFUITAEM TLSKHFDTHGRKEVLA/YEMF RSLMYWMTVQYDSMGRVIKR ELKLGYPANTTKYTYDYDGGG QLQSVACNDRPTWRYSYELNG NLHLLNPGNSVRLMPLRYDLR DRITRLGDVQY/KIDDDGYLCQ RGSDIFEYNFNAGPTKTLSSQAS GILQSLQGLHEVHRNPACSDFA
4666	35034	A	4707	1	663	MMLLLLALLGAGLLGASLLTS WHAPARNKIPRAQKWREPD DPKPILEPLAELAQQLRTEELS LESILCSYLKQALKVHQEVNCL MDFLGECEELQALKKLLKKE RGLLYGVPMMLKDTYDSMFLE KPATKDGVMKVLKAQGAIPFV KTNIPLTLRLSLKRASWALNAA TPIYQGMLSPNLNKKTCGGSS/G GDHGGWPHGPGRGEPAVPCK

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4667	35035	A	4708	2	624	SDARLHKDDTDICFSKTLNSCK VPQIRYASVERLLERLTDLRFLS IDFLNTFLHTYRIFTTAAVVLGK LSDIYKRPFITSPVARRARKLSLT SPLNSKIGALDLTSSSPPTTTTQ SPAASPPPHGTGQIPLDLRGLSS PEQSPGTQPEVSGSSPHSTAQSK IWSLVWKQYWLMAPSHAKKT CHAARLARTFVTSSSATKVHCA ISLK
4668	35036	A	4709	1	195	
4669	35037	A	4710	1	1845	MAEAEPRGPRGERGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPDKKEIVICDRASVKE FKEEISRFRKAQQDQLVLISGK ILKDGDTLNQHGKIDGLTVHLV IKTPQKAQDPAATASSPSTPDP ASAPSTTPASPTTTPQSTSDSA SSDAGSGSRSSGGGSPGTGE GSPSATA SILSGFGILGLGSLG LGSANFMELQQQMQRQLMSNP EMLLQIMENPLVQDMMSNPDL MRHMIIAKPQMQLMERNPEIS HMLNPNELMRQTMELARNPAV MQEMMRNQDRALSNLEIPGG YNALRRMYTDIQEPMFSAARE QFGNPFSSLAGNSDSSSSQPLR TENREPLRNP/WSPSPPTSQAPG SGGEGTGGSGTSQP/GSGMFNS PEMQALLQIQISENPQLMQNVIS APYMRSMMQTLAQNPDFAAQ MMVNVNPLFAGNPQLQEQLRLQ LPVFLQQMQNPESLSILTNPRA MQALLQIQQGLQLQTEAPGL VPVSLVSGMSRTPAPSAGSNAG STPEAPTSSPATPATSSPTGASST QQQLMQQMIQLLAGSGNSQVQ TSEVRFQQQLEQLNSMGFINRE ANLQALATGGDINAAIERLLGS
4670	35038	C	4711	59	464	

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4671	35039	A	4712	1	1902	MAEAEPRGRPGERGGGGAGRAG GRPGGGGGMAEPSGAETRPPIR VTVKTPKDKEEIVICDRASVKE FKEEISRRFKAQQDQLVLIISGK ILKDGDTLNQHGKIDGLTVHLV IKTPQKAQDPAATASSPSTPD ASAPSTTPASPPTPTQPSTSDSA SSDAGSGSRRSSGGGPGTGE GSPSATA SILSGFGILGLGSLG LGSANFMELQQMQRQLMSNP EMLLQIMENPLVQDMMNSPDL MRHMIIAKPQMQLMEERNPEIS HMLNPNELMRQTMELARNPAV MQEMMRNQDRALSNLESI YNALRRMYTDIQEPMFSAARE QFGNNPFSSLAGNSDSSSSQPLR TENREPLPNPWSPPSTSQAPGS GGEGTGGSGTSQVHPTVLNPF INAASLRSGMFNSPEMQALLQ ISENPQLMQNVISAPYMRSM QTLAQNPDFAAQMMVNVPLFA G/NPQLQEQLRLQLPVFLQQMQ NPESLSILTNPRAMQALLQIQ GLQTLQTEAPGLVPSLVSF RTPAPSAGSNAGVYPPRPPLPH ATPSHIFSNRG/SPAPQQQLMQ MIQLLAGSGNSQVQTPEVRFQ Q/QLLEQLNSMGFINREANLQALI ATGGDINAAIERLLGSQLS
4672	35040	B	4713	309	527	

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4673	35041	A	4714	1111	2506	KKDQRETRNQKGLGFLDRDPQ WVSGMKMQECLQ/HWNAMAI NNHRAVAIFPKRRRHGREDGLLS NLPTFGSYAPLRRVSNFIASAV QRILLERRALPHGNCKLGGGLTP QFMNRKNALVLEVLARAIHQE KEIKGIQLGKEEVKLSLFADDM IVYLENPVSAQNLKLLSNFSK VSGYKINVQKSAFLYTNNRQ TESQIMSELPFTIASKRKYLGIQ LTRDVKDLFKENYKPLLNEIKE DTNKWKNIPCSWVGRINIVKM AILPKVIYRFNAIPIKLPMTFTTE LEKTTLKFIWNQKRARIKSILS QKNKAGGITLPDFKLHYKATV TKTAWYWFQNTDIDQWNRTEP SEIMPHIYNLYIFDNPEKNKQW GTDLFNKCWENWLAICRKL KLDPFLLTPYTKIKSRWIKDINVR PKTIKALEENLGTIQDIGMGK DFMSETPKAMTTKVVIDKWDL IKLKSF
4674	35042	A	4715	3	372	SVGVLRPWKRE/RAASERRSS SGGGGGGGGGGGGGGGSGS GQ/HAPAAAPAGGIEAVNMAAS YHISNLLGLAALAVTQALP YPSAVAGSFSAPKSPAHRSAGL PIPAEPLSSPLLQPPPP
4675	35043	A	4716	1	1008	
4676	35044	A	4717	1	2619	
4677	35045	A	4718	449	801	VLLSSMSRRKCQSLYVDLLM KKETE*SMEKEKLTMHPLSCTH I*PRPQAPADKQMR*TEEQN CRMWQKKKEHLNAKRS LSA GSGWRDQPLDGKAPGEDHLP IPSPFQLPHPI
4678	35046	A	4719	1	1255	
4679	35047	A	4720	2	843	CLHGFYGRIRDSELQKIHRAAV KGDAAGVERCLARRSGDDLAL NK/TAQIAGAQPREEACTVILLE HGTNPNLKDIIYRNTALHYAVY SESTSLAEKLFHFGANIEALDK VLSISFLSKILMSSLKTCGRDAE DYTISHHLTKIQQJILRKKKIL KKEKRGKASEFLNSLGGPTL DKKIRNVEISDESAVSILHEL CV DSLPAALDDEVLSVATKCVPEKV SEPLCRPSHEKGNRIYVNGK GEG SEECCLPAAHRLRCGERLYLPP RLGCERLCLATIPSEK
4680	35048	A	4721	295	1050	

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4681	35049	B	4722	306	554	
4682	35050	A	4723	2	7973	
4683	35051	A	4724	2	316	
4684	35052	A	4725	81	228	DPPLCLGLL/LHRAISIVQKRIYF QDEGSLTKKLCEQGKTLKHSQ QMFFK
4685	35053	A	4726	1	1043	MELEWKVNVKVNQSDTNHHG SLQLARGEAAAVKFGMRMSKKQ RDSLYAEVQKHQRLQEQRQQ QSGEAEALARVYSSISNGLSN LNNETSGTYANGHVIDLPKSEG YYNVDSGQSPDQSGLDMTGI KQIKQEPYDLTSVPNLFYSSF NNVQLAPGITMTEIEIVAAEF PLIYKQSFLLTVLSFGGGGSVIC GPTFAKVSSRRFIHHGDKIQPS INALGWTFMEETPQIFKCRNT HGKELEHDLPEHSSGQGSTRRK SSCLRRDNNPMLLSGGRFYEKI HNFTGTFDVRKMEHAEGKTS LVHVGFQAIKMPSSLKQEA SNGLIKLEEASGARMKTGHK
4686	35054	A	4727	467	584	
4687	35055	A	4728	1	1794	
4688	35056	A	4729	110	1797	PSQPEPGSGTSLRYCWAQTL PSVTMKLVWSALLMAWFGVLS CVQAEFFTSIGHMTDLIYAEKE LVQSLKEYILVEEAKLSKISW ANKMEALTSKSAADAEGYLAH PVNAYKLVKRLNTDWPALDEL VLQDSAAAGFIANLSVQRQFFPT DEDEIGAAKALMRLQDTYRLD PGTISRGLPGTKYQAMLSVDD CFGMGRSAYNEGDDYHTVLW MEQVLKQLDAGEEATTTKSQV LDYLSYAVFQLGDLHRALELTR RLLSLDPSHERAGGN/LCRYFE QLLEEREKTLTNQTEAELTTP EGIYERPVDYLPEDVYESLCR GEGVKLTPTRRQKRLFCRYHHG NRAPQLLIAPFKEEDEDWSPHI VRYDDVMSDEEIERIKEIAKPK LARATVRDPKTGVLTVASRV SKSSWLEEDDPVVARVNRRM QHITGLTVKTAELLQVANYGV GGQYEPHDFSRNDRDITFKHL GTGNRVATFLNYMSDVEAGGA TVFPDLGAAIWPKKGTAVFWY NLLRSRGGDYRTRHAACPVLV GCKWVSNKWFHERGQEFRLPC
4689	35057	B	4730	1	2433	

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4690	35058	A	4731	425	1079	PMGTSFLYECANFQSVSLGDPQ EPSCLCGGPPQGAAGSSGSED ALLCLWDLQARKWKFEMSYTS GNIRGSSFCQFKSSFLVYFKALL KFRELFAQFKSFMGEKKLSLAP PMSDSSGDIIRKIDYASCKRSG SSIRALPKTYQQP/EVLNDTWV SFPSWSEDSTFVSSKKTPEEQL HRCEDERFEEMKTAGFASFGER SKTGVPNLRVTDWYRLVAC
4691	35059	A	4732	3	425	GASSEEAEAGASEP/GAPGGWG APGSQAQEGGDLQEAEESEQE GGDPRKPRSPRKVERHRKAGA PGRDLGRPSLTVLLNHCVLQR LRKIYHSSIKPLEQSYKYNELRQ HEITGQRCPCCEPKPQHQUERA LFVVSENRI
4692	35060	B	4733	1	1056	
4693	35061	A	4734	171	511	LLSVRHVVNTQETANDVQVW /LDREGGSKI/NTGVCFLDHMLD QIATAVSRMEINVKGDLYIDD HHTVIEDTGLALGEALKIAPGD KPGICRFQFVLMDECLACAL DISGGPH
4694	35062	A	4735	563	763	
4695	35063	A	4736	365	1644	RTSQMSSSAWRQNRARPSAI LPSSLSLGHAPLPQFSQRMPAT ASQLPGMVGVLQGYGQTAASP GSVSSCPACSSCLGCVWPSS WPSCRLHPLHGRPIAHCLPE/VL TTTTTTTITTSQAAGTPKGGQE SGVSPSPQSTCGLLSGPRGFFS SPNYPDPYPNTHCVWHIQTAT DHAQLKIEALSIESVASCLFDR LELSEPEGLLRVCGRVPPPTL NTNASHLLVVFVSDSSVEGFGF HAWYQAMAPGRGSCAHDEFR CDQLICLLPDSVCDGFANCADG SDETNCSAKFSGCCGNLTGLQG TFSTPSYLQYYPHQLLCTWHIS VPAGHSIELQFHNFSLAQDEC KFDYVEVYETSSSGAFSLGRF CGAEPHPHLVSSHHLAVLFRF DHGSSGGFSATYLAFNATERL CLVESTSS
4696	35064	A	4737	1	154	

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4697	35065	A	4738	1	700	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVILRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTALGGILKKKGHHE AEIKPRGTVSNA TKHKIPVKVT WRSSPECINQVLQSKHPGDFGA IDAQGAMKQGP GSCFRKDNWP PTYKELGLSRAKPLAGFPTPNPS WAPGFKRERGLISV
4698	35066	A	4739	1	154	
4699	35067	A	4740	1	617	GSRPQFPGHTRVRASGWRPCSL KPQLLGPVHPVSPYLLFLSSSDC AMGLIDGEWQLVLNVWGKVE ADIPGHGQEVILRLFKGHPETLE KFDKFKHLKSEDEMKASEDLK KHGATVLTALGGILKKKGHHE AEIKPRGTVSNA TKHKIPVKVT WRSSPECINQVLQSKHPGDFGA IDAQGAMNKALELFRKDMAS NYKELGFQG
4700	35068	C	4741	46	522	
4701	35069	A	4742	78	617	TKELLHSKRNC HQSEQATYKM GENFCNLLI*QSANIQLQRT*T NLQEK NKQPHQKVGE GYEQTL LNRRSLCSQKTHEKILIITGHQR NANQNHNEIPSHTS*NGNH*KV RKQQVSYKLL*MRPRTRQVT Q*RREPETSLAKETPGNPTNTN AKFKTRGARISHYSSNGERLP RTVC
4702	35070	B	4743	1	6477	
4703	35071	A	4744	1	623	MSSDISEVEDKNEFLTEQLSKP QIKFNTLKDKFLKTRDTLARKKS LALETVHNHLSQTQQQIKEMK EMYENAEAKENNSTGKWSCVE ERICQLQHENPCIEQQLDDVHQ KECLPSRKEKFKSEPPAFLSGN QVKSSSCSLQTLFPDDLILYLE NPKDSTKKLLELINKFRVTGYK IKLQKSAFLNDKNEQSKEENQ ECNPIYNNYK
4704	35072	A	4745	2	3272	
4705	35073	A	4746	1	579	
4706	35074	A	4747	3	510	

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4707	35075	A	4748	1	1261	MEAVDTFLVFNALNFLTSQTT GCSSSCDPGHLGGQSGNRPFI AAASARTAEAAKWWFSNNDYS NVLQLDPKKT EYHIHEKRFSD SRILCYYPEFGKVEEILTAMKH DWFGRHKKDDKIEKTKGIQIE SFTSEEEIRIMKQEQERIQAKTR EFRE\RQARERDYAEIQDFHRTF GCDDLMYGGVSSYEGSMALN ARQSPREGHMMDA\LYAQVK KPRNSKSPVPSKGVVLGEADP VYPRRNPTEGNASSLPVSFSE SPPVRAAFAGYHYVAFPWLQK LMSGTSGKDPEKADLARVVT LRVVTLRITHVKTLAFTAALL QQLACIDVGMDKQNDVYTYN KILLSFKRKEILTHTTTRMSLED IILSEINQWQEDKYRFGLYEVA QVVKLIETESKVVVSRDGGRG
4708	35076	A	4749	10	2051	
4709	35077	A	4750	2	2118	
4710	35078	A	4751	1	658	MWNSKTLAARPCPKDPLNFE LERDNLAYLAEEIPKQSIQYIT WMILKAFSHMHLQRDNLKLEL MFKRKAKHKGLKNLHPDHVIE KKNLFSAEKFKPAEIIYISNEEP NVNSQDNGKKCLQGMSEIFAA APAITDNTSDKTTLIKVSSWPVI ADRRCPVLNVTRDSPSEDVPF LRTLKGQDWFGEKALQGWGL\ KGIHHVSAQEPVCLLLPFMTPR
4711	35079	B	4752	1	471	
4712	35080	A	4753	315	407	
4713	35081	A	4754	411	1042	
4714	35082	A	4755	1	423	
4715	35083	C	4756	202	321	
4716	35084	A	4757	5	413	CCCCFFETESHFVTQAGVQWR DLGSLQSPPPGFTPF/S/QPPKE PGPQAPATTGQSFALVEMGF HHVSQ/EVSIS*PRDPPASASQS AGTTGVSHRAWTFCLRLQSLA LSPDWSA VARSQLTATSASVV QVSR
4717	35085	C	4758	150	491	

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4718	35086	A	4759	1	548	GIAFCI.NI.IK.TL.KI.PNFKSCVIL L.G.L.L.L.Y.D.V/FFVFITPFITKNGE SIMVELAAGPFGNNEKNDGNL VEATGQPSAPHEKL.PV.VIR.VPK LIYFSVMVCLMPVSILGFGDII VPGLLIAYCRRFDVQTGSSYIY YVSVSTVAYAI.GMIL.TFVV.VL.VLM KKGQPALL.VLPCTLITASVVA
4719	35087	B	4760	642	1985	
4720	35088	A	4761	39	252	
4721	35089	A	4762	1	783	
4722	35090	C	4763	218	358	
4723	35091	B	4764	372	374	
4724	35092	B	4765	129	1036	
4725	35093	A	4766	1211	1983	SQSLI.L.Q.EDFAP.IAGEQEAEQ HQED.I.RALLRASLQGQCSRQP GTRLHGSA.PWPGEAQNRSLPLP GDSPSLDRYRG/SDAVGKSRSG DIGSSLR.VEAGDKRTQASPERQ PHCGA.HDAQDISGGEIFKPRQ LPGSAIWSIKVGHGSGFPKRR PRGAGLSGRGGRGRSKLKSIGI AVVLPGVSTADISSNKDDENS V.LDMVVLFSSSDKFTLN/QVCG SFGQGAEGRL.LACSQCGQCYH PYCVSIKMDACSSSELKY
4726	35094	A	4767	1	603	MANFND.CVLDKEKVCIAAKFIT HAPAGEFNEV.FSDIRLLCNDS LLRERA.ARAFAHYNMDQFTPV KMEGCE.DQTHIACIESHECQPKN FWNGRWRSEWKFTITPPTAQV VGVLKIQVHY.YEDGSVQLVSH KDVQDSL.TVSND.AQTAKFIKII ENAENEYQTAISENCQTMSDTT FK.VLRRQLPVTRTKIDWNKILS YNI
4727	35095	A	4768	1	867	MADFDDR.VSDEEKVRIAAKFIT HAPPGFNEV.FNDVRLLLNND NL.LREGAAHAF.AQYNMDQFH AVKIEGYEDQV.LITEHG/DI.GN SR.VL.DPRNKIS.FKFDHLRKEAS DPQPEEADGGL.KSWRESCDSA LRAYVKDHY.SNGFCTVYAKTI DGQQTTHIACIESHQFQPKNFWN GRWRSEWKVPITPPSAQ/VVG VLKIQVHY.YEDGNVQLVSHKD VQDSL.TVSNEA.QTAKFIKIIIE NAENEYQTAICGN.YQTMSDTT FKALRRQLPVTRTKIDWNKILS YKIGKEMQNA

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4728	35096	A	4769	2	690	WPSGSASRPRLRAPEPV/GKA GKNKGAGLTPA/AGTSGCAGR AESRGPPPTGSHGSEPSRGSKGL CGRGTRSLPERGAELPHLPAQ TSPQLGSQGAWP/RHPRKPRFP AARAGTQPPGFVPSTPALLKVL YRSAHTQHSGRAAPEPSRLALG PTLQQKRHMGMHRRNLTFSTY NKKCGFGWAVEMRFSALLDVT TTPSRVAFWGSRGPPGLMERQL QLLSGYS PDGWLSTSM
4729	35097	A	4770	1	590	MDTRIGTDTGTGYGKVEGARR MRLKKLPHEYAYYYLDDEICTS NPCEFPGYGIERYPCETSGPLE LTVQEDQGEFPQREELTRKKT KVCRGSPLAWATGVKPKLKKK RRRRKEERRKKKEEGEGEGEEEE EEEEEEEEEEEEEEEEEEEEEEEE EE/EEEEEEEEEEEEEEEEEEEE EEEEESDPCTSWNTSQP
4730	35098	A	4771	1	288	
4731	35099	A	4772	1	237	MRSSVIGPRSHIPSRQKSGIQEE EEEEEFQEEEEEEEEEEEEEEEE EEEEEEEEEEKGLDQEAARHLV LPAATQCKPKM
4732	35100	A	4773	1	794	MASHSSPMGSGYQYYGFGPD AMHALNTVVSEKDLTDLGL VARNKRCGPHYSYLNTHLLHA CLRLPTQRENTTLKTFIPQGW HTDQVEREAECQPGRLKICVHD TAQELPLASTARNALLGRNLCP FRQSTTQMPDEIPISLDDRM PSLKKKK/VVGEEEEEEEEKEK EEEEEE/DEGEEEEEEEEEEEE EEEEEEEEEGGGGGVGE EEGEGEGGGGGEDEEE*EEEE EQKKKEKKKKEQEEGGGEGG
4733	35101	A	4774	115	341	
4734	35102	A	4775	1	651	
4735	35103	A	4776	189	618	SLCHKEAEGGHGKAHVEGKRA PSNLQPSAPAE LSGNNSISPHHE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEDLLYNFI YHFSKMPTKVPSLWDSKLGAE QAAPEENKKEQEEYQGKSF SFLNLTECWP
4736	35104	A	4777	1	414	

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4737	35105	A	4778	189	692	SLCHKEAEGGGHGAHVGEKRA PSNLQPSAPAEISGNNISIFHHE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEDLLYNF IYIIFSKMPTKAMSISSMFKFAT KIRMTVTNPKCCWIPVFPAYL STSKAAKCMHHTAHHGQEKSD HCISPSPIAP
4738	35106	A	4779	2	3815	
4739	35107	A	4780	957	1493	KNNRYNKLRLPQCNPTRTQD* ETHSKPLNYMETEQSP*LLG T*RNEGRHKAVL*NQ*EKRHNI PESLGH/AKQCVEGNL*H*MPT RESRKDLKLT*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQELVF*KDQ QN**TASKTNKEEKREESNRN KKC
4740	35108	A	4781	1	4962	
4741	35109	A	4782	2421	3011	NQACQPGQAGAAARAGQCFPRV AQRPGPGPAGMALAHPDLYL HSAAGDQCR*DEEADPPQGAPT HFQVHPAGGLHLLDRLAAPH QAGTQGGQPGRRH*PAARSS PVEPPSTGSPSRPTTMMWPSCSR RQGGGLGGL*CVQQPHLLDAP GTLPLVGLALVCRLOPWRLCL GGGGGVGGSQRPFGGGGGNG GRNWG
4742	35110	A	4783	1	932	MRTPKSSIKPSLGEKENYRGS LKETAAPSLQKEWAEQSSKSQET VGKVGITRHFQVSTLLERREDR KSKEPPLLIPTQTVSGVDLQQT TDLQLSVLTVRRKTNKQKQHP HQKPICTSPSSNTKVNLEKQL DEWLTRITNAEKSSKDRMELKT KARELHDECTSLSSRCDQLEER VSVTEDEMNMKRGEKFKREKR IKRNEQSLQEIWDYVKRPNLCL IGVPESDGENGTLENTLDIIQ ENFPNLARQANIQEI/RENAT KILLEKSNSKTHNCQIHQS*NEG KNVKGSRERSGYPQREAHQT
4743	35111	A	4784	477	638	LLCCGFELPLLARRSLIV*SLLS THQSHSPSFVPLLVRSCLPEEE RRSDF
4744	35112	B	4785	1	1509	

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4745	35113	A	4786	3	832	ERHHPPQAGPHPPRRRKERN HRQPTPQPHGA/WKISVPQT TNGISSITSTQRNPQATTVEKA HNESTRTPPEPKGAVRGTR*KK KKTSRDTPQT*EKSSSATRNK AGGKSDSKRERKATEDQTTPS KRRKLHPMAKKLTLKKN*MN G*LE*PMQSP*RT*WS*KPRHE NYVMNAQASVTDAINWKKGPP PRPTTNDKIVTRPTHPTCSHH RPPRKPPRTHPTPTQNKISQ* NGYTPPRGKRVREDRCKPPQAP TSAPRAAKQRQS
4746	35114	B	4787	1580	4673	
4747	35115	A	4788	1	462	MKLEHQAQRSGQGREKRR WPEGKAGPGCEGAWILCPESQ DDSKQEGDNNMIVVSRNAVRS VKAEFQGDNLNWECSAEIIV QGRDNGVPHKAHGLGTEEGT VLKISERQNWLDLVDIFLLGGD LFHENKPSRKTLHTCLELLRKY CMGDRPVQFEILDQSVNFGFR KLNRKDIHTKNPSVRHHQRP KVDETIKMGKTQSRKTRNSKN QSTSPPPKERSSPAIEQSWMEN DFDELKEEGFRRSNYSELKEEV RTNGKEVKNLEKKLDKWITRIT NAEKSLKDLMLKTLIAQLRDE CTSLSNQCDQLEERSVSMEDQ MNMKREEKFREKRIKRNESQ LQEIWDYVVRPNLCLIGVPESD GENGTKLENTLQDIQVNFNL ARQANIQIEIQRMPQYSLRR ETPRHIVRFTKVEMKEMLR AREKGLECSGAGLAHCKLWLL GPSDPPDCSSVSPVLRVHLVLP SLPHSVGTPLGVSVPSPVPRFP DRVHFPYPYTHYCDNLKTCHT SHGSVMAETAVINHKKRKNP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRL YSVINPYLIPFFIGLQNRFTQFR LSEKTEITNPYAMRLYESLCQY

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4748	35116	A	4789	1314	2221	KNRNYNKLRLRPQCNPTRTQD* ETHSKPLNYMETEQSPSE*LLG T*RNENGRHKA VL*NQ*EK RHNI PESLGHI/AKQCVENGLH*MPT RESRKDLKLT*/PSQLKELEKQ EQTHSKAGRRQE/TN*DQSRIEG DRDTKNPSKNQ*IQLVF*KDQ QN**TASKT/IQRRKERRIK*TO* KMLKEDITDPTIEIKTHREYYK HLYAHNLENLEEMDKFLDYTT LPRLNQEEAESLNRPITNSEIET VINSLKEKAQDQKDLQLNSTRA LFTIAKAWNQPKCPSMTDEIK/I NVEHIIHGILCSHQKE
4749	35117	A	4790	2	2260	TKDKNHHMISIDGGKAFDKIQQ PFMLKTLNKLIGDGYTLKRIRAI FDKPTANILNGQKLEAPLKTG TRQGCPLSPLLFNIVLEVLARVI RQEKEIKGIQFGKEEVKLSLFA DDMTVYLENPIFSAQNLLKLIS NFSNVSGYKINVQKSQAFLYTN NSQIMSELPFTIATKRITYLGQL ARDVKDLFKENYKPLLNEIKED TNKWKNIPCSQIGRILWPYCP QEDENFNSLLQNGDILNSSTEE KFKAHDKKDFNLPEYDLNVEE RLVLEIKSVDSTATADDT HKLD HINMNLNKLITNDTFQPEIMERS KTQDIVLGTSFLSINSKEETEL ENGKNYPNLESVNVKVNHGSEE TSQSPNRTEPHSDSCSVDLGISK STEDLSQKSGPVGSVVKSHSIT NMEIGGLKIYDILSDNGPQPST TVKITSADV DGNIVRSKSATLL YDQPLQVFTGSSSSSDLSIGTKA IFKFDSNNHNPEEPNIIRGPTSGPQ SAPQIVYGPQYNIQYSSAAVK DTLWHISKQNPQIDHASFPQPLL PRSESTENQSYAKHSANMNFN HNNVRANTAYHLHQRLGPARRH GEMWAISPNDRLIPAVTRSTIQ QSSVSSTASVNLGDPGSTRRAQ IPEGDYLSYREFHSAGRTPPMM PGSQRPLSARTYSIDGPNASRPQ SARPSINEIPERTMSVSDFNYSR TSPSKRPNARVGSEHSLDPPG
4750	35118	A	4791	1516	1729	ILAPHSLACRVSAERSAVSPM GFPLWVTQPFSLAALN/DFLHF NFG/RJ*QLCVLELLFSRSIVVAF SEFP

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4751	35119	A	4792	3	1426	RRYDELQNSSGRDGKPRAMAV TRSTSSTSSGSNSNVLVPVSWK RPQYSQKRAKEKL VHVLSLCC QEVGLSKNPSVIFSSCGDLDLLE HQTSLVSSSEDGAREQENMDDT NSEQQFRVFRDFFDL DVELEDG EELQGESMDNFNWGVRRRLSD SLDKCDMQILEERQLSGSTPSL NKMHHEDFDESSEEDLTASQI LEHSDLIMTLSPSEETNPMELLT TACDSTPPEPHSFNTRMSSFDAS LPDMNNLQISEGSKAEAVREE EDTTVHEDDLSSINELPAAFEC SDSFSLDMTEGEEKGNRALDQF TLASFGEGRGVSPPPSPFFSAI LAAFQPAACDDAEAWRSHIN QLMCDSDGSCAVYTFHVSSLF KNIQKRFCFLTCDAASYLDNLL RGIGSKFVSSSQMLTSCSLDKL KFSVLELQEYLDYNNRKEATL SWLANCKATFAGGSRDGVITC QPGDSEEEKVIKAC
4752	35120	C	4793	60	164	
4753	35121	B	4794	44	2547	
4754	35122	A	4795	401	9546	PRADITTCDDRITPGTCRPLPV LPASLYAADMASQQDSGFFEISI KYLLKSWSNTPSPVNGYIKPPV PPASGTHREKGPPTMLPINVDP DSKPGEYVLKSLFVNFTTQAE KIRIIMAEPLKPLTKSLQRGED PQFDQVISSMSSLSEYCLPSILRT LFDWYKRQNGIEDESHEYRPT SNKSKSDEQQRDYL MERRDLAI DFIFSLVLEVLKQPLHPVIDSLI HDVINLAFKHFYKGYLGPNTP GNMHI
4755	35123	A	4796	2	6107	GERKPKIDLFRTCVAAIPRLLPD GMSKLEIDLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNLLREVNDMHHTLL DSSKLKLLQLLTQWKLVIQTQG KVVEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDVDL GVDVDVGVDVDADVDVDVD MGVDVDVDRIYGFCKCGCDR DVDRVVDVDVDIDVDVDVDM DVNIDVDVGLGAGVDVDMVD HIDMDMDVDIGSDNQLSALRR

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4756	35124	A	4797	3	565	MLPGHLFLAKAGKEEQEEKG QHTRKTITPQNIPGGAHITATH RGRCTVATKFSGGGLCKEPNRLT WY/GPPLKGAHGGGR/GPSSRVPS FPAAGQPPIGGALHGAGSRGLA RTRAQLGGPPGGELRGTSNGG DGGQPDGDSRKSGLRPSHL/P DPAAVAGAPVSGHLQTPGHHA GRRQQAGPRGAGLP
4757	35125	A	4798	1	417	
4758	35126	A	4799	1	1069	MPRPVPPANALGARGEAVRLG LQGEELRLQEVSVRLHQINYL SDRISLHRRLLPVRWNPLCKEKK YDYDNLPRTSVTKAFYNEAWS TLRLTVYSVLETSPIILLEEVIL VDDYSREHLKERLANELSGLP KVRLIRANKREG/LVRARLLGA SAARGDVLTFLDCHCECHGW LEPLLQRIHEEESAVVCPVTDVI DWNTEYLGNSGEPQIGGFDW RLVFRWHTVPERERIRMQSPV DVIRSPTMAGGLFAVSKKYFEY LGSYDTGMEVWGGENLEFSFRI WQCGGVLETHPCSHVGHVFPK QAPYSRNKALANSVRAAEVW MDEFKELYHYHRNPRARLGLAC DECSIKAGWWL
4759	35127	A	4800	1	1152	MHNSDGIEVMRQQAIEIGRVG GLEGIQLGVTEIVNGARMLES YNCKAELGATGLVNYQISVKC SNQFKLEVYLLNAENKVVNDQ AGTQGGQLKVLGTNLWWPYLM HEHPAYLYSWEGRPDGAQAVG ALTPGTLAVIEVWLTAQKSLGP/ SDFYTLPVGLRTVAVTESQFLIS GKPFYFHGVNKHEDADIQGGK FNWPLLKDFNLLCWLGAFT CTSHYPYTEMLQICYRYGIVVI DECPAPSGHTGPSVPSLLARW QLFNNVSMHHHMWVVEEPVL RDKNHPAMVMWSLAKEPASFL ESAGYSFKSLTMEQTRVLDLDD TGEAVLQYRSRPRGAHKTLGK KRKISSYNVDLTSCQLAKEKCL KGPSSFLQSRQERMNSLRDN
4760	35128	A	4801	293	535	
4761	35129	A	4802	94	686	
4762	35130	B	4803	1	2187	

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4763	35131	A	4804	596	1789	MFHVIERPYECKECGKNFRSGY QLTLHQRFHTGDIHKGKGPYEC KECKKTFTLYRNLTRHQNIHTG EKLFECKQCGKTYTTGSKLFLQI QKTHTEKPYECKECGKAFTSL YGYLKQHQKIHTGMKHFECKE CKKTFTLYRNLTRHQNIHTGKK LFECQECGKAYSTGSNLJQHRK THTGEKPYKCECGKTFSLHG YLNQHQKIHTGVKPYECKKIHT GGKPYECKECGKAFTSRASNLV QHERIHTGEKPYVCKQCGKTFR YGSALKAHQRIHRSIKVNQWL DSPRHKSINCDPMSPRTRKTRE RSHVSGRSLCQRLLGQAQLRE FKQPPNRFRFVCGLVARNTPF RGLRGRASRRNAASRLEDA VAELLKARCSALGSGSGLPEGLS
4764	35132	A	4805	2	489	CQEGAKWEGQMTGRRVWVG PPASSTPPHS/HFWLLVLSRGLV GIGEASYSTIAPTIGDLFTKNTR TLMLSVFYFAIPLGSGGLGYITGS SVKQAAGDWHCALRESFLQLV RLLKVTHLLQQLQLLYPTNGK RQDTNHTRSQCAHYLPHLDFQ VALCAYAVLQC
4765	35133	A	4806	1	327	
4766	35134	A	4807	899	1219	ANRKASTMRWYVRPFCSGLST LSREKLYPLRLMRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPAAWMSFTI WAVRLPL*KAWAPSMASVS
4767	35135	A	4808	2152	2633	SRLDCGQGLVNGSCDYHHGCT GDTPRRPEWHRSLAHCMSPPV SLPGCAVSGSSDPWEVSWLWQ QVDRCDNREE/VMW*QRLGFP SPTVSFPQRAVSASKPLQ*APS WISLHSTLSQCRASDLRGRHTV PEVVYVWSPCALPTHREHPNAI MEGWPPPQAWWA
4768	35136	A	4809	2	387	SNASVILEGEDLRFSCSVMAG RLQGRFSVIWQLVDRQNRKSDI MWLDR/DGTVQPGSSYWERSSE GSVQMEQVQPNFSFLGIFNSRK EDEGQYECHEVTEWVRVVDGE WQIVGERRASTPISIALGE

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4769	35137	A	4810	46	3753	EIRSWEKRRRLVLCLEAADM KCFFPVLSCLAVLGVVSAQRQV TVQEGPLYRTEGSHITWCNV GYQGQPSQNFQWSIYLPSSP EVQIVSTMDSSFPIYITQRVR GGKIFIERVQGNSTLLHITDLQA RDAGEYECHTPSTDKQYFGSYS AKMNLVVIPDSLQTTAMPQTL HRVEQDPLELTCEVASETIQHS HLSVAWLRQKVGEKPVEVISLS RDFMLHSSSEYAQRQSLGEVRL DKLGRITFRLTIFH
4770	35138	A	4811	1	3728	MKCFPPVLSCLAVLGVVSAQR QVTQEGPLYRTEGSHITWCN VSGYQGQPSQNFQWSIYLPSSP EREVQIVSTMDSSFPIYITQR VRGGKIFIERVQGNSTLLHITDL QARDAGEYECHTPSTDKQYFG SYSAKMNLVVIPDSLQTTAMPQ TLHRVEQDPLELTCEVASETIQ HSHLSVAWLRQKVGEKPVEVIS LSRDFMLHSSSEYAQRQSLGEV RLDKLGRITFRLTIFHLPQSDQ GEFYCEAAEWIQDP
4771	35139	A	4812	897	1217	ANRKASTMRWYVRPFCSGLST LSREKLYPLRMLRMRASTGPLS GALGMYSTASPRLMFSGCSISS AR*LFRSSAVTMPAAWMSFTI WAVRLPL*KAWAPSMASVS

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4772	35140	A	4813	1	1507	MWNSKINHDIIDDOFLKTYTVL ESSISVGVASNASVILEGDDDLRF SCSVRMAGRPOGRFSVIWQLV DRQNCRSNIMWLD RDGT VQPG SSYWERSFFGSVQMEQVQPNF SLGIFNSRKEDEGQYECHEVTEW VRVVDGEWQIVGERRASTPISII ALEMGFAVTAISRTPGVTVSDS FDLQCIKPHYPAQVPVSVTWR FQPVGTVEFHDLVTFTRDGGV QWGD R S S F R T R T A T E K A E S S N NVRLLIIRASDTEAGKYQCVAE LWVKNYNTWTQLAERTSNL LVIRVLQPD RMGVSARALRGEP SPSQMPQACCHGNTGALVIGIN EPESL PCLQTVTKLQVSKSKRT LTLVENKPIQLNCVSKSQT SQN SHFAVLWYVHKPSDANGKLIL KTHNSAFEYGTYYEEGLRAR LQFERHVS GDLFSLTVQRAEWL LSPNYAWYKLAEVSGRTEVT VKQPGGSLGLGCSVSGWAAEP VCTQGRPCSWNTPLALTAAC
4773	35141	A	4814	1	627	
4774	35142	A	4815	166	435	
4775	35143	B	4816	1	240	
4776	35144	A	4817	1	288	VVPASSPGAASEPRRRRCLQP EKSVPSPGGGHRDPPKARPPR PPSAPKP*RRPFS*LARSLCFPA AGCAYGVGVGGAGGGRAGLR QVPVAE
4777	35145	A	4818	206	1041	VSVGSAPSDMPAAATRW/CNSR COHQRLSAR/PVAGPGT/RTSS FPWLA PRNVVPGSLEMPGTA GPORGSHSSPGSSALLSFS/CV HNVESKEPVCLLLPSMASRLT PRGTCRPVPGCLQHPLSLPPVL VGTQSPSQAPKS AKRPSQPQL GWLQLHPGSGSLCLLPAPAGS MECAALESVPSQLGIGAPGPCW AQAGVQGWNSVATSSSPGSA QGQPRAPPCLVCGPAQCGTSGS RSRATGLRPSCLECQVWWSQV CGANPGDTTSSQDAGTRCSKV
4778	35146	A	4819	2	487	

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4779	35147	A	4820	152	758	RGARGPEWDGQLDGPQSGMC GMAAPRLRRSGVRAAAGHPV QQPRLLDGLSLTDESDSCVSFEP PSHPSSSSGPVTALSRGWNFLK AFPLMGETQERER/VLTHFSRR YQCQNPDAQPSDEGHI/TLTCA LMLLNTDLHGHVIGEVGTETN RTDKQQNRTEQSKRQANADKH NEHANNEQQHEHDKDNDTRTR DTEMRHAKRDNA
4780	35148	A	4821	100	220	
4781	35149	A	4822	100	1588	CLKISTGYTGSMFAEEASGNLTI MAEEGEAGTSTHGQSRKRE KEEVLHPFKQPDVRSYRENS KEEICPHDSVTSQITPPPTLGITI RHEIAASICHVADTAGVAGDA MMRKTDLIPPFIGLTLQGGSA DMGNQKKWRKGSENLATLVA MASERFHWQYSGNSTIQPKQK QHGMITRLVTAAPVCPGLVQPPL CAVGLRNIMSLSSHTCALQNTK QAWEGYDDCHSQRVSQPGEN MTKLFLNLLNQMPWSWEGGKM VPADFGSGCWEGTGTGSPAGSQ VSFLNRHNDGQLAGDSPGLPPP PCPRGLQGAEQRSALRRHKAD VHRDQWLVISFSKKLRTSARK WYEAGPFGVPRVLPAQAQGG TDFPFSPSEEPFQSPFSMVQAH TVRSKPQFHFAAGENCNLRSE LSRNQGLQARVGPLAIMSSDPS GDFVLYTPTILGVGLEVLVSR EGTFLWRYSTCP/LNYKLWLPP GYLGLLVPKDQKVRAVFLGM
4782	35150	A	4823	1329	1881	AHLEAAGWSSSVQPGSPRVLG RAEEHQQSRAKEIGHKIPKE TFDELTALETISSK/CLYLAKK NQVIQELLSMKEVQKCKKL EEVKNILEQEVVNLKTHEKNM VEFGDVEECKLQLEERAGQEI KLEEINLQRACLSAKKVRAEGE LEPRRHNNHILGFTGEPWGLM SVITGAYDLIR
4783	35151	A	4824	176	308	LGNLTSPPFN*KHRSTKGTFTLS TVALLTLGHVGKITSNCHPGY

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4784	35152	A	4825	1467	1890	DWFDeltaETISSKICLYLAK KNQVIQELLSSMKEVQQCKK LEEVNKILEQEVVNLKTHEKN MVEFGDVEEKLQLEFRAGQE EKLEELNQRACLSAKKVRAG ELEPRRHHNHTLGFTEGPWGL MSVITGAYDLIR
4785	35153	B	4826	1	753	
4786	35154	A	4827	225	410	
4787	35155	A	4828	225	410	
4788	35156	A	4829	225	411	
4789	35157	A	4830	141	1001	GGVRGVQKETCAFKVLESIG KLG/LALSVAGGAENSALYNVD AGHRAVIFDRFRGEQDIVVGE THFLIPWVQK/PIIFDCRSRPRN VPVITGSKDLQNVNITLRIPLRP VASQLPRIFTSIGEDYDERVLP TTENLKSVMVAPFDAGELITQRE LVSRQVSDDLATERAATFGLIL DDVSLTHLTFGKEFTEAVEAKQ VAQQEAQARFVVEKAQEQKK AAIISAEGDSKAAELIANSLATA GDGLIELRKLEAAEDIAYQLSR SRNITYLPTG/QSVLLQLPQ
4790	35158	A	4831	194	453	QPLPELELRPKAL*LTSPQFSA *RLKTAARLPKPWAVLPQGFT DTPPHFSQAQISSSVTYLSIILV KTHVLCSPFHRTGVV
4791	35159	A	4832	1	86	PCESYLEHL*WSCRLRLRLGSV SLQLLS
4792	35160	C	4833	191	263	
4793	35161	B	4834	1	741	
4794	35162	A	4835	3	96	
4795	35163	A	4836	1	301	QEQQKMNTLQGPVSFKDVAVD FTQEEWRQLDPDEKITYGDVM LENYSHLVSLAYEVATSTCTSEIL KPSNLPKSFSSH*QDMISPSQT SSLSWSRERSG
4796	35164	A	4837	3	273	VLHFISAGNTFAHQEHSPRKG PNNLSKRKLLPAVIGPRVFHGE DRHIL/LFSTRKE*ARSLCYVQG GVQAPAAAFCSLLSLGWGAGC AFWC

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4797	35165	A	4838	3062	3688	RSVTRAPPRTSTFPLAQAPSRS HIREPTSPHLGRLGSHRGPPS RPLPPALAAALSLETLQPRLLHP HLHLALHDQGRACVRAYAHPS YLWRCHALGVWVES/ARLRPS ALPPAHSPPLAAPLLSSSVQPPA PALEPPPRPPAAGAAARCLAAQ HHHPSRLGVRRQPLAVGALGST WPPQAPAPPELSALEQDRVGA QPPPPPSQGA
4798	35166	A	4839	1	197	
4799	35167	C	4840	26	358	
4800	35168	A	4841	84	433	PASAPLGLSATVSACFQEQQKM NTLQGPVSFKDVAVDFTQEEW RQLDPDEKITYGDVMLENYSH LVSLAYEVATCTSEILKPSNLP KSFFFSH*QDMISPSQTSLSWS RERSCG
4801	35169	A	4842	1	372	VQWLFMQICLGGKHQQLRHQG VQEKMLPLEGS*VIEAGSPTLIG ETLSLEIINYIIGAGLESVHTHKS RQLGGWTRPGSHFQVQLIPAHT PMNLEPSQLSLEPRLVPAQQSL PSAPTSPKALSQ
4802	35170	B	4843	7	267	
4803	35171	B	4844	213	3895	
4804	35172	C	4845	141	359	

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4805	35173	A	4846	831	3017	RRRLHYSGSTRPWRTRAMLPRL TLSLRPHLSLHLPLPCLLLHLA LPTHLPKPKHQPTVREL/ARRC RLPRACHPAQNLLQQPLRPSH LQRH/LSLLPPLGLSQSGPPG/LA PQPLL*LQTPDHFAGADPCSIHG TSH*HQGTSNPSGRDGYQTPSH ICPSPAPKQSFLEGTQNTSPSSP AAPAASSAPPMFKPIFTAPPKSE KEGTPPGPSVTATAPSSSLPT TTSTTAPTQPVFSSMGPPASVP LPAPFFKQTTPATPTTAPLFL TGLASATSAPITSAASPTDSA SKPAFGFGINSVSSSVSTTTST ATAASQPFLFGAPQASAASTP AMGSIFQFGKPPALPTTTVTTF SQLHTAVPTATSSAADFSFG GSTLATSAPATSSQPTLTFSNTS TPTFNIPFGSSAKSPLPSYPGAN PQPAFGAAEGQPPGAAPALAP SFGSSFTFGNSAAPATAPTPA PASTIKIVPAHVPTPIQPTFGGAT HSAFGLKATASAFGAPASSQPA FGGSTAVFSFGAATSSGFGATT QTASSGSSSVFGSTTSPFTFG GSAAPAGSGSFGINVATPGSSA TTGAFSFGAGQSGSTATSTPFT GGLGQNALGTTGQSTPFAFNV GSTTESKPVFGGTATPTFGQNT PAPVGVTSGSSLFGASSAPAQ GFVGVAFFGNTFAHQQEHSPR KGPNNLSKRKLLPAVRAQGPPR
4806	35174	A	4847	9	935	IPCFCGAMPYQTRRQENDLR TASIAV*RRKQDDH*QKRRW QNIQRKGPKRYIVIAGNSQSHQ PMIFSMLRKLPKVTCRDVLPPIR AICIEIGCWMQSYSTSLTDSY LKYIGWTLHDKHREVRVKCVK ALKGLYGNRDLTARLELFTGRF KDWVMVSMIMDREYSVAEAV RLILILKNNMEGVLMVDVDCES VYPIV*ASN*ALASAVEGFYLYW KLFYPECEIRTMGGREQRQSPG AQRFTFQLLLSFFVESKSHFVTQ GGSGGQFAHRNLCPLGSGNFI VSASRVAGIAGAPHTWLIYVF
4807	35175	A	4848	1	1749	
4808	35176	B	4849	282	1227	

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4809	35177	A	4850	221	907	FEDSFNIRGVKKKAARPLKTPP VAKYPKKGSQAVHRHSRKQSE PPANDIFNAAKAASDMQHRE VRVKCVKALKGLYGNRDLTAR LELFTGRFKDWMVMSIMDRE YSVAVEAVRLILILKNMEGVL MDVDCESVYPIVLKYPECEIRT MGGREQRQSPGAQRTFFQLLS FFVESKLHDHAAAYLVNLDWDC AGTQLKDWEGLTSLLEKQDS TCHMEPGPGTFHLLG
4810	35178	B	4851	1	2361	
4811	35179	B	4852	1	878	
4812	35180	A	4853	1	313	MPHTPRCLFRPQASCLVHFLEQ QNKLLKLETKLQFFQNRCECKSNL EPLFEGYTLRREAECMEANS RLASELNHVQEVLEGYKKKYE EEVALKATAENEFVALKK
4813	35181	A	4854	188	354	
4814	35182	A	4855	405	647	LPLISDQVSYSPLMSKSLASLY QESY*TLARLPLISPFVNSLST DLFILLIGNTSIAIAFEGVSAISL PSCNSLE
4815	35183	A	4856	1	585	MSSGEGKRTWLGLWGGRVVP VPPICGLRVAVTSAAGTSSFLA PKPTRIRGERGKGQGRG/SSGN GGGRGRAGASAGSGREVVSV NDGRWRGRGRGVGCPRSSKRE DNRFAKHGRASGKAWEPHPPS QALRALFGPIRRRGRAAETRI YWKDRQLTNRDSTILELQKVL KTCCAQSMKIFCCLWNFVYKQ
4816	35184	C	4857	12	468	
4817	35185	A	4858	1	1156	MAFRKKIITAGCIDHVLVSVD QQMQANLTQRTEAIRKQTQIA PTFPAHSLPDKYLGFALLNRKII GTFLVFNMCNRNHEDKNEAFT VLREKKVFNLEFCTLQNYSEV KEKERQRFSKQTLREFATRK ALKEMLVQLQRYKERKHIRKR NVKYSADHTTDTANQADPNQ QEPHVPGHAPDNKTIQKQNK HKDNTTRKHNQMTSDTSRTNT KVSQQRPGKQTRRRHERQQA RERQGRHQRK/RDAQTRHTQR QRQARAE/QVIENKREEKRTS ERTNDSTRREGTRRPRTEKGE RQEEGDRATATHRKDHDRQPP HGAPHCSRSSRHGAPTPLYCC SPLPGTPSCTICTVQYGRWLPH MATEQLNMAGPNQDFQDVVW

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4818	35186	A	4859	1	1580	MAPALLLLLASGAAACPLPCV CQNLSESLSTLCAHRLGLFVPP NVDRRITVELRLADNFQALGPP DFRNMGTGLVDLTLSRNAITRIG ARAFGDLESRLSLHLDGNQAG GAGHPRALRGPVNLQHLILSGN QLGRIAPGAFDDFLESLEDLDS YNNLRQVPWAGIGAMPALHTL NLDHNLIDALPPGAFAQLGQLS RLDL.TSNRLATLAPDPLFSRGR DAEASAPLVLSFSGNPLHCNC ELLWLRLARPDDLETASP LAGRYFWAVPEGEFSCEPLIA RHTQRLVWLEGGQATLRCRAL GDPAPTMHVVGPDRLVGNSS RARAFPNGLTLEIGVTGAGDAG GYTCIATNPAGEATARVELRVL ALPHGGNSSAEGGRPGPRTSPP PLALLPRYNSSDETLIYRIVPA SSHHFLLKHLVPGADYDLCLLA LSPAAGPSDLTATRLLGCAHFS TLPASPLCHALQAHVLGGTLTV LVGGVVLVAALLVFTVALLVRG RGAGNGRLPLKLSHVQSQTNA
4819	35187	A	4860	2	403	
4820	35188	A	4861	87	442	PVFPWHYPYKQKESQSVLVI WQKTAGGGWSTW/WLSFSPET EKVVKK/AHVDTL*NEMWDVT K*TAFKIPSC*T*HQHP*SFFRK SESQVIVFAGQGVKIH*YILLHS NVIHYMNEI
4821	35189	A	4862	2	651	EFIKQWDADKFEHIQTLEGHQ EIWCLAVSPSGDYVVSSSHDKS LRLWERTREPLILEEREMERE AEYESVAKEDQPA/VPGIQQ DSYFT*KKTITVK/AERIMEA FELYREETAKMKEHKAICKAA GKEVPLPSNPILMAYGSISPSAY VLEIFKGIKSSELESLLVLPSFY VPDILKLFNEFIQLGSDVELICR CLFLLRIHFGQITS

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4822	35190	A	4863	1	703	MGLTKQYLRYVASAVFGVIGS KQGNVFFVTLRGEKGRYVAVP ACEHVFVWDLRKGEKGLKQEV TCLCSPDGLHLAVGYEDGSIRI FSLLSGEGNVTFNGHKAAITTL KYDQLGRLASGSK/RQPGGIV FTESILAYSSACQDKQNHVWGS SQ*CADFVIQLRQYCCSFCS*F H*NMEQVYTAVYSHNDL*ICTL LILCTW**TGSNRNKAPKTMFP RCTEGLDRGNRPATHS
4823	35191	B	4864	1	2616	
4824	35192	A	4865	3	674	PECTGRTLRSASQHQHDTFYILA CELNSLADDAQRYDVPNSCL YPPDLWPRVPMQAKKKELARR DDIEDGDSMISSATSDTGSAGR KSKKNIRKQRMKILFNVVLEAR EPGSGRRLCDLFMVKPSKKDYP DYIIHLEPMDLKIIEHNIRNDKY AGEEGMIEDMKLMFRNARHYN EEGSQVYNDAHILEKLLKEKRR ELGPLDDDDMASPKLKLKSA ASHFII
4825	35193	A	4866	3	425	
4826	35194	A	4867	1	1115	LCSVPTLCLASSHLVSNLSTFKQ VTSSFIRHVATLLGLYLALFCF GWYALHFLVQSGISYICIMIIIGV ENMHNYCFVFALGYLTVQCVT RVYIFDYGQYSADFSGPMIIT QKITSACEIHDGMFRKDEELT SSQRDLAVRRMPSILEYLSYNC NFMGILAGPLCSYKDYITFIEGR SYHITQSGENGKEETQYERTEP SPNTAVVQKLLVCGLALLFHLT ICTTLPEYNIIDEHFQATASWPT KIYLYISLLAARPKYYFAWTLG TAPRKWSPCPGPQCIQLRAADP SGPEPLMLSSQERQPKAKPPK EAHADIAGTPREGEKTRTGGPG KAFLRDPGASSVELSRTQLWV LTPPIAKAPCECLQ
4827	35195	B	4868	218	656	
4828	35196	A	4869	1	180	
4829	35197	A	4870	12	199	GLFPLEPGANGI*GC/SGRIRAQ RWLPGRPKFTGESFIR*PPRVAK ESGQLIWFCVPTQISS

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4830	35198	A	4871	1	5058	MKLRGVSLAAGLFLALSLWG QPAEAAACYGCSPGSKCDCSGI KGEKGERGFPGLEGHPLPGFP GPEGPPGRGQKGGDIPGPPG PKGIRGPPGLPGFPGTPGLPGMP GHDGAPGPQGIPEGCNGTKGER GFPGPSGFPGLQGPPGPPGIPGM KGEPGSIISSSLPGPKGNPGYPG PPGIQGLPGPTGIPGPIPPGPPG LMGPPGPPGLPGPKGNMGI.NF QGPKGEKGEQGLQGPPGPPGQ! SEQKRPIDVEF
4831	35199	A	4872	3	1646	EDEGRAKGHHTWQQTRENEQ AKGETPYKTIRFRETY YHKNSM GETTMIQLSFTGSLPQHVGIM GATIQDKIWVTPGLPGFPGTPG LPVKRGFPGPSGFPGLQGPPVIP GPTGIPGPIGPPGPPGLMVTGP PGLPGPKVNMGLNFQGPKEK VKQGLQGPPGPPGQISEQKRPI VEFQKGDQVIPGDRGPPGPPGI RGPPVTPGGEKGEKGEQGEPE KRVKPGKDGENGQPGIPVMPG DPGYPGEPGRDG/EKGNAVMG PPGPPGFPGERGQKGGDEGPPGIS IPGPPGLDGQFGAPGLPGPPGA GPHIPPENKGDTCFNCIGTGISG PPGQPLPGLPGPPGIPGAPGA PGFPGSKGEPDILTFPGMKGD KGELGSPGAPGLPGLPGTPGQD GLPGLPGPKGEPVRITFKGERGP PGNPLPGLPGNIGPMGPPGFG PPGPVGEKGIQGVAGNPGQPGI PGNKGDGPGTTITQPKPLPGN PGRDGDVGLPGIPGLPGQPLP GIPGSKGEPGIPGIGLPGPPGPK
4832	35200	A	4873	110	256	CSGT YRCYSF/HSRDPYLWSAPS DPLE/LVVTGPARQY YTKGNLV RIASGL
4833	35201	A	4874	2	2888	LSDPCSSRWDRSLSQRSRSWS YNGYYSDLSTARHSGHHKRR KEKKVKHKKKGKKQKCHRRH KQTKRRILIPSDIESSKSSTR MKSSCDRESRSSSSLSHHSSK RDWSKSDKDVQSSLTSSSRDSY RSKSHSQSYSRGSSRSRTASKSS SHSRSRKSRSSSKSGHRKRAS KSPRKASQSENKPVKTEPLR ATMAQENVVVQPVVAENIPV IPLSDSPPSRWKPGQKPKWPKS YERIQEMKAKTTHL

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4834	35202	A	4875	350	986	LWGGGSARLLRLPRGPCLPPAS PSSPSSSELSS*CSLGPSSSSSSSS SSSCLCPSSSSSSSP*LPSSSS SSSRPLPPSSSSSSSSSSSSSSSS SECLCPSSRPRTTVAGLGAPAG FPSGPVDTCSVWLLRFTSTMW DCSLRL*VPEPPSSSSNSPPSSL HKLAGPPASTPPSFSSLLKKG WAGPMVAGTVPPAVPAPSSSTR TE
4835	35203	A	4876	1	496	SQSYSVRGSSRSRTASKSSSHSRS RSKSRSSSKSAVLASTARCAGS RKQCVPPLPRLCQLQSRSLQPS MVPWRWGLTGPRGIALPPAAR PGPLHEAPRWGPPRRRAPRPWP PGARPGRRRRRAAASPSSCG PRASGAAGGRGAPIGARASA GAAVWTPISTT
4836	35204	A	4877	3	4578	TLAVFVPTLAGFSVALGGPAW GRRRRSVSGVGVLWQQCFLF CSRGPAQAGGQPALAATSVAM GAQDRPQCHFIDIEINREPVGRI MFQLFSDICPKTKNCLCLCSG EKGGLGKTTGKKLCYKGSTFHR VVKNFMIQGGDFSEGNGKGGE SIYGGYFKDENFILKHIDRAFLLS MANRGKHTNGSQFFITTKPAPH LDGVHVVFGLVISGFEVIEQIEN LKTDAASRPYADVRVIDCGVL ATKSIKDVFEKKRKKPT
4837	35205	A	4878	1	1689	

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4838	35206	A	4879	1	1604	MGISCPGSSKMLNSRALPVLKL TQGALRDCCKERANYTNFNLYK AVESQKGFVCLVYNGQSQPEY VMIPCTSVPTGQEVPEDRGMR MVMKNKPNKPSKMQLKSSKH LTNSVIVIAVGIFSVTLQARDP QLDDAIEQLRGVCIRAWEKITS GGEQYPSFSAIKQGPKEPYIDFI ARLQESLKKMIADSAQDIVLQ LLAFDNPDPQAAALRPARGKA HLVDCIKACDDIGDSSNGKAS YFGSKSKVFQTSYSAQKAEVL AVIEVLTAFDMPINVISDSYM VYSTQLIENALRFHTDEQLMT LFTQLQTAFRSTMHPFYITHIRA RHPTPLPGPLTEGNQMADECLVA NAISNARHFHNLTHVNASGLK HRYSTITWKEAKNIQRCPTQCM VHSSFRGGVNPRLGEPNSLWQ MDVTHIPLFGLRAYVHKRRIR GGGGGEGEGEGEGEGEEEEEEE EEEEEEEEEEEEEEEEEQEQEQE EQEQEQEQEQEQEQERRRKDTE ELSYSLPLNRTQPCWHPDFGLP
4839	35207	A	4880	1	1146	
4840	35208	A	4881	1	1577	MGQVWALVHSTLETFTHDEEE GEYNEVTEQVCLPAKAGSAAV DLCCCTKAVSLLPGESPQKVPTG AGGPLPAGMTGLLLGRSSLNIK AVQVQTGVTDSDYNGEIQVTS TSVPWKAKPGDHIAQLLIVPKK FUEGLKEPLQVERQSSCQGLGY/ PFLMAAIVKPEPIPLKWLTDKP IWTEQWPLSKEKLEALEDLITQ QLKKGHIAPTFSPWNSPVFIKK KSAEQDCEWVFVTLAVNNLQL KPAKRFHWKVLPGQPNQPIWI PSRYLKYPHYKPDACEEIPESQ GFPVAAMSRLTLRRTPVTISNT HRTQPPTWGQIEKLQMAEENL RKAGQPVITISNWLPRITKFKPI EGAENVFTDSSNGKASYSGSK GPLTEGNQMAADRLVAKVISNA RHFNHNLTHVNASGLKRRYSIT WKEAKAIHQRCPTQVMLSAEE QHLQKSAAKTEAEKLVWWRD PITKSREIGKIITWGRGYACVSP GPNQQPIWIPSKHLKPHYKPD GEKISGNGCGRPHPRQLQPCPD

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4841	35209	A	4882	1	420	MTNISTTLKDLKDAGMIDPIKS TFNL/PIWIPQKPDGSWKTANN /R/KLNQATISIAAIVLDVASLPG KARSYHGFSSHAGRVIDSNQK DIEGCTYILNVAGKNMFGIQLR RSVIFPCPNLMYTDNCSSHGPR GPSDYDSDP
4842	35210	A	4883	213	687	PEHILPGAQEGPSC/PLEPELE/V *NMSSWNLTSECKMHGDLKY L.FVITAKDQQ/VSIAAST/*GFC WNQ*VSASPSQAPGMPLVLGR RLWQGSRLGGLSISLDDCHGA HNHSFKRVTTLQVFSWTVPQ AEPAMDCIHTA/DSRQRLP*QA HESVAEVIIT
4843	35211	A	4884	1	648	MSSWNPLPESFKHIGYLLYLFV ITAKDQQ/VSITASTWGFYWNH SQGKNPEQMEASQKPVAGLWA WWNLISLSAASHGAQNHPFKR VTTTLQSQGWNKDLWIMRELL CNNRPEQLLQETATIKAPIAPAD PWSQEVIVNFCNAVSSVSCMPF NIHFNISNIPPESSGDWRMQQP KVEQSILGAQRGGGCRPGSLR ELFPCLLAEPNMEEEVAALRA
4844	35212	A	4885	3	597	GTLEPAEWSVLLGVHSDQGP LDGAHTRAVAAIVVPANYSQV ELGADLALLRLASPASLGPV WPVCLPRASHRFVHGTACWAT GWGDVQEADPLPLPWVLQVEVE LRLLGATCQCLYSQPGPFNL LQILPGMLCAGYPEGRRDTCQP SPEPGPMCIS/SHIQRLRDAVS HTWQRGTPEARLGSWERRQRQ QQQGPV
4845	35213	B	4886	387	552	
4846	35214	A	4887	20	612	
4847	35215	A	4888	792	959	TGLSSSQNPKATKSIPWHNRLL PNVDSQVQQNSQAIHVTN*GNS ESQYPFSKMDT
4848	35216	A	4889	268	500	
4849	35217	A	4890	1	529	
4850	35218	B	4891	259	1672	
4851	35219	A	4892	480	657	
4852	35220	A	4893	2	377	WCDPSSSLHRSVQALRTFCVTL SGAFVRDCTTVLSSTICEPSTD V/CWAMNIVSVLLLYGSEEEA FWLLVALCERMLPDYYNTRV VVIRTYDQRYEQCDVLDGLP TTLFTTDDWHVWPDLTGLP

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4853	35221	A	4894	1	251	TEARKAAAVMPKTAVLAAERPKKAWGVLIIPKSKTKRTPKAFAGGGCW/TKVGVWSKVAKKVPKPEASKPKKAAPKTRRYKSTLTKTK
4854	35222	A	4895	283	427	PSVSKESPLNSPASQAGSATFATPLTPPK/PAATSSVAAAALLPALPR
4855	35223	A	4896	111	1095	SRGWSRLPVPCCAPALLSPWAVNGIRRRGAGDGTTRGGSGCAGAHSAGLVASGPESWIPGPVPPGAEPPIRRGDSGLARCPAGHPSPRASPQRPAEGFDALAAAPSRVPGDSRQLSRNNTRSRCEGRGGKTTPAWAGVHRHGGPPPAAPPGRARVHGHRLRGGLPGGGKRGLPGCCPRAADPRGRP/GETSRSGERGPPGRSAPLSLQPRHRTGLET/RQPSPLARSRPGLGPRPSARRPSRPA PPPPPPELHRGAPQGRVVASQTRPGARARPAADTHSSLKSPASQAGSAAAFATAPLTPQKPOLRAPWQPLHSFRPCRGVTSRLRTAPP
4856	35224	B	4897	243	452	
4857	35225	A	4898	3	353	RRYLSPKYIKMFVLDEADEMLS RGFKDQIYDIFQKLSNNTQVVL SATMPSDVLEVTKKFMRDPIRILVKKEELTLEGIRQFYINVERE EWKLDLTLCDLSAMHGDMQKERDVMIR
4858	35226	A	4899	3	410	NLQEWKLDLTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFTVSAMVCLPAASLLWVCPSEVSYLKPGLFPRCLPGLLHICFLFQHGDMDQKERDVIMREFRSGSSRLVITDDLVSRLGN**QRQKGGSKVI
4859	35227	A	4900	1	235	MLSYVLEVTKKFMRDPIWILVKKEELILESIIHQFCINVEQEKWKLDTLRDLYETLTITQAVIFINTRRRKCCSKVREI
4860	35228	A	4901	3	48	NSNVEREEWKLDLTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFTVSAMHGDMQKERDVIMREFRSGSSRLVITDDLVSRLGN**QRGTRGVEAGHTM

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4861	35229	A	4902	2	879	AQFPTRLDLKATQALVLAPTRE LAQHIQKVVMALGDYMGASC HACIGGTNVRAEVQKLQMEAP HIIIVGTPGRVDFMLNRRYLSPK YIKMFVLDEADEMLSRGFKDQI YDIFQKLNSTQVVLLSATMPS DVLEVTKKFMRDPILVKKEE LTLEGIRQFYINVEREEWKLDL LCDLYETLTITQAVIFINTRRKV DWLTEKMHARDFTVSAMHGD MDQKERDVMREFRSGSSRVLI TTDLLARGIDVQQVSLVINYL PTNRENYIHRJRGGRFGRKGV AINMVTEDDK
4862	35230	A	4903	1	1764	MASLEEGIYSLKINSKRSSYNS MNPQFTAGSEGGNETEEPKNFKQ SRKGRPQDSGSSLSVLQEIQL DDIPKVKEEAVISSQSDLGECPY CGERPARNATIFAPQKEKESAP EMSSSCDKRVTVNPPEKFSEGR PKTQNTLICEKCSQPSNFLDDY NPHVIIQKRLSNQSRVICEKSSP PLNVDPNYSNSHVIQKHKEKM AIERPSSGSDWSDVGGTTVIFSE EKPFSCLCPVVSEPPYYATDYT TFPPHYSFPHDYTSSWFSSTKS SCYPSLGSSNTLQAGKSSCSSS SRSNNNIFQGERSSHQFSLDYS TSFPVSSENTSRLKMTTEGRS KNSSLFYYSRNVAAEAEKERVY QEETLGHYPYGGGRASSFPRTIW QPEQPGFIDTHCLDLLYSRLPF KGTFTKFRKIYSNTFFKEFQGC SCFCNPQNLNDNLWEDQLKDD LVWGVFGCRPHFAHYNNYQE RSILKALRHPKAVAFGEMGLD YSSKCTTHIPEQQKVFKRLRL AVSLKVKPMMIHCRAEDDLLG ILKKYVPSDHKMYQHCFGTGSYP VIKPLLSCFPNLYVGFMAILTYS SAEQARETVKK

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4863	35231	A	4904	125	820	VLAPNYHITFRNLSSVSSPVSTA EPVLQAGQARELSFSSLHPASPL LVPSTPALTLHAFNALVLFPSFP LEKAAKRERPKSKIQTARVGK MRRTWSPHTTISAGGSVNGAST LKNLSLVWEAKPADTINPTPTT HPNPGPTPTNTNRHPPPHHPLT NTPAPPHQPPATT/PSQ/TQTPN YCPNTDHTTPTHTDTPNPVPPTR RTPPNRTGKRNTNTSQNYRLVSP APKIHWEA
4864	35232	A	4905	407	757	
4865	35233	A	4906	5	426	GKSTKSQNASSPPKDHNSSPA REQN/WIENEFNELTEVGFRIT SLEKNINDLMELKNTARELREA YTSINSQINQVEERISEIEDQLNE IKHEDKIREKRMKRNNQSLQEI WDYVVRPNRLRLIGVPESDIENG TKLENTL
4866	35234	A	4907	1	2267	MTGQFQDQDVVREEARPLPNRIM RLRFNFHATECSWDHLVYVDG DSIYAPLVAAFRCEVENRYQGN PLRGTCYYTLIDYQTFSLSQE DDRYYTAINFVATPDEETPPIRG RQTAAHTGELQLTSGGYPGSMK LPEEGTGERNRITINKDVHTET PSKGHQHQRPVKDKSTKIKKN QRKKAENSKNKNASSPEDHN SSPAREQNWMENEFDELTEVG FRRWVITNSSKLKKHVLTCQKE AKNLEKRLGQLLTRITSLEKNV KELMELKNKAQELCEAYTSINS QIDQAEESISEIEDQLNEIKHED KIREKRIKRNKQSLQEIWDYVK RPNRLRLIGVPESDGNGTKLEN TLQDIVQDNFPLARQANIQIQE ILKTPQRYFSRRATPRNIITFTK VEIKGKMLRAVREKDHSAIKLE LRIKKLTQNCCTMWKLNLL NEYWVHNEIKAEINKFFETNEK KDTTYQDLWDATAKAVFKGKFI ALNAHRRKWERSRIDTLTSQK ELEKQEQTNSKASKRQETKIR AELKEIETQKTLQKINESRSWFF EKINKIDRLRLARPIKKKREKNQI DTIKNDKGDITTEPTQMOTTIRE YYKHLIYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPTTSSE IEAIINSPLTKKSPGPDGFTAKL YQRYKEEVVPLLLKLFQTVGK EGPLNSFYWANILIPKGRHT

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4867	35235	C	4908	605	760	
4868	35236	A	4909	94	400	
4869	35237	A	4910	I	1538	MPIQMOPYQYKLVENKTQPPV YQYWPADLQYRPPPEVKYRP QVVCVPVNSTAPYQQPTAVVF NPTAPPSGGIIAQNTDLVEWF FLPHSTIKTFTLYLDQMATLIGQ ARLRIKLCESDSKIIIVPLNKEQ VRQAFINSGAWQIGLADFVGII DNHYPKTKIFQLKLTWILPKI TRHKPLENALTFTDGSNGKA AYTRPKERLIETQYHWAQRAE LVAVITVLQDFNQSINIVSDSA YVVQATKDVETALIKYSIDDQL NQLFNMLQQTVRKRNFYVVT HIRAHTNLPEPLTKANEQVDLL VSSAFLEAQELHALTHVYATGL KNKFEDITWKQAKNIVQHYTQC QIPHLPTEAGVNPREQHFTGK KNSPHEGKLIWWKDKKNTW EIGKVITWERGACVSGENQL PGWIPTRNLKFYNEPLGDAKKS ASAETKNQPLSIIDSPGKAPGCL MPTTQNLWVEVPTVSATSKFT YHMYVPPAPKRQRPARTGHND DGSFVKKGDM
4870	35238	A	4911	I	759	FRMVIRCLPQRELDGDRGNWT ATSaelTGJKWRRYNFGGHGD CGPIISVPAQDDPILLSFIRCLQA NLLCVWRDV*PDC*ELWIFW WGDEPNLVGVYIMNCRLLWKK DSGKMAFPMNVGRC/FFKAIHN LLERCLMDKNFVRIGKWFVRP YEKDEKPVNKSEHLSCAF/TFFL \HGESNVCTSV EIAQHQP IYLN EEHIIHMAQSSPAPFQVL VSPYG LNGTLTGQAYKMSDPATRKLLIE EWQYFPMVLKKKKK
4871	35239	A	4912	I	539	MRHPCDGNLSLYFDHISYNMLA VMLYYGFGRVSIGKTGLRGVQ RHLWPLPLDASSTKTVSSSHSD KGEIFSPFPCLINCNFEMRNT TKCLMDKNFVRIGKWFVRPYE KDEKPVNKRVTSEIWLDFEY\ GVSLPCFAVERCALLPLCLLPR LMISISSTRQRPQYISRRGLKAKI SWVV
4872	35240	A	4913	198	620	

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4873	35241	A	4914	63	1267	RNRILRMEFFDWFVAFWSWLL NMIRSQNAKDSSNSMENTDSP WCELFRELCINALDVPDSSLV RGNEFSASVHNTFDHMMWRTKE RYEAGWLLSSADRMKEND LRDSVSWLQKQILSLKSAKIAL SGSLISYRERAEIVEKQTQTLIM RVADLQQKGYINSPALCHNLW RDLDFHSFPYDITLFHYIDDIML IGSSEFEVANTLDILKGQRFVLT VIDTYSRYWFASPECNAA/KT TIHGFTECIHYHGPHISIASYQG THFMAEEPWASKNQGEVETPF TITPSDPVATFLLVPVMTLRSG LEVLPVEGGTLPFGDTTMIPLN WMLRLPPGHFGLLLPLSQQAK KGVTVLAVVIDPDYQDEISLLF HNGAIIISDGNVILIGLLQWFST
4874	35242	A	4915	2	2210	
4875	35243	A	4916	1	2036	MDTFLDTYTLRLNQEEVESLN RPITGAIEIVAINSLPTKKSPGD GFTAIFYQRYKEELVPFLQLQF QSIEKEGILPNSFYEASIIIPKPG RETTKKENFRPISLMNIDAKIVN KILAKRIQQHIKKLIHHDQVGFI PGMQGWLNTCKSINVIQHINRA KDKNHMIIISIDA EKAFDKIQPF MLKTLKKLGTGDTYFKIVRAIY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPFLFNIVLEVLARAIR QKEIKGIQLGKEEVILSLFADD MIVYLENPVSAQNLLKLISNFS KVSIGYKTNVQKSQAFLYTNNI QTGSQIMSDLPFTIASKRIKYL IQLTRDMKDLFKNYKPLITEM/ KTKKWKNNIPCS/WELEKTLTKFI /WNRKRARIAKSILSQKNKAG ITLPDFKLYYKATVTKTAYWY DQNRDIDQWNRTEPSEITPHIY NYLIFDKPEKNKQWGKESLFN KWCWENWLAICRKLKLDPLT PYTKINSRWIKDLNLRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATQAKIDKWEIKLKSFT AKETIIRVNRQPTKWEKIFTTYS SDKGLISRIYNELKQIYKKKKQP HQKDFAYHFTVFVFFYGFALL AAATSLHDLHCNTTITG/HATPE **PV*HKRSSLTITVLCRSG*IIW WCDPHTHS
4876	35244	A	4917	1	1359	

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4877	35245	B	4918	1	948	
4878	35246	A	4919	1	981	
4879	35247	A	4920	1	3747	
4880	35248	A	4921	1	1875	
4881	35249	A	4922	1	2238	
4882	35250	A	4923	1	3924	
4883	35251	A	4924	1	1068	
4884	35252	B	4925	62	389	
4885	35253	B	4926	1	3663	
4886	35254	A	4927	1	1474	MAVSTTVRVDMPCCAVMLYC WGRSGKEQQPDEALKKGFTV CFEGLRFQKPGSYFSLDQIGH VEIQMITPPWRGTTLSTKRGG KRGKTESDREHNLAPPKGRDTP KKEGAHVRRGGLSGTPTTEKK GKARSPRYGDTHRGEGLNKT RAPQNFSESEPTINKIDRPLAR LIKKKREKNQIDTIKNDKGDTT NPTEIQTIREYYKHLIYANKLE NLEETDKFLDTYTLPRLNQEEV ESLNRPIGTGSEIEAIIISLP(TKKS) PGTDGFTAIFYQRYKEELVPFL LKLFSQIEKEGILPNSFYEAII PKPGRDQTQKENFRPISLMNID AKIVSKILANRIQVHIKKLIHHD QVGFIPGMQGCVGSSARAIGQE KEIKGIQLGKEEAKLSLFADDTI ECLNPIVSAQNLFLISNFSKV SGYKIHVPKSVSFLYTNNIAES QIKNAIFPTIASKRIKYLGIQLTL EVKELYNKNYKTLKEIRDE
4887	35255	A	4928	419	1002	CYQRWKVLKSSGGLARL/IKK REKNQIDAINKDGDITDPTTEI QTTIREYYKHLIYNKLENLEET DKFLDTYTLPRLNQEEVESLNR PITGSEIEAIIISLQTKKSPGPG FTAKLYQRYKEELVIYRFNAIPI KLPMFTFFTELEKTTLKFTWNQK RIRIAKSILSQKNKAGGITLPDF KLYYKATVTKTAWYW

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4888	35256	A	4929	1	2502	MFFETNENKDDTTYQNLWDTFK AVCRGKFIALNTHRRKQERSKI DTLTSQKKEPEKQEQTTHSKASR RQEITKIRAEKKEIETQKTLQKIL QKINESRSWFFEEINKIDRLLAR LIKKKKREKNQIDAIGNDKGDIT DRTEIQTTIREYYKHLANKLE NLEEMDKFLDTYNLPRLNQEE VESLHRLITGSEIEAIINSLPTKK SPGPDGFTAKFYQRYKEELVVP LLKLFQSEKEGILPNSFYEANI LIPKPGDITTKENFRPISLMNI DVKILNKILANRIQQQIKKLIHH DQVGFIGMGQGFENIHKINVI QHINRTKDKNHMISIDAEEKAF DKIQQPFMLKSLNKL VLEVLR AIRQEKEMKGIQLGKEEVKLSL FADDMIVYLENPIISAQDLLKLI SNFSKVSGYEINVQKSQASLYT NNRQTESQIMSELPFTIASKRIK YLGQLTTRDVKDLFKENYKPLL NEIKEDTNKWKNPICSWVGRIN IVKMAILPKVIYRFNAILIKLPM TFFTELEKVTTLKFIRNQKRACIA KSILSKKEKAGGIMLPEFKL*Y KATVTKTVVYWCQNRYIDQW NRTEPSEIIPHIYNHLIFDKPDKN KKWGKDSLFNKWCVEHWLAI CRKLLKDPFLTPYTKINSRWIK DLNVPRPKTIKLAGHLGNITRDI GLGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETAIRVNR
4889	35257	A	4930	1	4187	MGDFTNPLSTLDRSMRQKVNK DSQELNSALHQAADLTIDICRTLH PKSTEYTFFAAPHHTYSKIDHIV GSKALFSKCKRTEIITNCLSDHS AIKLELRIKKLTQNRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDTFKAVY RGKFIKAVCRGKFIALNAQN RKQERSKIDTLTSQKLEKEQE QTHSKASRRQEITKIRAEKKEI TQKTLQKISESRSWFFKTNKI DRPLARLIKKR

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4890	35258	A	4931	1	1818	MSSRGPCTLETLINPSPSVADDI PHLRPKPVYITTTDRDNIYSTK IPYMAARVVFIKWIVTFLEKK YLTATQNTKNGVDVLPKIIQTV GGGAVQERAPELDGGGPTEQD KSHSNSSTLSDRRLSNSLCSIE EEHRMVYEMVQRILLSTRGYV NFVNEVFHQAFLLPSCIAVTR KVVQVYRKWILQDKPVFMEEP DRKDVQAQEDAELGFSETDSK EASSESSGHKRSSSWGTHNSFT SAMSRGCVTEEG/TIQMLKAGV QALLQPVLCVFPLIPLPPLCNQA ARPAVVISPLGDLPLWLSVLGG PADQWHLSYLKPEGSSAYACIL EALASAGKGLWKVSAVGRKP WTRGRSDRKGTVGHQVQFLFF KDEGRVDSRILTLMVAVIRPN LCVYISRELWDDFLGVLISL TE WEELINEWANIMDSLTAVLAR TVYGVEMTNLPDLKLEQKEK KQRGKGCVLDPQKGTTVGRSF SLSWRSHPDVTEPMRFRSATT GAPGVEKARNIVRQKATAKRS QSISSNCVHLSALPATKSVPLLL HTLYKNKALKALGQPVGKAD QLVVAGSPSVCCVEDQWGRSN LEAMVLWLYCIPPDGDVLYL
4891	35259	C	4932	96	278	
4892	35260	A	4933	1	261	KLRLPFGHFGLLLLLSQAKKG VTVLAVIDPDYHNEISLLHN GGKKTRPAEMLAEGKGNTE WVGEEVSHQYQL*PHDQLQKR
4893	35261	C	4934	36	385	
4894	35262	A	4935	1	2349	
4895	35263	A	4936	207	561	QLAEPHPWIPGTRKDAQCLVGL FGFWRQHPIHLGGLLWPIYRVT QKAASFEGWGP*EKALQIQPS VQAALPLGP*DLADPMVLEVS MADRACAGWSLWQAPIGELQQ KPLGFWSKALP

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4896	35264	A	4937	1	1375	MSTTQLDITMGAESLCNMTVQ VEDEGIQKLKEIRMVVEWITPFRP THPSCEGPEDIPLTNALQNTFVR AAPASLKSPPVVALLLSPVGYRT HAVVISPVPECRFGIDILSSWQN PHIGSLAGRAHQKQFVGSWQG QQYAFTVLPQGHINSLALCHNL IWRDLDFHLLSQGITLVHYTDD IMLIGSNLADPMVLEVSMADRC AGWSLWQAPIGELQKPLGFW SKALPSSADNYSFPERQFFACY WALVETECPLTGHQLTMQPEL PIMNWVLSDPSSHKVWHGQSG HGGRDSGYSWTQQHGLPLTKG DLSMTTAEQIFQQRPILSPRY GTIPWGDQPATWRQKWQRFVL TGIDTYSRYEFAYPACHASTKT TIHGLMEFLIHHHGIPHSIASDQ GTHLMAKEVRQWAHAHGIHW SYHVPHHPEVAGLIERWNEIGL LKSQQLQHQLVNRRLRRELQCWL
4897	35265	A	4938	1	324	INCLRNCKTYQA/RKPLWFYNT SLKFFLNKP/MLADVVEIQGTT VPAHRAILV/ARCEVMAAMFN AGIFQAMCLLCAE/MYQVSRL QHICELFII/TQLQSMPSRELAS NL

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4898	35266	A	4939	108	2304	VAAAYPPASPWPSPARSLAGA APAPLCVGAAPAAVEAREGDAAG DERIAGELAAARGPREAVSRCFS PSRRPALGFEIMSIHIVALGNEG DTFHQDNRPGLIRTYLGRSPL VSGDESSLLNAASTVARPVFT EYQASAFGNVKLVVHDCPVW DIFDSDWYTSRNLIGGADIIVIK YNVNDKFSFHEVKDNYIPVIKR ALNSVPVIAAVGTRQNEELPCT CPLCTSDRGSCVSTTEGIQLAKE LGATYLELHSLDDFYIGKYFGG VLEYFMIQALNQKTSEKMKKR KMSNSFHGIRPPQLEQPEKMPV LKAESHIYNSDLNLLFCCQC VDVVFYNPDLKKVVEAHKIVL CAVSHVFMLLFNVKSPDTIQDS SIIRTTQDLFAINRDTAFPGASH ESSGNPPLRVIVKDALFCSCLS ILRFIYSGAFQWEELEEDIRKKL KDSGDVSNVIEKVKCILKTPGKI NCLRNCKTYQARKPLWFFYNTS LKFFLNKPMADVVREIQGYG QCPAHRALIVAPCEVMAAMF NGNLHGKAKSVLIPVYGVSKE TFLSFLEYLYTDSCCPA/GIFQAM CLLICAEMYQVSRLQHICELFI TQLQSMPSRGTGHPWNLDIS/ DLL*KGPSFHHSWIAFSTWAYF HFHCYLYTYLIFQFKRPGIFRDL FSEGRNGSFLFGKRHRWGSPNM LLGRQLAGITGKYFTSPGNVG
4899	35267	B	4940	1	3117	MRVCARACVTRTRMVCVYAH TCVCVRTYAYVVRVVRVHVRA RVRVCA YARTRVRNSLSILPFIQ LTLATPIHHIIHQEEFNIRGIVPV LRRVKPDLAIGIDITPSCDTPDLH DYSEVRINQGVGITCLNYHGRG TLAGLITPPRLRMLEQTALEHN IPVQREVAPGVITETGYIQLFLP GWEIGFSPALLLAFLCSTSPGF GDPDGLGVIA YQDTVVRNAAT AISELNA LAVKGVILTGDNPRA AAAIAAGELGLEFKAGLLPEDKV KAVTELNQHAPLAMVGDGIND APAMKAAAGIAGMSGTDOAL ETADAALTHNHLRGLVQMIEL ARATHANIRQNITIALGLKGIFL V'TLUMTGLWLA VLADTGATV LVTANALRLRRR
4900	35268	A	4941	1	1162	

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4901	35269	A	4942	1889	3387	QWAIKQFKHAEKENPYLFGGG HLRAIFR*SGFQ*RQLHTMHWG AS/QQAEHP/LAQPSTRAQLRTP P/TADS/QRALVSGSGMKPRLNG ERVLICAAGKHPADAFTGLINE LESAGQTVVLVVRNDDVLGVI ALQDTRLADAATAISELNALGV KGVILTGDNPRAAAAIAAGELGL EFKAGLLPEDKVKAIVTELNQH APLAMVGDGINDAPAMKAAAI GIAMSGGTDVALETADAALTH NHLRGLVQMIELARATHANIRQ NITIALGLKGIFLVTTLLGMTGL WLAVLADTGATVLFPPRLFEAR NSQVGNGETNQTRFLCAAPG GTFIADFTAGTGRRARPRNRNR RVVVSDFHQNMRRFLMEIVA ARFVVSXVAHFRTFHYGGVIF ISRENVWIRGFESIFDHLERFR LLFTIDNPVGKVFVAALVGRV LGKHIQFDVVRVTTKLCESILQI VNFIFRQSAKTQVSVDRQLTA LPQQINAGNRSRLMVGKQLLCI
4902	35270	B	4943	1	2104	
4903	35271	C	4944	1	1215	
4904	35272	A	4945	3	268	YEFNRPYPEIQRSGIS/KLLEPLL FAATSDSQLSKTEISSIKINSETV PVYQLRYNGNNALMFATYQD KMLVFSSTDMFLFKDDQDTEA
4905	35273	B	4946	1	1725	
4906	35274	A	4947	1	1437	
4907	35275	A	4948	2	736	QCPYPYIAATGRILVVTHTLICLA PQIVENQVTVPLTTTMLSVPGA KTVRGFSQFGDSYVVYVIFEDGT DPYWARSRLVLEYNQVQGMPL AGVSAELGPDATGVGWIEYA LVDRSGKHDLADRLSLQDWIL KYELETIPCVSEVASVGGVVK YQVVIDPQRLAQYGISLAEVKS ALDASNQEAAGGSISIELAEAEY MGGTCSAHGRALSRGVLWCRF SAIVRGPPRGMFCAGAAAPNLI
4908	35276	A	4949	531	632	
4909	35277	A	4950	532	609	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4910	35278	A	4951	1	525	LGVEATAMGDFGKAAEKLVPV VELAQACAHVMKSGIDLAVS YCMQVNHGFAQPLEFLLGGLD KVPVLLVFINGVATPLPGFQRT RMLGEAIGRFTSTPQYAGDTVN DEDISNTIRALFATGNFEDVRVL RDGELRKFTCESDDNFRPVT SVNYVIRHDWVGIRRVVPENE
4911	35279	A	4952	1	2769	
4912	35280	A	4953	1	681	
4913	35281	A	4954	1	1230	
4914	35282	A	4955	1	774	MLRTSDRPPYQPKRCIPLSVL EVLRCARRWSLRPYQLARAYI /ERYRHDRDIEREKRGRNLNQE RGLVEQTNASLLNENANKD AHERGDIHYHDLDSYSPFPMFN CMLIDLKGMLTQGFKMGNAEI EPPKSISTATAVTAQIGSVHIYG GTTINRIDEVLAFFVTASYNKH RKTAEAWNIPDAAGYANSRTIK ECYDAFQSLLEYEVNLTHTANV EGLTGDDGIAYEALKKNSQKPR MSASHNCELVSRLGRQYT
4915	35283	A	4956	1	1278	
4916	35284	A	4957	461	1002	SLSTKGYYAAKWCSTACAGS/T LLLVLLVWFIPKGFPGQDNGI IQGTILQAPQSISFANMAQLQRQ VADVILQDPAVQSLTSFVGVDG TNPSLNSARLQINLKPLDERDD RVQKVIA RLHTAVDKVPGVDL FLQPTQDLTIDTQGSRTQYQFT LHATSLDALNTWVPQLMEKI/Q QLPKLS
4917	35285	A	4958	1	291	MNPVDRPLLDIGLRLRLEFLRISG KGLAAGLTIA PALLSLGCKQED IDSGTVGLINTPKGVLVTQRRAR CTGCHRCIEISCTNFNDGSGVTF FSRIKPH
4918	35286	A	4959	1	306	MKNFEVLQPLQNSLSGLPLVW SERILQQINQLTHYEPVIGIMGK TGAGKSSLCNALFAGEVSPVSD VAGCTRDPLRFRLQIGEHFMTI VDLPGVGESGVRD
4919	35287	A	4960	2666	2775	
4920	35288	A	4961	9	308	GDLGDSRRHRAFLCHLPVELKTA LMFPVTLTRALMETAY/ATAVS A/NFRTESRGH/SRFDPP/RDD ENWL/CHSLYLPESESMTRRSV NMNPKLRPAFPKIRT
4921	35289	A	4962	1	1132	

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4922	35290	A	4963	1170	1352	RNLPDAAAGQSCAGEIRLYRQQT QRSRLQRWLHLACFRRCNLHR RELDATA*QHVRSRWR
4923	35291	A	4964	1	312	MRKLTALFVASTLALGAANLA HAADTTTAAAPADAKPMMHHK GKFGPHQDMMFKDLNLTDQA KQQIREIMKGQRDQMKRPPLE ERRAMHDIIASDTFDKVKA EA
4924	35292	A	4965	3	205	KDHIKGVLEAQNSLSTQVSLFF *SFFG*NSNMRLIQIYRSL/CTK AI*LMNFKRHK NQLVINYLRSR
4925	35293	A	4966	1	915	MTGVATARAGRLRRPLSVGQV PPFARLWKGVQTVERHMLANI GTGSQHPGCGFQLINQNSVIVF AAGEVNGFTSGDVQCLKMRSG DMNDIQRRQRLLPDGNKFGEIQ TTIREYYKHYANKLEDLEEM DKFLDTYTLRLNQEEVESLNR PITGSEIEAVVNSLPTKKSPGPE RLTAEFYQRYKEELVPFLKLF QTTEKEGLLPNSFYEASVLLIPK PGKDDTTKENFRPISLMNIDVKI LNKILANRIQQHIKKLIHNNQV GFIIIGVQGWFNICKSTNVIYHV NRTNDKNHIIISIDTEKAFD
4926	35294	A	4967	1	1338	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
4927	35295	A	4968	1	1928	PPLVIHRQTGSGEDLQQTPTDL QLRLVTIRRRKTNKQKQGHPHQNP ISSRRHEITKIRAELEKETETQKTL QKKSMNPRSWFFERINKIDRL ARLIKKKREKNQIDAIAKNDKW DITHRIPTEIETIAREYKHLTY NKLLENLEEMDKFLDTYTLPR LNQEEVESLAHRLITGSEIEAITN SLTVIKKSPGPDGFVAEFYQRY KEELVPFLLKLFQSEIEGILPNS FYEASIIISKPGDITTKENFR PISLMNIDAKILNKILANQIQQHI KKLIHHHQVGFIPGMQGWFNIL KSNVVIHHNRTKDKNHMHISIEA EKAFDKIQQPFMLKTLNKL GID GTYLTYLKIIRAVYEKPTANIIL NGQKLEAFPLKTGTTRGQCPLSP LLFNVLVVLVGLVGAIRQEKEIG IQLGKEDVKLSLFADDMIVYLE NPVSAQNLLKLISNPFSEVSGYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDV KDLFKENYKPLLNEIKEDTNK WKNIPCSWGRINIVKMAILPKT LNQKFSYWFRVNVKHYHRTFP LKETEFTIATLYNGASP/RTAP KSTGTNGHQASGLPRF*RIAFCS ALVKSRRKLYQGYLPGQTD RR EEGVSWCPGGP
4928	35296	A	4969	2	237	QPVEDTWLSTPAAPMVDSL LIAR VRVMARGNAITLPVCGRDVK/F TLEVLRGDSVEKTSRVW/SGIET YQELVTEDALDDL
4929	35297	A	4970	1	1752	
4930	35298	A	4971	1	723	
4931	35299	A	4972	1	1701	
4932	35300	A	4973	1	1446	
4933	35301	A	4974	1	403	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAAADLVGVSSQAIRDAEAKGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGLRLRAEDVFPVPV GVAAHKG/LALKGLRVLLVEV RHRV
4934	35302	A	4975	1	1374	

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4935	35303	A	4976	1	2259	MKLMETLNQCINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQRVGVTIEQI NHMRDVFGRRLRAEDVFPPVI GVA AHKGGVYKTSVSVHLAQ DLAL/KGLRVLLVEVHKRWS*N DEGYRHCTV***HPEARKITRR WRIGEAAADLVGVSSQAIRDAEK AGRLPHDPMEIRGRVEQRILVIQ LNKLIIICVMCLVRDCDVLKTYF HR*SGLLPIKVAFTKP/HVSVHL AQDLALKGLRVLLVEPPSAPN LGIGTINVVCAADVLIVPTPAEL FDYTSALQFFDMLRDLKNVD LKGFEPPDVRILLTKYSNSNGSQ SPWMEEQIRDAWGSVMVKNV VRETDEVGKAAPMVDSLIARV GVMARGNAITLPVCGRDVKFT LEVLRGDSVEKTSRCDNLKTCH TSHGSVMAETA VINHKKRKN PRIVQSNDLTEAAYSLSRDQKR MLYLFVDQIRKSDGTLQEHDI CEIHVAKYAEIFGLTSAEASKDI RQALKSFAGKEVVFYRPEEDA GDEKGYESFPWFIKRAHSPSRG LYSVHINPYLIPFFIGLQNRFTQF RLSETKEITNPYAMRLYESLCQ YHPLTIEKVMKPLITSNTVTDEI ERANVEKMGNGK WYLF TDSRGS KMTIDGINSNDIYMLGYVNSNL TGPYKPLNKTGLVLQMGLDPN
4936	35304	B	4977	1	1744	
4937	35305	A	4978	1	2367	
4938	35306	A	4979	1	1215	
4939	35307	A	4980	1	946	MKLMETLNQCINAGHEMTKAI AIAQFNDDSP EARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHDPMEIRGRVEQRVGVTIEQI NHMRDVFGRRLRAEDVFPPVI GVA AHKGGVYKTSVSVHLAQ DLAL/KGLRVLLVEGNDPQGT A SMYHGWVVDLHIHAEDTL L PF YLGEKDDVTYAIKPTCWPGLDI IPSCALALHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVCAADVL VPTPAELFDYTSALQFFDMLRD LKNVDLKGQAPCMK\LTMS SSSAPSPWML
4940	35308	A	4981	1	1572	

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4941	35309	A	4982	1	1617	
4942	35310	A	4983	1	550	
4943	35311	A	4984	1	3818	
4944	35312	A	4985	607	3777	
4945	35313	A	4986	671	3091	ARCQRPVGRPVDDLRLCLPRAT TPAPSPAPGLVVRRLAAPVPAA APVPAAPVPAAPVPAAPVPAAPV AAAPVPAAPVPAAPVPAAPVPA VPAAPVPAAPVPAAPVPAAPVPA AAPVPAAPVPAAPVPAAPVPAAP VPRFQSPNQASTSDSPHIGQLP HQTVPISDSFHTGQSPHRTDSTP DSPHTGQLPHRTVPTPD/ELPHR TVPTPDSFHTRQSPHQTASTPDS PHIGQLPHQTVPIQDSFHTRQSP HQTASTQDSPHTGQIPHRTVPT PDSFHTRQSPYRTASTPDSPHIG QLAHRVTPDPSFHTGQSPHRT DSTPDSPHTRQLPHQTVPIQDSF HTGQSPYRTASTPDSPHTRQLP HQTASTPDSPHTRQSPHRTVPT PDSSPHQTVSTPDSPHTRQLPH QTVPTPDPSFHTRQSPHQTVPPT DSPHTRQLPHQTASTPDSPTPD SPHTGQSPHQFPHQTVPTADSP HTRQLPHQTVPTADSPTPDSFH TRHSPHQTASTPDSPHIGQLPHR TVPTPDSFHTRQSPHQTASTPDT PHTRQLPQQTVPPTADSPTPDSF HTRQSPHQTVPPTDPSHTRQSP HRTVPTPDPSFHTRQYYPQRTVPT QTASTPGSPHTKQSPHQTVPPT DCPHTGQSPYQTVSTPDSPHTR HSPHQTASTPDSPHIGQLPHQT ASTLDSPHIGRHPRQMAPTPESP HARQLPCQMAPTPDPTLDGPH
4946	35314	B	4987	1	891	
4947	35315	A	4988	157	1990	
4948	35316	B	4989	1	2157	
4949	35317	A	4990	1	378	MSIKGTLYLKVIAIYDKPTASSI LNGENLKAFLLRTGTGQCPLY KINVYKSVALLYTTNDQGENQI NNSTPYTTAPRKIKYIGIYLTKE VKDLYKENYKTLLEKVIDDT/R WKHIPCWMGRINIV
4950	35318	A	4991	1	392	

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4951	35319	A	4992	3	1570	ETDFAFVGGAGVQWCDLSSPQ PLPPWVQAILLPQPPRGCCWSG IPKWSGISDEVQVWKNCKLDL AAATGKNCLGQGEALLTQMR TGNQREVSDDWEEFVYLRNRN PLMVNSNYMMDFLYVTPTPL QAAAGNAVHALLLYRHLNR QEIPVVRGPQWVRDGGVVLWP LGHVGPGRQLTAHGFIQTLLM GMRPLCSAQYEKIFNTTRIPGV QKDYIRHLHDSQHVAVFHRGR FFRMGTHSRNLLSPRALEQQF QRILDDPSPACPHHEHLAALTA APRGTTWAQVRLSLKTAQAEAL EAVEGAFFVSLDAPPAIGLTL EDPAASLDAYAHALLAGRGHD RWFVDKSFSLIVFSGKGLSV EHSWADCPISGHMWEFTLATE CFQLGYSTDGHCKGHPDPTLPQ PQRLQWALPDHHSISLALRG AKILSENVDCHVVPFSLFGKSF RRCHLSLDSFIQIALQLAHFRDR GQFCLTYESAMTRLFLEGRTE VRSCTREACNFVRAMEDKKKT
4952	35320	A	4993	1	1027	MPAKSPGQDVLGTDNIKIDVFK QTNQKSHTEKPYCEPCGKAF SEKSRRLRKHQRTHTGKPYKC DGCDKAFSAKSLRIHQRTHTG EKPFECEHCGKSFNYKSILIVHQ RTHTEKPFECNECGKSFHMS GLRNHRRTHTERPYKCDCEG KAFKLKSGLRKHHRTHTEKPY YKCNQCGKAFGQKSLRGHH RIHSGEKPYKCNHCGEAFSQKS NLRVHHRTHTEKPYQCECG KTFRQKSNLRGHQRTHSGEKP YECNECGKAFSEKSVLRKHQR THTEKPYNCNQCCEAFSQKS NLRVHQRTHTGKPYKCDKCG RTFSQKSLREHQKAHPGD
4953	35321	A	4994	154	331	IPAAATCMGSLGGE*ETPGLWA RRSVKSRGLFPGLPSPRASVRS LLLLPAWAAFLGIVDTRPTAW RAFPWTLFLSVFCQFLDFPETSL DSQKSLDTPSF

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4954	35322	A	4995	657	1455	PEPKAAVAPPPESPLPAGDSEC CLQPGHLLPASPRLPRPQAAS LAHRPEKSA PGADCPGSR/IGR PWTCGGLSGPAAAPRPCPLAPA FAPAFALGAQR/GPGPEQGGH ERQAERPGRRRRTRAYSARIY LPVAAEWPMGPGPEPGAGGRR RGEVPGGAQRSPARRRRGGPA AVSSGGRGVGGLRGAVLFQHP EQQRPVGLAGLGAQQAHPV WRYGPLST/PPALGPAAARGP\A GRRILFPFSFSPSAGAPGAASRP SPRRSP
4955	35323	A	4996	1	415	
4956	35324	B	4997	8	211	
4957	35325	A	4998	1	563	MDPNHEEIPDLPEKEFRRVKSK NHMTISIDA EKA FDN IQH R FMI KTL SKIGIQGTHFN IKA IYDKP TAS IILNGENLKA FPLRTGTSTIVL EVLARAIRREKEIKGIGKKEEV KLLLFADDMIVYLENPKDSYRK LLEQIKEFSKVSRYKINVQKSIA LLYANS DQAENQINNPTSFTIA AKNKK
4958	35326	A	4999	667	960	
4959	35327	A	5000	317	1157	EFRMDPAIALVLALSLTVPKLT VPDSPLRLYRSFCTSACTSNLV VHFA*KEK WPDV*LYTDSWAV ANGLAGWSGTWKKHDWKIDD NEIWGRGMWIDLSEWSKTVKIF VSHESAHHIT*KSSAEEDFNQ VDRMIHVSVDTRPLSPATPVITQ WAHEQSGHGD RDGGYAWAQQ HGLPLTKADLAMVTAECPIQQ QRPTLSP*YGTIPRGDQPA TW QVDYIGPLSSWKGQRFLVTGID/ TSGYEFAYPARSSANSTIRGLM ECLIIHHHGIPHSIASNQLYS
4960	35328	A	5001	2	15246	

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4961	35329	A	5002	1	951	MALALNRYL/CLAVLPLITKCA PLFAG/TEHRAIMVDSMLHTVY R/LSRGRSLTKAQRDVIED/CLM SLCRLRLRLVFDVPIILNEFA/K MPLKLLTNHYERCWKY/YCLPT GWANFGVTSEEE/LHLTRKLFW GIFDSLAK/KKY/DPELYRMAM PCLCAIAG/ALPPDYVDASYSK AE/KKATVDAEGNFDPRPVET/L NV/IIPEKLSDFINKFAEYT/HEK WAFDK/DKEIYRWPIKESLKAM /AWEWTIEKAREDLDPREGYN PQPPDLASV/TLRELQAMAEQ LAENYHN/TWGRKKKQLEAK GGGTHPLLVP/YDTLTAKEKAR DREKAQSY
4962	35330	A	5003	273	478	
4963	35331	A	5004	2	622	GAPRSLSEKERQLMGMINQLSS FREQLLHAHYEQKKLAASQIEK QRQHMKLGKQ/QEQIARQQQ RLIQQHKINLLQQIQQLYAA QLAAMQVSPGGKLPQPGNL GAAVSPSTIHTDKSTNSPPPKSK TCCLLLWEDEHSASIPVTNQI HLHLASSITDHGGKVIWERCLE ESGKGVTFPDPWSPRWGRIPPE GSKEGFTKE
4964	35332	A	5005	3	512	
4965	35333	A	5006	1	642	MHAQTYAHTDTRAQCTSMK QVSLKPTTEAHKKERKPKPG KYICQYCSRPC/AKPSVLQKH SHTGYGCEMYPHGLEMERIPG EEFEPTGESTDSEETSATSG HPAELSPRPKQPLSSGLYSSGS HSSSHERCSLSQSTASQLEDPP PFVEPSSEHPLSHKPEDTHTIKQ KLALRLSERKKHQVIDRLSGSI LAGLSWQLLPQGEAL
4966	35334	A	5007	341	1020	TLNRRQGCCGSLWTRNSGILL FEISRPTYLPILLFLVKR/HKL KMSVLNMVVRHDGPGSTESAKA KEELIFRCRSHFRASPLFSQHA AADKHKFQRFLTADMALAVTV YAPTTFPPSLLLFKQKSNMGH NLIATGHLLVDPNRMVIRRV LSDPPFKICTKMAVVCYMFN EDVQWFKPVELRTKWSRRGHI QEPSGTHGRMKCSFDRKLKSQ NTELMNLYK

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4967	35335	A	5008	1	847	EKAQAELELAGFKDPAPGHTE ESMTHDKTKIPCKSPPELVDT ATSSKKWPRACGQKVEVKEEL LAVGKLTQTSGETTHTNKEPEG EGKGMKAFKQPAKQKLDPEN TGSRRLLPRVPKEKAQPLEDLAS FQELSQTGHTTELANGADSFT SAPKQAPDSGKPLKISRRVLQA PKVEPVGDLVGTGR/D/PVKSQSK SNTSLPPLPFKRGGCKDGSVTG TKRPHCMPAPEEIEELPASKKQ R/VVAPVRVGKSPPELVIMKRS LRTSAKRIEPAEDLNSNMKTNN
4968	35336	A	5009	9	1094	IRHEEESMTDDKTTIPCKSPPEL EDTATSSKRRPRTAQQKVEVKE ELLAVGKLTQTSGETTHTDKEP VGEKGVTGKAFKQPAKRKLDA EDVIGSRRQPRAPKEKAQPLED LASFQELSQTGHTTELANGAA DSFTSAPKQTPDSGKPLKISRRV LRAPKVEPVGDVVSTRDPVKS QSKSNTSLPPLPFKRGGCKDGS VTGTKRLRCMPAPEEIEELPTV SKKQRVAPRARGKSSEPVVIM KRSRLRTSAKRIEPAEELNSND MKTNKEEHKLQDSVPENKGI SLRSRRQNKTEAEQQITEVFVLA ERIEINRNEKKPMKTSPENDIQNP DDGARKPIPRDKVTENKRCRLRS ARQNESSQP
4969	35337	A	5010	1	459	MAKPWRALCILLRSLDSFLQLS ASLTCFGFMHNTYKNNRPWGV LRSSTERSPRKGTAGDMRAGGRF NAPLIGQDLLFKEHFASKALDT CTNIARSAKTQGGPVAAIILLL AFGPCIFNLRVVFVSSRIKAIKL QM/RLTIYRGPLDRPAGPSTGL
4970	35338	B	5011	1	687	
4971	35339	C	5012	194	418	
4972	35340	A	5013	17	396	
4973	35341	A	5014	1	70	

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4974	35342	A	5015	1	994	MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVNTRDIIICQ IAVARIEGIMIVCAAYAPELPK/ YGVK\VGLTNYAAAYCTGLLA GPAGFFHRFGMDK FYEG/QVEV TGDEYNVESIDGGQGLHPAY WDA RPLPRTSPLAIKVFWLP*R GA\VDGGLVLFPPQYPNRPFWL WIPESQGNLNARRYHREGTIHG PRIVAGLHAPTLMEDEDA\YK KQFVRQYVKNSVTPD\MMEE MYKKAHAARIAENPVYEKKPK KEV\KRKRWNR\PKMSLAQKK DRVAQKKASPL\RAQERAAEKL NQTIIFYKDFSDIAN
4975	35343	C	5016	27	308	
4976	35344	C	5017	68	307	
4977	35345	A	5018	388	1485	
4978	35346	A	5019	3	1940	RDRMILLKMEQEIIIDFIADNNN HYKKFPQMSSYQRMVLVHRVA AYFGLDHNVDQTKSVIINKTS STRIPEQRFCHEHLKDEKGEESQ KRFILKRDNSSIDKEDNQSVCS QESLFVENSRLLEDNSNICNETYK KRQLFRGNRDGSGRTSGSRQSS SENELKWSHDHRAWSTSDSDS SNRNLKAMTKTASFGGITVLT RGDSTSSTRSTGKLSKAGSESS SAGSSGSLSRTHPPLQSTPLVAG VAAGSPGCVPIYPENGIGGQVA PSSTSYILLPLEAATGIPPGSILL NPHTGQPFVNPDGTPIAYNPPTS QQPLRSAMVGSSQQQPPQQQP SPQPQQQVQPPQPMAGPLVT QSIPAKKELNAFRVRNQEQRDT GTLHEGSGKISRMVLGWEPLSP YAPDRDDVATQFGQMTLSRQS SGETPEPPSPGVYPSLLMPQPAQ QPSYVIASITGQLPTGGFSGSGP PISQVQLQPPSPQGFVQPPPA QMPVYYYPSGQYPTSTTQQYR PMAVPQYNAQRSSQMPQAAQ QAVLEVLSPVSTVMPKLAVAL VMAGFRLRLLESVLLQALW WSDHLSSFSELLCRLPDVLPSP LLPLEYDHQKDAQGQDYLTCM VLVTLLESPTGIQEDDSNEISVI

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4979	35347	A	5020	3	1353	GDAYALVLRVTLYCGKCHVNE VVLAIPFEILSTESIQDQI.PYSV MLMSMLAITEGRRSFVSVENA CSNYVTTVQVKEVNQMHSFN SCNAIHPRDHILEISGIPHTLTQ VEELEDASIQMSQTL.LLLIEHDP VSRSPAQLRLDAWLSPHTQNA GHPHALSTLDTKDNLEGLTRRC SLRLSNSISKSPSSPKPEPLLS RDISCWESLCCSSTYSKQNRSC DLIHGEVLGKGFFGQAIVTHK ATGKVLVMKELMRCDEENQK TFLTEVKVTLPSNLLPPGHDLL QTGAREQTGILKTGGLSVPGGA GHAAACRAGGVGPHCEHAVRP DPRLTPLALAQPPAGGCSTASIA PLFSIPAVSRVFRASRGLAACLE AEQAGRILTCEVCKLVVGLSL DSQQQLSSVLCGWLCCLSCPQL WSLNRHPQHHLVEMQNLKS HPRPGETESAL
4980	35348	A	5021	1	588	MEYPDGGSTLDLLEPGPLDETQ IITILREILKGLDYLHSEKKIHRG VKAANVLLSEHCEVKLVDFGM AGQLADTQTKRNTFVGTPFWI APENNPTLEENYSKPLKEFVE ACLNKELSFRTAKELLKHKFIL RDTKKTSYLTELIDRYKRWRA KQSQEDSSSEDSNSETDGGDSIG GSDSGDWIFTIQEKDPKNL
4981	35349	A	5022	1	1380	GPRASPPRARRGPAVPSQEVA VLSAMAHSPVQSLPGMQNLK ADPEELFTKLEKIGKSGFGEVF KGIDNRTQKVVAIKIIDLEAEAD EIEDIQEITVLSQCDSPYVTKY YGSYLKDKTLWIIMEYLGGS ALDLEPGPLDETQIATILREILK GLDYLHSEKKIHRDIKAANVLL SEHGEVKLADFGVAGQLTDTQI KRNTFVGTPFWWMVPEVIKQAG YDSKADIWSLGITAIELARGEPP HSELHPMKVLFIPKNNPPTLE GNYSKPLKEFVEACLNKPSFIP TAKELLKHKFILRNAKIKTSYLT ELIDRYKRWKAQESHDDSSSE DSDAETDGGASGGSDSGDWIF TIREKDPKNLENGALQPSDLDR NKMKDIPKRPSQWLSTIISPLF AELKEKSQACGGELGGPLKEL RGAIFYLAEACPGISDTMVAQL VQRLQRYSLSGGGTSSH

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4982	35350	A	5023	1	346	MAGEKVEKPDTKKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGGDKNGGTQVF QIITYSSYTQKVQLPKSTLKQRQ GPCPQ GAL
4983	35351	A	5024	67	599	SAKSEMAKGEKVEKPDTKKK PEAKKVDAGGKVKKGNLAK KPKKGKPHCSRNPVLVRGIGRY SRSAMYSRKAMYKRKYSAAK SKVEKKKKEKVLRLNLLQNQVG GDKNGGTRVGLNFRKM PRLVY PTEADVPKRLLSHGQKNPFSQH V/REKLASITPGTILILTGRHR GKRVVFLN
4984	35352	A	5025	101	202	PVPGTSSCTDRYHYKKH**KIN TKLVSKYILNM
4985	35353	A	5026	2	562	LRTVPDLPGRFRFRAMRTGQRR* PELPPDMNSLEQAEDLKAFERR LTEYIHCLQPATGRWRMLLIVV SVCTATGAWNWLIDPETQKVS FFTSLVNHPFFTISCITLIGLFFA GIHKRVVAPSIIAARCRTVLA EY NMSCDDTGKLLKPRPHVQ*QS SLIVMGLRIAFLRISDTAKSHKG FLRLDM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4986	35354	A	5027	1	2090	MGAVFFMLFSWWITSGHIQLLC TRRRATVSTHQEFVVTVPFSL GLVVSGLDADTAMPGSAAEEQ FQWQSQDGGKDIEDELTTGLEL VDSICRSLQESGILDPQDYSTGE RVIHFGKTLGLSSEDSIMEKG QMVKEVTVTQVSVLKANETM ASALCGEQEGHDDPLLLTVQMS TGNHYIKDNLFPVWVKWPSLLS QSALQLNSKPEGSFYYPASYHS NQTALGETTPSQLPARGTOAR ATGQSFSGQTTSRAGHLAGEPEP APPPPPPPREPFAPSLGSAPHLPD APPAALAAALYSSSTLPAPPP GGSPLAAPGGSPTKLQRGGS PEGATYAAPRGSSPKQSPSRLA KSYSTSSPINIVVSSAGLSPIRV SPPTVQSTISSSPHQLSSTIGTY ATLSPTKRLVHASEQYSKHSQE LYATATLQRPGLAAGSRASYS SQHGLGPELRLQSPHHIDPI YEDRVYQKPPMRSLSQSQGDP LPPAHTGTYRTSTAPSSPGVDS VPLQRTGSGHGPQNAATAATFQ RASAAAGPASNYADPYRQLQY CPSVESPYKSGPALPPEGTLAR SPSIDSIQKDPKSPYILCDGGNPF CALVYRPPSSRERASSL/LKSMCY Q*NRLYPKFRRLVLSGFEGMQ RRFCASKGIKGRFCGSSLEQDC EHGGQHPCYPKLVPTLWNP HQ REGNQKNSE RV
4987	35355	A	5028	123	3825	
4988	35356	A	5029	1	593	MQVCSSGGRIILRVSGTERQLRR EGGRFCLGRGVRLREGGALR APFTAPSLTALPPDIVDIK PAN MEDL TEVTTASESHPHHCNLFV YSSSKGFLRLCDMRAAALCDK HSKHPCDDIGPIQIIGHLRTSR GWMHLPALQSTFCRCRMDQNL RAFLAPRLCDFSTSQPQGSPEQ PVMSGLISPWTKPSRSSVFSM
4989	35357	A	5030	1	894	

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4990	35358	A	5031	1	3115	RQICSMASELGARDDGGCTELA KPLYLQYLERALRLDHLRQTS AIFNRNISSDDSEGLDDSNPLL PQSGDPLIQVKEEPPNSLLGETS GAGSSGMLNTYSLNGVLQSES KCDKGNLYNFSKLLKSRKWLK SILLSDESEADSQSEDDDEEEL NLSREELHNMLRLHKYKKLIQ NKYSKDKELQQYQYYSAGLLS TYDPFYEQQRHLLGPKKKFKF EEKKLKAKLKVKKKRRRDEE LSSEESPRHHHQTKV
4991	35359	A	5032	1	1522	MVAQASGQTIREAEVGGSLTA QEVEATSILLSDESEADSQSED DDEEELNLSREELHNMLRLHK YKKLHQNKYSKDKWMSQLA ALNYLLAGGDEQKLLDLSYSP QNRQPAKAKAHNNNNNNNN NNNNHNKKNPKRLDERELLY STATQSFDTNRNTRSFDEDAKES RAAALRAANKSGTGFGESYSL ANPSIRAGEDIPOPTIFNGKLG YQLKGMNWLANLYEQRLERL RFLQLEQEHTCPQEGRAERLRG QPLKLWALLHFIMPTLFDShEE FNEWFSKDIESHAENKSAIDET KLKKVKKKRRRDEELSSEESPR RHHHQTKVFAKFSHDAPPGT KKKHLISIEQLNARRRKVWLSIV KKELPKKTLTYQDAPFHVVITS NQLVVQDVKYFQVRKWQYMY LDEAQAALKSSSLTRSNARYPL VSSQRKIHDQVQVTTDKSSKMDP KEEEYIPAKHEMENTKLQFYLS AIGEKQVRWKILLQFQCRNRL LLTGTPIONTMAE
4992	35360	A	5033	1	974	MGFIIHVARAGLELLTSGMCCY FAQDLRPEQSIKASLQRIILRKY EKCGHHNLQKKGKYKSVDEYK VHKGSYNGFNQCLTTTQSKIFQ CDKYVVKDFHKFSNSNRHMTKE NPFKCKEKGKSFVLSHLTQHK RIHTTVNSYKLEECGKAFFNVSS TLSQHMRHTGQKHYYCQGEM GIAFNKSSHLNTHKIIHTGEKSY KREECGKAFFNISHLTTHKIIHT GENAYKCKEKGKAFFNQSSLT RHKIIHAGEKPYICEHCGRFAN QSSNLTCHKRIHTGDKPYKCEE CGKAFFNVSSLTQHKRIQQQQQ QTIKQTKNLLNNNNKKLVV

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4993	35361	B	5034	22	684	
4994	35362	A	5035	1	1338	
4995	35363	A	5036	1	596	MGMTDMGKSKKKSQPPSPFP GGAPPPAIGAPAGRERPPGTGD PFNQRPDNLKTCHTSHGSM AETAVINHKRRKNSPRIVQSND LTEAAYSLSRDQKRMPLYLFD QIRKSDGTLQEHGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSPE*RRGKFPPTQM GQD
4996	35364	A	5037	787	1692	
4997	35365	A	5038	289	1338	
4998	35366	A	5039	982	1347	
4999	35367	A	5040	1	780	
5000	35368	B	5041	148	334	
5001	35369	A	5042	2	545	
5002	35370	A	5043	1	732	
5003	35371	A	5044	1	1110	
5004	35372	A	5045	1	1170	
5005	35373	A	5046	1	870	
5006	35374	A	5047	1	1254	
5007	35375	A	5048	614	1236	TARVAAARRRCQWGSAGCS ALTLPRTSSLTLTETPIVQTRM VVRCPATSLPSQWRSCPSSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRTGRTEKARIW EVTDRTVRTWIGEA VAAAAAD GVTFSPVPTPHTRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5008	35376	B	5049	1	1281	
5009	35377	A	5050	2	893	
5010	35378	A	5051	1	1416	
5011	35379	B	5052	49	768	
5012	35380	A	5053	1	792	
5013	35381	C	5054	1	1461	
5014	35382	A	5055	887	1203	RPEKAR/IWGVTDRTVTRTWIGR AVAAAAADGVTFSPVPPTPHTR RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYVYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS

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5015	35383	A	5056	740	1431	CCQTLPVFHPHPHSLGPRPCPP TH/HLPSEHRSLEAACHDS LEPLNLSSGSKTKSPSPPKAKK PKGLEISA/RPAGALRHRHLR PQQSPPLGIPHPSLLTAAQVFIR DKLMERRNRRTRTEKARIWE VTDRTVRTWIGEA VAAAAADG VTFSPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
5016	35384	A	5057	1040	1477	
5017	35385	A	5058	1	1422	
5018	35386	B	5059	1	1404	
5019	35387	A	5060	353	870	AWSSPRSRCPLHRSRTPSLPRVEG QAHIGPGL/HRYQQGHQDLFIL RSDLPSQVFIRDKLMERRNRRTR GRTEKARIWEVTDRTVRTWIGEA VAAAAAADGVTFSPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
5020	35388	B	5061	1	1612	
5021	35389	A	5062	2	429	WGHWASPRLWWAWGSPGPAG LKPPGTVAASTGFSQWLLYIETI SRTPELELKNSKVRKDVLS/R GPHSLYLVDQAQLEHAMEIAK VSVQALQAYRAPPRMEQANP KTPPDANLYKKGSPSPRRANT TRLGSRATKTIHPDS
5022	35390	A	5063	508	1007	PPLAQKQAVASQSHSPCGGFHR RWFMRMTGEIMKIITCFKLVP EEQDIVVTPEYTLNFDNADAKI SQFDLNAIEAASQLATDDDEIA ALTVGGSLQNSKVRKDVLSR GPHSLYLVDQAQLEHALPLDT AKALAAIEKIGFDLLIWTSSRI QAVALASPLSNT

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5023	35391	A	5064	1	1670	MNIEFFDPPIRVSGTLNLRNIQH PFHLTGIRYCIDERQRTVNDVL QAHAGRVLQYQLPAPATATFR CQSRNRTENPQFLVCQWAGED QITQLLQEQWRVLIWMIFRTHN HMAGPRRWFRMLTGEIMKIIT CFKLVP EEQDIVVTPEYTLNFD NADAKISQFDLNAIEAASQLAT DDDEIAA/LVGGSSLQNSKVR KDVLSRGP HSLYLVQDAQLEH ALPLDTAKALAAALEKIGFDLL IFVKGTCLVLLVAFGLVTTTHFQ PCLFGVQNGEQETVQILLVG VV GGMERAERIIPFTLAINNQPTT RLTKTIAQGMPIIQRNIPNPRIS LQPAPTPRHSANPATMQPHAQ ATPTPKPHTRITPTPRPPHQRSA TPGTQRTPTPGPQTARDRAKPK DHTRPQT AHTAHTSNDPQQR HRTQRHTNKQHPHPAPRLPT LPQNNKRQKPAESDTRKHHTP HMRQPTAHAETTARNTQAAQH CHTQNT PQANRHATGDRPEHH QARDRTRIDPKPNPDRTITTGHT KGTTYAHKHTPLATHHMT RPT TGHRRGTHH
5024	35392	A	5065	548	924	GLLRPRFSVNSPIIFNTWLLSAN SINWR*YGFMP SLLILL*LNPM GRYSGASLVSRMASTTLPGHS IAMRQPVCGIFALTRAISI/AM WDFHVEDFMPERMA LNLVLNS AI*LPKIFPARWMKFS
5025	35393	A	5066	33	424	CRFDESFWCDA/HAI FVAPTLY AYDFYADKTLVPLTDALANTW QKQFPLDYKGRLWGSVAFVI GSALTGKLVTFDYRVILALLT LGVASMLLGLIRPTIQPGASL QQUESTGWSAWLALVRQNWRF LA
5026	35394	B	5067	1	265	
5027	35395	A	5068	142	609	CLFRQVSAPHITRVCITRSAATI QTIDLNNLDTGD*LQAPFPVW LISPGPFHPTPSVTRVPLEKEIRT FAQLRSVLHGINAEFFDKPLFS SLVLTLRDEGYISDSGDAEP AE TMKVYQLQTNIVIIHKCFKAGF TLAVGNQFLLINKQRASHQN

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5028	35396	A	5069	983	1387	LVWKVIPWRPAWKITLCLVNS CRRACLFAPAT*TANRLQAVC/ WLQSANPSINRGTLKESRTVA QRLSVLHGINAPEFFDKAVFSSL VLTLDREGYISDSGDAEPAETM KVYQLLAELITSDVRLTIESATQ GEG
5029	35397	A	5070	1	1815	
5030	35398	C	5071	1	354	
5031	35399	A	5072	1	678	MTDKQQGEKQKQKTEDKTKT KQKQRKNKTDKRRKTKTERNT QRTPERQTNTNQTRTKQ/RRPD TGVQTADTRQDTSARRLMRQP RSAAA WMAALRGARDPKLITM VPHSKISRSIVRKGLPMTETQRR TETSKNYRPREQQTRNRQQQD PRQQRITVQTHQQEERRETKDN NTHTKPHETLARRHRRHNIHAL AAADLVIEAASEVWKSCKRSL HSWRKFAPTNIDH
5032	35400	A	5073	93	729	SADPRNRDRTRAAKTRDAGK TDC*NL*THIETPDGDRYSRAG SCGPG/PLKRRNLNWKSKKRS HSWRKFARHKRY*PLTLRQSLY TAIAAEIKNPERVAGLHFFNPAP VMKLVEVVSGLATAAEVVEQL CELTLSWGKQPVRCHSTPGFIV NRVARPYSEAWRALEEQVAA PEVIDAALRDGAGFPMGPLELT GPDWAGPPFCCHLFGV
5033	35401	A	5074	145	1038	SILRLRQKRKQLTAYDFADNCD KALY*RNHRLREILALVCAHD RQKK/YLPSLAGFL*LKNEINRL SVRGW/SRRRSFSVR*/PFTNTD RARSHFYQFVIIDELQSLFQSHA DRRNQNNGFVSTGSTHVQGFL TGQAVYSQVVRAMNTDNLTF VNFCTVTEQLTAILQTEQRER DRFTLTVRDQYAVLTLTHTFRT YVVVVAEGGVQQTSTGSHGHE LRTEANQTTAWDHVVETAAAF TVWVHFVQVALTFAQLRHVRT LMLFFNVQSHVFIRLLFTTVDF EDNFRGTGYRQFETFTTH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5034	35402	A	5075	39	4329	YAPATFSAATQPTPKKINNVPV RNSAMHWQTRIQQAQNGYWL EREQWLA VGEQWFWRMWWSG PHRAAAGRLCHHHGNDATWH RG*FHLCFRPCV**RIEQPQEGY AIIMETTPPGTG VNFVFSDDPAF DKGYAFDFFCLEPMSHAPDDH HRPEGGDLIALAPGESTTSEMS LRVPVANCAVTTASLDSYYGE AMAIGERAPVALLDFAASARL AVGEALTNIATQIGDIKRIKLS ANWMAAAGHPGEDAGLYEA
5035	35403	A	5076	1	625	MRASGTDEAVVLVPPIRMTLEQ ALEFIDDDDELVEGAAAFAFEAL MMGSGRDREIRYGE GSPWFDI VLP CGGGITLTLHKLRS AQPLL AVLNRLEQKKPVGLRYDPQAQ SLVCLPTQTRTGWNLNGFEASI THRALRTSRYDGQYYCQGPR LTIRRTVIMTGSSDPHDTTDSNN DRVLGPSRYDGQYYCQGPRTL TIRRTVIMTGS
5036	35404	A	5077	3	516	ATLSCEVLENLAASPVVTTLE YTLFDGERV VHS SAIDHLAIEK LTSASLAFTVEQPQWSAESPY LYHLVMTLKDANGNVLEVVPQ RVGFRDIKVRDGLFWINRYV MLHGVNRHNDHRKRRGVGM DRVEKDLQMLKQHNINSVRNA HYRKRNRKEVRTKKKIESIEEK
5037	35405	A	5078	3	678	ASYCYCTRNDELVA VCD SRLS QRQALAEYGNASVWDDPQA MLLAVKPDVVSVCSPNRFHYE HTLMALEAGCHVIAQAREM/CD TARKLGKVLAYDFHHRFALDT QQLREQVTNGVLGEIYVTAR ALRRCGVPWG VFTNKLQGG GPLIDIGHMLDAA MYVLGFPR /SVEDSLCGTIELHSGCILWLETS FALNIREHAIMNIRFCGDKAGA SVFPAHIYTTATQR
5038	35406	A	5079	2	294	YSFMV/PIFGRRRWTVFSTAIL/I PCVWLGIAVQNPNT/PFGIFVIA LLCGFAGAN/FASSMGNISFFFP KAKQGA/PVFAF/LGVNGVPQA DGSVMSLAMPH
5039	35407	A	5080	1	834	
5040	35408	A	5081	2	135	QYASALVSTAIALLVCLAFLY PAANSEIHLGLVSIFWGD PDG

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5041	35409	A	5082	1	324	MQGGYNIHPLDALDDAKLAPI AAKALSHTLLMFDNFYDVEEK AKRGNEYA/QVMQSWAD/AEW FLNRPALAEKLTVTVFVKVTGET NTDDLSPAPDAWSRPDIPLHAL GC
5042	35410	A	5083	1	866	MGLAQAKLLIEAPVNGGRNRYN GPKVAKFLVGGASLNDVYLHQ HDKYRYDRYHLIRNREKTHIM PEWVTQNMNGRGVNRLLDDVN RPKSPEIKNDIRLFRQELRDAAY HFQGDADNDQLSVTPLVGLGK SSLLIK/TIFHRMRWAEQNLSICS SSFNRPAlFVRNIIQLREGKKV EITVGDKEHENDFYIPEDEPFKIIG ALPYLYEINLRRFLSRLQYYVN TDQLVVRVWKEDDNITYHLAK GWGWDKWMVITGINKLDPR AWRLDLENAILIHDPLQLELAPQ REKELE
5043	35411	A	5084	1	3483	VMFFFLPGLLMASWATRTPAIR DILSVSIAEMGGVLFGLSIGSMS GIL/SLGVVSETLWDT*/CHSW RCPAH*SG**Y*/VLALWLTSP LFAVGLGVFGASFGSAEVAINV EGAAGEREMNKTLGLPMMHGF YSLGTLAGAGVGMALTAFGVP ATVHILLAAALVAQIAAWYKAL QEIQIPDFIPRAPQRMADVAK TLAGEGRHLAIEAPTGVGKTL SYLIPGIAIAREEQKTLVVSTAN VALQDQIYSKDLP
5044	35412	A	5085	1	848	MLVGKVVVSEGA SFRTHGAVD TSKAYVSLNSGWTHIADITTTN QNTLLNLNLANLMSDANVIMMD EPVTRSSVTASAENITLTTNTL SGNGNFYMRDTMANHQSDQL NVTGQATAGDSLTLVTTGGGD AAFTLGNAGRVFDIGTYEYTL DNGNHSWSLAENRAQITPSTTD VLNMAAAQPLVFDAELDTVRE RLGSGVKGVSYDTAMWSSAINT RNNVTTDAGLRAQAIKTVHHR QNRLIHFSLNGSTFNVYRHFR TKTCPKDAETNGKEQGRCQPE CQT
5045	35413	B	5086	75	1777	

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5046	35414	A	5087	1	860	MKAPGLPADQQFFADLFSGLV LNPQLLGRVWFASQPASLPVGS LCIDFPRLDIVLRGEYGNLEAK QORLVEGEMLFIPARAANLPVN NKPVMLLSLVFAPTWLGSLFY DSRTTSLHPARQIQLPASLQRG EGEAMLSALTLSRSPLEQNIQ PLVLSLLHLCGSVVNMPPGNSQ PRGDFLYHSICTWVQDNYAQF LTRESVAQFFNITPNHLSKLFAQ HGTMRFIEYVRVWRMAKARMI LQKYHLSIHEVAQRCGFPDSY FCRVFRRQFGLTPGEYSARFQG
5047	35415	C	5088	86	601	
5048	35416	A	5089	1	870	
5049	35417	A	5090	305	625	VAPGDRHAFPLAPSGLSPELTLP QTQCCAQATVQGLEGRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEE/EEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEAKTQ
5050	35418	B	5091	1	552	
5051	35419	A	5092	2810	3117	LTLNSHMAPALIPILAMSAPMT PMKN/LSQVHAQGLVIRDLPLIA SNFRNTEDLSSYLKRHNIVAIA DIDTRKHAACAVPNTLVARGL RKHLKRVAAPQHWIAG

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5052	35420	A	5093	2	1902	LKYPMKRVGKRGEGKFERISW DEALDTISDNLRLKDYGNEA VHVLVYGTGVDGGNITNSNVPY RLMNSCGFLSRYGSYSTAQIS AAMSYMFGANDGNSPDDIANT KLVMFMGNNPAETRMSSGGGVT YYVEQARERSNARMIVIDPRYN DTAAGREDEWLPIRPGTDGAL ACAIAWVLITENMVDPFLDK YCVGYDEKTLPANAPRNAHYK AYILGEGPDGIAKTPewaakIT SIPAEKIIQLAREIGSAKPAYICQ GWGPQRHSNGEQTSRAIAMLS VLTGNVVGINGGNSGVREGATG SAVGEEVVFNTSMGTGYQEITD\
5053	35421	A	5094	8	456	LPIPSNRYSISYPILAMSAPMTP MKN/LSQVHAQGLVIRDPLIAS \NFRNTEDLSSYLKRHNIVAI\
5054	35422	A	5095	377	1228	DIDTRKLTLLREKGAQNGCIIA GDNPDAAALALEKARAFPGNG MDLAKEVTTAEAYSWTQGSW TLTGGLPEAKKEDELPHVVAY DFGAKRNILRMLVDRGRLTIV PAQTSADVLKMNPDGIFLSNG PGDPAPCDYAITAIQKFLTEDVP VFGICLGHQLLALASDVEKNVV MITAQNHGFAVDEATLPANLR VTHKS/LFDRYVTGHSSHR*TG\
5055	35423	A	5096	1	519	FSFQRHPEASPGPHDA/APLFD KQARGRLCPAKPGWSCPWPW QPTFC/GQCCLKVRPGVIGDHF GALKFDCPTGTRTCLGRITPLFL PSSPIWNGCIFPIPVPGDCEG VQIRSLSCMVHSGSISHAAGR EDALCGEMPFDQSLKQLCSVP CPGDCHLTWSEWSTCELTCD GRSFETVGRQSRRTFIIQSFE QDSCPQVLETRPCTGGCSPQA RPAAIRQCIPACRKPF SYCTQGG VCGCEKGYTEIMKSNGLDYC MKVPGSEDKKADVKNLSGKNR PVNSKIHDFKGSWLSQLDP

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5056	35424	A	5097	1	743	MCPAIDAVLVVYVNRKWTNLSDD PMPVGMGTVPKYVLM SAPATT ASYIQLDFSPVVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVNI QDTMIGELPPQITKTLARFIPEV AVA YPKSKPLTTQIKIKKPPKV AMKTGKSLHLHSTLEMF AAR WRRKAPMSLFLEE HFN LKGQ HSLHENQLQMATS LDRRG N/YT GFITSYLEEAVIPV VNDVLQVG LPLPDFLAMNY
5057	35425	A	5098	2327	3435	KTTTLEDNLGNTIQDIGPKDF MMKIPKANATKIKIDEWDLIKL KSFCTAKATTKR VNKQDESLRS HYE*WGMLTDCVVMRDPNTK RSRGC GFV TYATVEEVD AATN ARPHKVDGKVVEPKRTVSR ED SQRPGAHLTVKKIFVGKIGEDT EGFAVTFDDHDSVDKIVIPKY HTVNGHNCEVRKALSKQEMAS ASSSQRGRSGRG GFGGNENFG CGGNFSGHGGFGSGHDGGGYG GSGDGYNGFGNDGGYPGGGPG YSGGSRGYSGGQCGNQDQSG YGRSGSYDSCNKGGRGGFGSG SGSNFGGGGSYNDFGNYNQY SNFGPMKGGN/ GGRSGP*GD GGQYFAKPPNHSGYGGSSSSSS
5058	35426	A	5099	1	636	MRDPNTKRSRGGFVTCATVE EVDAA MNARPCKVVGRTVEPK RAVSREDSQRPEDETELHLRDY FEQYGKIEVIEIMTDQSGGKKR GFAFVTFDNHDSMDKTVIQKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGSGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVYNNQSSHFGPM
5059	35427	A	5100	1	3622	MTGICYTEDERSYKKNQAQPTA ASKKQKETQKFCLRV DGGQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPE PVALET RSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRLAMPGRPEPPVFRSQEVV ETMCPVPAATSNVHMVKKISI TERSCDGAEMKWEDQNIGD

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5060	35428	A	5101	1	782	MRRRLQLDSSLHPPSCFSSTLK CGKAAAAACDSSDQIQLRLQT GHLPCSEASTICPPNHHSSQSLR PPLPPPHNHTLSHHSSANSLSN RNSLTNRRSQIHAPAPAPNDLA ITPESVQLQDSWVLNSNVPLET RFWCCQRFLVFPGLQLQLHTLS LPVWSHGALPVSLCIFTWLSH KDTSHFGLRVHLLSLPLEAKYS FYPGCPVLEAPAPNPLKGPWCLW GVGTFRRYCTTFLFNESEPKDL VGEKFKSDRLCREAHLQE
5061	35429	A	5102	3	1864	
5062	35430	B	5103	1	525	
5063	35431	A	5104	2	351	RPAVGAESKNPSKRHRDRUNA EULDHLASLLPFPDIISKLDKLS VLRLSVSYLRVKSFFQVVRQRR EIHGRNCQKRNQNLKDRGWQ WQMPKMWMITRANEGPCRS GPEHWTPRP
5064	35432	A	5105	1	375	RPLQKQRPVGAESKNPSKRHR DRLNAELDHLASLLPFPDIISK LDKLSVLRLSVSYLVGKSFFQ QGLAVADAEDVDHTGERRP MSFRPRALDTQALRRRTQFGLH LLMVNIAGLIATDRL
5065	35433	A	5106	407	910	NVTPAHYDEQQNFFAQIKGYIR CILFPDPQFECLYPPVHHPCYR QSQV*LDNPDYERFPNFQNVVG YETVVGPGDVLYIPMYWVHHI ESLLNGGITITVNFYKGAFTP KRIEYPLKAHNKVAIMKNIEKM LGEALGNPQEVGPLLNTMIKGP IQLACQGSRRPAR
5066	35434	A	5107	237	908	HEKPGRQRETRSQNHSHHHHHH HHHHQEKIRIQTFTFP*EDTER SDCPQAKKRSRRNQPC*HLDF ELPAARAATQPVNSGARAGRA GATVPRHTATLLHHQRRDYA GGSLCDIDRAPDAKQGGKS*ES ETDSRFWKGTVC*DHTAGWVH GRPTTPHHSSPDSRNGGQFLHQ QIALAAGWREGASRPKQEP LQP GPEQQRGRREPVQGKAPSG HQS WP AE

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5067	35435	A	5108	57	873	SGLCTAAFFHHQMEVVHT*SVSSRS*R/PTTPVIAQWAHEQSGHGRHGGYAWTQQHGLPLTKADLAMATAECPICQQQKPTLSPRYGTIPQGDQPATWWQVDYIGPLASRKGGORYGFAYLARNVSAKTTHHGLMECLJHHHGIPHHASDQGTFFVAKEVRQWAHAHGHIFHHVAYHPEAGGLTEWWNGLKKSQQLRQLGDNTLQDWGKVPQKAMYALICQPIYGIVSPIARIHRSRNQGVKVEAPFTTIPSDPLAKCLLPVLVTLRSAGL
5068	35436	A	5109	1	311	QITMQPELPIMNWVLSVPSSHKMGHAQQHIQEV AQMPRVSTPATLPSLPQPALMAPWTVPYDQLMEEFKARARYAGTIQKWTAALQPLSRTSLKDSGEGTSKW
5069	35437	A	5110	3	591	DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYSFFKRQLLACYWVLVEIEHLMGHQVTMRPELPINC\VLSDPCHKVGHAQQHSIIKWRWYIHDWAEGETSKI.HEEVAQIPMVSTPSLPQPAPMASWEVPPYDQLTEEEKTRA WFTDGSARHAGATQKWTAVALQPLSGTSLQDSSEKSSQW
5070	35438	A	5111	1	582	
5071	35439	A	5112	1	635	

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5072	35440	A	5113	2	1538	FFPIGFWRQHPIRLSVLLQHIY* VT*KAASFEGWPKQEAL*QV QAVVQVALPLGPYPADPMLL EVSVAADKDAGCSLWQAPIGES QWRSLGFRSKALPSSADNYSSF ERQLLACYWALVETECLTLGH QVTI*PELPIMNWVLSDPSSHKV GHEQQHSIIKWRWYICDWAVV GRESTINGLAGWSETWKKHH WEMGEKQIWGRSMWMESEW SKTVKIFVSYVSAHQCVTSTEE DFNNQWDGMTCSVDTTPLSL TTSVIAKWAHEQSDHGGRYGG YAGAQQHGLPLTKADLAMTTA ECPICQQQRPSLSPQYGTISQGD QPATWWQVDYIGPLPSWKQR FVLTVIDTYSYGFGAYPEHNTS AKTTVNGPMECLIHRRHIGPHGI ASDQGTFRFTAKEVWQWAHAH GIHWFYVYPHPEAAGLIGWW NGLLSQLQCCQDNTLQGWG KVLQKAVCALNQHPYGTVSP VARIHGRNQGEVEVAFPIITS SDRLAKFLLPVSSTSCSAGL
5073	35441	A	5114	488	966	ILVSGKQGSVCPGPSSSGTRGSS SPGVAVSNKAAATVGPQ*VTQ QEGGPGSRQRTRAGSPVLPAG PSAVEGEEGSWTPGGPVPRKR SAAPSRQR*HWLRCTPA*QRRG DWPRAAGRCHARRPPAAGSRA PTKISARPTRISRLGPRAASKAQ RLQRL
5074	35442	A	5115	197	421	KLKATMNSFHKS*SCALVSTRP CSPRGDPRLATTTIPALVEPPCG TQDPKMAAEAPQRPGKRLGRN LLRRRRPT
5075	35443	A	5116	3	5649	LLEKLRQRIHDKAVALERAIDE KFSALEEKEKELRQLRLAVRER DHDLERLRDLVSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ WLKEEMETKFSRWQKEQESIQQ QLQTSLHDRNKEVEDLSATLLC KLGPGQSEIAEELCQRLQRKER MLQDLLSDRNKQVLEHEMEIQ GLLSQSVSTREQESQAAAEKLVQ ALMERNSELQALRQYLGGGRDS LMSQAPISNQAEVTPTRGLGK QTDQGSMPQRSDDST
5076	35444	A	5117	2	157	YLGRLHCLFSEHEHSSRKEMV LVEGLCSEQGRG*TLASSSER KPLENER

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5077	35445	A	5118	248	621	TDEPSLLSHTFCPKGALLSACSG ACPLSSGTQAGMPPSTEALQPC RGLTVPHQ/LG*RPQGMLWWK ALAADWSVEWQKGRRLGKA LSVTSRTGRLLCR*GSAEAAAS PLAASPRRSSRALGAGIP
5078	35446	A	5119	2	157	YLGRHLCFSEHEEHSSRKEMV LVEGLCSEQGRG*TLASSSER KPLENER
5079	35447	B	5120	125	994	
5080	35448	A	5121	1	550	RRYRPRRVQDPGGPAEAERGPP RRLLNARVHVCRAEASERAPGP CGRVSAHVERARDPRLE*QLED KAAPRQDFTQQLRGPEKH VWQEKEDMHKQLVEASETLKS QAKELKDAHQQQKLALQEFLE LNELMAELYSQKQKVWDKEEE MEVAMQKADMMWQE!*RSKK LRKRMLFSQMRWL
5081	35449	A	5122	135	638	GSFPGAPLQTLVTLGLAWQS SGWILRGWLVPVPRACKSPRGQ ALAICLSLRGLGARSTWAETRP QGPRGSLASLCPAHMDLSIWKT GDGGPRSAFVKVHQGSLNTFG VDTAARRLSQARTAPSPSV\SAP SSAAAPASAGPPAPGAPPTPA QALRPAPPSPRPAER
5082	35450	A	5123	193	610	VGELLPFRFKISLRPFLALCSSL GPCRQPHSGSVPA*NPLLGPR KSSPHSGCGLAPFAIPPELLRRLP LEGSAHCPAPEGAA SPPTSWDS ADPPCRETSIFAPPRVVLTPGPS APQASPSQPLFLTPRWDRLPES VL
5083	35451	A	5124	2446	2630	VGFFFFFWWGERGTGSYSVTQ ARVQ*YDLGSLQLLPPSFKGF CLSLPGSWYYRHGPPRLG
5084	35452	A	5125	3	710	EDGDWDQRRGGEAGDQDQRR GGEDEDQDQRRGGEDGNRDQ KRDGENDWDWKREDENDQDQ DEKREGEDGNQDQRRGGEDGD QDQRRGGEDGNQDQRRGGKD GDQDQGRGGEDGDQDQREG EDGDQEQRRRGEDGE*QDQRRG GEDGGQDQKRGGEDGNQDWS REGEDRD*HWRRGGEGVE*QD RRGGEDGE*GQRRGSEDGDWD RSRGGEDGDQDQRSVGHLC HSGPPASGCVS

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5085	35453	A	5126	506	882	RCSGGGFDGNKGTALPTISA DTRCWRTRLRVQTMTCRFRRF KAFFGIMSCGRTGRILFPSPCS MSWIPCRANKS*GNVISQSPSK NR/WQIMMVIQLLNFYLPGLDFV SFRIMLKGNWEVTRTRG
5086	35454	A	5127	107	1327	ERRKRAVGGFDLVLGEQPSDKI FR*VIV*GLALWPLSKSFVIP AELAINPSAKCKTDMTVMEDA VEVR*VWLQD*GLDSLEVLLDS FGPVRDCSKDNGGCSKNFRCIS DRKLDSTGCVVGLPCKLVVDS SGCYDRHIGVDCSDGFNGGCE QLCLQMQAPFPDPDTLYNILMF CG*VELPARPLDGRSCQLITETC PEGSDCGESRELP MNQTLFGEM FFGYNNHSKEVAAGQVLKGT R*TSYT*N*YQQLPDGLVVATV PLENQCLEEISEPTDPDFLTGE CAFSTLFGYPVLQHWKVR SVM YHIKLNQVAISQGEHCRLSCD GATSRADFVALLDQFGNHYIQE AIYGFEECSIWYPNKKVQRRRL WLEYEDISKGEWHACWQILSTF PWIVISLHNCLP
5087	35455	A	5128	3	23	FYSAFLVADKVIVTSKHNNDTQ HIWESDSNEFSVIADPRGNTLG RGTTIT*VSIPPSL

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5088	35456	A	5129	1	2462	MRALWVLGLCCVLLTFGSVRA DDEVDVDGTVVEEDLGKREGS RTDDEVVQREEEAIQLDGLNAS QIRELREKSEKFAQAEVNR MKLIHSL* [*] NGIFLERLISNSS CVALDRLSLISLTDENALSVNE* LTVNKKCDKEKNLLHVQHTGV GMTREELVKNLGTIAQIWDQ ASFLNKM* [*] SHRKMGPVNLPEL IGPVWVSGFLFPPLVADKIVIT SKHKQPIQHIWGVWTPNGIFL * [*] LLDPRGKHS* [*] DRGNRQFTLCP * [*] KEEASDLPWNLDTIKNLRQKN IHSFIKLFLLIYVWSSKTETV* [*] GA PWGEEAAKEEKEESDDEAAIV EEEEEEKKPKTKKVEKTVWDW ELMNDIKPIWQRPSEVEEY KAFYKFSKESDDPMAYIHFTA EGEVTFKSILFVPTAPRGLFDE YGSKKS [*] DIKLYVRRVFTDDF HDMMPKYLNFVKGVVSDDL PLNVSR [*] ETLQHQHLLK [*] VIRKKL VRKTLDMIKKIADDKYNDTFW KEFGTNIKLGVIEDHSNRTRLA KLLRFQSSHHPTDITSLDQYVE RMKEKQDKIYFMAGSSRKEAE SSPFVERLLKKGYEVIYLTPEVD EYCIQALPEFDGKRQNVAKG VKFDESEKTKESREAVEKEFEP LLNWMKDKALKDKIEKAVVSQ RLTESPCALVASQYQWSGNME RIMKAQAYQTGKDISTNYAS
5089	35457	A	5130	45	416	RWGLAMFPSLDNKSSETLSQKK KKKDLCPHISFEMDLTTADAR WVQDAATRLLATRCPPNSRG SR** [*] ISWRAGCCPGWAGPHW GHDGCL* [*] PSCVSSS
5090	35458	A	5131	3	477	GRLPRHRGGEPGAQAPAGRQ RGGAATAAGAPRAGGGAAA GNARRCREAAARDPHHGECSG PEPSQCEGAHQRAQRAQGD* GGSGATGEGRRGHDSHNLG RVRGSTLPPS** [*] N* [*] VGL* [*] VPSWP QCGPAHPPGQHPALQEIHQRLP LESGGHRV

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5091	35459	A	5132	3	446	RTGSWGWASASQQRHKKDRGL DSAGSGWVSHILPVAPPADADA RPSASRWRQGSHPGRTECP SVQPLCLPPAGHHRNHSIASPS QTPPPRSLPGSQDKSLFLPRDRR TGEGEHGMN*APLSAPGTSCRS GGSTSWLPEILGPTQ
5092	35460	A	5133	352	588	DIFKVGCGFLFKRLRCQQRFFL LIFSSSTQSA*RVSNQPYH*EIK MAVYYGELRKNGLIQESCDNIQ PRQGSFNMDSMQ
5093	35461	C	5134	13	144	
5094	35462	A	5135	587	1078	LSQRFLSSRIKLQRLSLQNGIP QIKELDYLFRTNSNQINFNLISH RVRRARPPAPPGRPNPSGPDPRP EPPARAGSSRRGPGEPPIRRQPQ RRFRRRGPDPRGRLSRGL*RRR ARPASQPQRQHHSRGPAGRPGV APRRPAGLAAAAERLTARGAA ASPAIPRA
5095	35463	A	5136	44	455	HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWENWLAICRKLKLD PFLTPTYTKINSRWIKD*NIRPKSI KNLEENLGNTIQLHG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP
5096	35464	A	5137	101	861	LIGYQPKMSRTRRIHSKRLPERIK YLGSQLIRDVKDLLKENYKPLL NEIKEDTNKWKNNIPCSWIGRISI VKMAIL/PQAICGKCLKDPFLTP YTKINSRWIKDLNVGPTTIKTLE ENLGNTIQAIGMGEDFMTKTPK AMATKAKIDKWDLIKLSFCT AKETTIRVNROPTEWENIFTIYP SDKGLISRIYKELNQYKKK/TR NPIKK*VRDMNRHFSKEDIYAA HRHMKKCSSLLDIREMQIKTTM RYHLTP
5097	35465	A	5138	3	314	LKSFCMAKETTIRVN*PTWE NIFAIYPSEKGLIYRIYNEATNK DLVRRSGPLKTPKKKSQTLVLN LVTFFKRTPALSEEKSAQVLWQ FKKPECVLTSKRVH

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5098	35466	A	5139	1	1278	MNIDAKILNKILANRIQQHIKKL IHHDQVGFPEMQGWVNIKCSI NIIQHINRTKDKNHHISIDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKTGTGQCPLSPLLFNIV LEVLRARAIMQEKEIKGIQLGKE EVKLSLFADDIMIVYLENPVSA RNLLKLISNFSKVSQYKINVQK SQTLHTNNRQRESQIMSELPFT IASKRIKYLEIQLTRDVKDLFKE NYKPLLN
5099	35467	A	5140	1	430	GGVFFLRTPTDCCGMLQGAAG STGFYASEARPRGPACSLDRGS SSLLSWGLHQDPLFPAKQHRH EAGRADQNSPRRLSTG*QTPT L*RRPAAATGRRRAQPPRATSV SAPASPPCPRARPPHARPPRVL ACQP*ATAPGP
5100	35468	A	5141	1	346	
5101	35469	A	5142	3	1336	
5102	35470	A	5143	5	283	
5103	35471	A	5144	1	1368	
5104	35472	B	5145	1	838	
5105	35473	A	5146	1	962	
5106	35474	A	5147	19	87	
5107	35475	A	5148	41	831	GLQNPKHQSSQLVDLKMKKSL LQCMFYQLIVLQ*YLK*YLGTO LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWIGRJNIVKMA ILPKDPTTAQLSPRGSTAQKGH WRPCPLPRGVPSPRGPTSH HHDPCCGGAPVNTGSEWRQ KLRSGPKSDWAGRAQAPSLGE GGAKNGKSHPGSHRAFSLPRAP RRLGPQSQGRFRGFLKQARGR AGEGHSAILLAPESPNAQVSNV TSATYRSNLSGLPRPCSVVLLG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5108	35476	A	5149	1	2233	MKAIEIKTFETNENKDDTYTQNL WDAFKAVCRGKFTALNAHKR KQERSKIDLTLSQLELEKQEQ THSKASRRQEITKIRAELEIET QKALQKINESRSWCFEKIHKID RPLARLIKKEKNQIDAIAKND KGDITIDPTEIQTITREYYKHLY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPTGSEIVAIINSL PTKNSPGPDGFTAIFYQRYKEE LRKLYGLQTRDVKDLFKENY KPLLNEIKEDTNKWKNI PCSW VGRINIVKMAILAQGNL*YIKFN AISIKLPFTFFIGL/EKNLTFKFIW NQKRS/RIAKSILSQKNKAGIGI TLPDFQITITYKATVTKTA/WY YQNRDIDQWNRTEPSEITPHIYT ILNFDKPEKNKHGGKASLFIK W/CWENWLANCRKLKLDPELT PYTTINSRWIKDLNLRQIIKTL EENLDNTIQDIDIGKDFMTKTP KAMATKAKIDKWDLIKLSFC TAKETTIRVNRQPIEREKIFAIYP SDKGLISKIYKELKQIYKKKNK QPHQKVGEYEQILLKRRHLCS QQTHESMAHHHWPCREMQINT TMRVHLYTPVRMAIIKKSNNRC WRGCGEIGTLLHCWWDCKL VPLWKS VWRFLRDLEIIPFDP AIPLGIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTM IDWIKKMWHIYTMYYAAIKID
5109	35477	A	5150	1390	3491	DLLTRTACAVPGWGCSRA TC QARGWRLSSPPHPSPVQPLLC HLPYPPSPFSLLSNLTPFLRAFP SLETS*KWART/WPGAVAHAC NPSSLGGRGRWIT*GREFETNL TNMEKPCLY
5110	35478	A	5151	310	445	YLTKIWPGA VAHTCNPSLTGGR GGWIT*GQEFETSLANMVKPHL Y
5111	35479	A	5152	44	1132	PQVIHPRAPKLLEIQEPWRWH DLNQDTPSALCQH*RTC*HRAE GVSWFKSWIHLGGSCNSSSLGA RGGWIT*GQEFETSLTNMAKPH
5112	35480	C	5153	183	323	
5113	35481	B	5154	504	2474	
5114	35482	C	5155	66	269	
5115	35483	B	5156	2414	3096	

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5116	35484	A	5157	9	239	HHHYCQHIIHHHHHHHHHHHHHHH LPAPCRNLRV*PVCFRYKLFWH YGKQHLLFLDFLLSHSEWCCEM VSHCGFDLHFSDD
5117	35485	A	5158	3	387	TDTKPLSCSSCPPRGKKPVSHR DQ*RRWGRRCRGEPGTEACWS AGALQF*KPRSRGGRTSKMTSG PSAEKGGG*AGRKPGRRHFGRR VLRHSCVLPVARELWGRHGPC GWRQKNVPWKWSELLPVVAP
5118	35486	A	5159	1	277	MPPPPPPSPGPGVGSRLPPG PAVTGNEKELRGN*VGLAPPR PRFRASRREGVTGKVHRPNRLQ LRAPPKG*SDQRGQNVPPSEAK SLC
5119	35487	A	5160	1	3285	
5120	35488	A	5161	3	194	IPLSLQSKVEGQQLQDDLKVL NELYSVNQMGCLAL*QAEGSSI WQLAAIVHQQQN*TPSWGQ
5121	35489	A	5162	520	844	VQAPGKCHAQMPAPAAPVPLG RSRNPGRLASAVPVSSLLRFLPF LQPIPPSDILPLSFEAVPSSPAE SGLHPCTRRRKARPPSC*VPLG LLSPQPHPPPHVWRKGIL
5122	35490	A	5163	1	794	FRGFLDRGDCAALPCTYPHSPC SH*GGNCLPSLLTRPCVKA*PQ MSGRKSSMRWRQRSLTAGT SS*TPTSSTMC*ALVGSSTWNC MLQAGSTAPGAGTPGSRPTWS SSSTCSWTAPSGRARCAASS SCAMSAARRGWTSACWRRTS RAWWTTSSPACASSATASVAA STASTWPAARTTGTAESSARP ARRASCTGSPARCWRRRPPT PSPGRPAPPSRRTRAQAGTSA LSPGACFGPRSCC*SSTCSSLSV APY
5123	35491	A	5164	3	57	RIGQGVPPVHS*VEGGPNVISIV LEYLRDTPPPVVCDSGRAS DILAFGHKYSEEGG*VKVFLWC THKWKEDPM
5124	35492	A	5165	1	1326	
5125	35493	A	5166	2	337	YSVTMTPGKLRLTCEIDWPALE VGWSSEGLDRSLV*KVLCPEL VPSGGFLVSLTSRMKPTLTGS VKVLKDGMSGVCSFRCDVSR VSSFWWVRGLAGWSTTLRLKL
5126	35494	C	5167	339	548	

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5127	35495	A	5168	3	413	SQAFLPAASRRERPPPEVDPKA TDPKSGTRRLPPRLPCQWTTPE HSHTSQLNLSRAFPKEPNPAAT Q*NPSGASPRERPHARAQEDRN GEC*EGNGSRPDLEEEASTPRA SPTPSD*PLWLHPRLPLVLEITPL LQL
5128	35496	A	5169	3	479	FLHSTHIYWAHSMHELLKTAV VSISSGQCTSLNTESGIWGGVPE NAR/CPPAEGTVPASLQPRDPPR LPGSH/ASLPSAPPSRHVWTPP EP/EAAGPKPS*IRCRWPPAGAT TKANPKESGRVLESMLPLPKSR SAPVTFSAFACSGLPERVHEVF RVGKLR
5129	35497	A	5170	81	329	QSVSSPSWFPQFPVQVQKVP QVYRGDLVV*KHIVAPPSPSS FSGHVRHDCFPFAFHDDRKFE ASPAMLPVSSLGPHYL
5130	35498	A	5171	335	467	MPSTPTARKPESPEALARVESIA CLPSPAP/PHCESPQASEETG
5131	35499	A	5172	1	2424	
5132	35500	A	5173	2	304	CLTKNTSATREKQVTELHRRSK LQFPAKTKALQTVIE*KDITLC *VKEHLYIVACWALRLHLVFLP TKAGISPALMKVSYPGKPLTLK QLGRLVILQE
5133	35501	A	5174	44	286	GVQNGVEELIVRRMQKSPGP GEMESGSLEKEPLGTQTGPVPS EGTE*TGPPRTPSLQTQGPQRT PSLQTQGPPTPSL*TTQGPLRTL SLQTQGPPTPSLQTQGPPTPS LQTQGPQRTPSLQTQGPPTPS
5134	35502	A	5175	206	384	KRVFAHQADGRARSQFISSAGP GSQAGPGQGTG*QREDVEAAG QPGSTAEGVRT*SDPG
5135	35503	A	5176	270	818	RNERKPSQRTAVGLGAGQLQP GQPGVQSEEPGLEAGCAAGV LPGPAEQDREGIYSK*KRVFAH QADGRARSQFISSAGPGSQAGP GQGTG*QREDVEAAGQPGSTA EGVRT*SDPGSSHPAAAFYEN IQDGEALGRCGAKRTATAAP*Q RG*EGF*AGPTAAEKNEEGPPP VFSLFNHSL
5136	35504	A	5177	122	436	LTSLSAISTKAKVSPLC SARAC SPSPAARAALGSPGFTC*GAGV APTPVVAAPAPATAPATAVAA AATTTVVSAAAMFTRRATRAAA ATGAWGFVAGAPWPLQT

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5137	35505	A	5178	20	1341	MRRCVAAPLAHRW*QKLGLP CTPTVCSFLSPQPPPRARSSSAT LSSGAPRAATPQPQTTPSSVQ PCAATPCARGGRPAPAGVTWP TTRPSMA*RTS*ASTTAPRMAP PRSHACARSHRPETARSARTAP RSAITRRAFTSTRPPPTTRTVAS SGTHTSGLSPTASRLARCRAPG RSSTIIT*TCRSPTRLCCPAQRPL PPASSPSSSRTSRSVWTRRCTRL RWTSSRPSPWMALRTVGTSTGP TA*RLRRCQASTWRSRSTSA PPSWCARWAAT*PLPSACQRK WSMLWRTGTARVSTSAACGAAP STSRSTSRPSTPMLRAPVPAGW QPPALHPQPPRPSHTRQWPWSA RRSCRWRTCTTRPASSTSSPRA T*TSHWPPTTRWRMSRCSTPTK TNCTCMRGLGTCQAGRLRGCP WPPGPSWAPWSRSPWCSLCSA
5138	35506	A	5179	47	598	ASGPASIVVLRRQFIKFFLDEICS LEERVWCRRKLCCLLYLWKEPR AVQAKSRCSDIRRELYRPVSLA GLSGDFLRAGRYSAHTVNGAW SAWTSWSQWA**SRGI.LLALH NMLKIIIAFCSLQVATRIQSTFIS SWHLSPSLGSRSPSLYMSFGS VLCPLFISHDTSSYSTKSQFSFSC LGWV
5139	35507	A	5180	236	690	LQNWSYLAEQCWNGGFIYLIM LRRFKHKAHSTYNGNSSNSEP GETPTL*LGDRATAKKGKRTKRF GVISRPANKAPEESKGSAGE VSSDPSTELENGDPDELGNHGV FQLENGPDSLKEVAGPHLERSE VDRGTEHRIPKTDAPLTTSN
5140	35508	A	5181	2	480	WPFWAMVQRPSSAILCGPATLP PNCRGACCACRATGALSAYP AIHRPATRPPAPPAGPLTSPPL SVQNSNPDPPLPSARPSGPAAPR HARHSPSELPAITLSARGSSAL CTKLKVEAAA*SCSASAWNWR LLPRNHVDSRCQPEPDGARARD GRGP
5141	35509	A	5182	3	153	
5142	35510	A	5183	3	239	
5143	35511	A	5184	1	394	
5144	35512	A	5185	1	435	
5145	35513	B	5186	84	2068	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 2009/054,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5146	35514	A	5187	149	832	DAGLSWREATRPGLHRPGC QDASTQMTFRPGDPGSSALFPLP SP*PEREELPMSSRRSPKPELPG EACSRPPTRPRPRTATRGPPLN GRLPRARLPVSAGAGALGGGR CRRRVAPRRVTPRLATRPSGVA PRGSG*AATTKLSLAFGVTPLA LTPWSRTPFRKREERPPF*YPRP ATPEASPAHVENFRSNQTRYTS AE*SGQQLERFSAIEISAQATVE PRSTI
5147	35515	A	5188	45	312	AEAQGGAAEAGHGCGGGPAPS QGCPARAAGARGWQAPAPSPQK PTPSDTTPPPRTQPPVTQCHP VTQPPVTQPPVTQPRHPMKIPP G
5148	35516	A	5189	15	549	PRHKEPESQAPGRAPQAAAY QQAASPAR*QGGSCSRCPG*A VEAAPAP*GQALGCVSQGPA*V GPTRSPHPTAGLSRPHGPPSVRS TGWSPSSRLQAQEAPWPVAPT HIPPPPLDPGQPHSCGLGAGCQP RAPAAPRAGHIP*EGAGPPPPWP SASAPPCASAPVWLWLRFPRET KT
5149	35517	A	5190	1	2445	
5150	35518	A	5191	1	708	FSEGRNRFNLVGPTFRFSTRQTL MWIPDSFFSLLSGRISTLRDET GAIFIDRDPAAFAPILNFLRTKE LDLRGVSINVLRHEAEFYGITPL EKIKMEYCFSCVMYS*QVCFE MFLVRRLLLCEELERSSCGSVL FHGYLPPPGIPSRKINNTVRSAD SRNGLNSTEGEARGNGTQPVLS GTGEETVRLANTIDSKYVAND DWLIFQYVDEEDLMNAIKDFSS VTKERTTFDTHL
5151	35519	A	5192	31	330	YGGTATVQRWAESRHVPFPSP QEQNANKICSCVEEKDSADSY GEIPWWQGPERCWPVRLMLAT LGDYKWVLTGIGTDS*LGFTIPT DHANAFSAKEIPQ

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5152	35520	A	5193	1	734	MISEVIVIQMLFLHAFSKVFSAL IKNNKKPLQDAQIKWKAISGLS GGMRRSECNRRERDQVTRTQCR DISQKIRGPGD*GMATSKNGAM A*QLGPGCQGDASTGNAEFGES AHAWSGGGRVPGVTGPDREEV GRSWQGTSCGGTSGCGRQL* DGVASRGRW/DPARPREQRAG VRQLAAPLGGP*SRRPWEPPGG SSCGRYLFAISSWSGVTVAQEG QRKRSGGK*RTERSGPGLRRL PPLLLTV
5153	35521	A	5194	3	449	EGQRSSSPATALLSSGPPSLKM ATSKNGAMA*QLGPGCQGDAS TGNAEFGESAHAWSGGGRVPG VTGPDREEVGRSWQGTSCGGG TSGCGRQL*DGVASRGRWDRR DRASSGRESGLHHSGARSLG APGSRPVEAPAGSEAKTPG
5154	35522	A	5195	606	841	CTVGFALPVFY*GFSH*CSSGIL V*NSRFLLCCLQALVSG*CWPH KMS*GGFPLLLTGIVSEGMPV ASLCISGRQL
5155	35523	A	5196	620	930	IPFISFSLIALARTSNTMLNRSG ERGHPCLPVVFKNAGSSFCPPS MILAVGLS*IALIILKYVPSIPNL LRVFSMKGC*ILSKAFSASIEIIM WFLSLALFI
5156	35524	C	5197	1	819	
5157	35525	A	5198	591	815	
5158	35526	A	5199	187	387	FFKTICFMVRVRKPPNRLCVS NMAVYFTWVQAGLHCSYPEH L*WSCRLPRRLGGVRL*PLEGE
5159	35527	A	5200	1	1197	
5160	35528	A	5201	119	375	ILDISPLSDE*IAKIFSHVSGCLFT LMVVSILA VQKLFSLIHSLSILA FVAIAFGVLDVK/CLVHA VVNLN GIA*VF*GFYGFRSNI
5161	35529	B	5202	1	1053	
5162	35530	A	5203	2	157	
5163	35531	A	5204	12	176	
5164	35532	A	5205	2	223	QTVLEDRSPRARWIF*G**GTIC SIPIPSFWWFSSNLSHSFVCRSPP SSSPGGLPMCTCVSKFPWAVW PFSRY
5165	35533	A	5206	61	308	

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5166	35534	A	5207	487	898	DFAEVAYQLGISSGVCRTTDFH EPRMLLSDRSSGSFVTHSVFLS FSSLKCL*SPLVHDALHQAHPH GKSRLRFLGSMACCMKFTCPP TLSTVPSSTPFSFCSLIKTRSAT LLKLWSISLRFLHWSWSSAFRV
5167	35535	A	5208	9	191	IPQHYYPPKTKPGRI*ISE*INNRR L*NCGNDQ*LINQKESRTRWIH SRILPKTNREP NHE
5168	35536	A	5209	1	1989	
5169	35537	B	5210	1	1488	
5170	35538	A	5211	929	1209	IPFISFSCPIALARTSNTMLNRC ERGHPCLPVPVFGNASSFCPPS MILAVGLS*IALIILRYVPSILNL FRVFSMKGC*TLKAFSVSIEII
5171	35539	A	5212	242	642	FSLKRSFTSLVSWIPRYFILFEAI VNGSSMLIWLVSCLLLMYRNA CDFFPILLYPETLKLKLLISSSLY LW*NSAVNLSGPGLFVGRLLII ASISEPAIGLFRDSPSSWFSLGR VYVSRNLSISSRFSSFLV
5172	35540	A	5213	747	885	
5173	35541	B	5214	115	1267	
5174	35542	A	5215	209	322	
5175	35543	B	5216	1	3321	
5176	35544	A	5217	390	655	CLFPVHYRLHAMMHQMKNP VLVLGIGGFILGILVIGGPVSLF KGS*KLLGIETGKISLDHPVPG GTPTKMALYEHFMNTKEFGIE
5177	35545	A	5218	3	221	
5178	35546	A	5219	798	914	FVFLWDRW*YPLYHFLCLFDS SLFFSLLVLLAVYQFC
5179	35547	A	5220	12	460	YLCMLHEVLVLCFSVPSPGHFSF SLN*LF*LA VPTVTFYQGLSFLA QA*ASQVDFRQLCWQQEFQAS GS*LAGLHSGSIH*ARPLGSWL QLPFQESEWFCLSGVPGATVVS /CTF**SPF*LV*DGISLWF*FAFL *WPVMMSIFFMCLLAA
5180	35548	A	5221	3	508	AERNRSRQGVGAGAGDHEVLQ LLPDKWKQKILCPVQLLRGAW SNYYSPDANRQP**VQGNALHF AECWPHGEDSQPTVPTSQGRM LAGPARHLPHPHVPSPSGSLRG SDSEDTHT*GTVAGSGCLHCLAP GHLHPGWPPSRVLPIDRSVHQ GPGRKAPPTPRVTLFT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5181	35549	A	5222	584	1052	LRKAAASGSFVFVAPDPNTDTG SSQCESESGSRGCSMGHQRS QHYYHHHHHHHHHHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPSGHRCI*LT GIEAA*CHSL*PYQKDACHHFE EHSPPP*RPFLPRHHLHPQSS
5182	35550	A	5223	1614	2308	LRKAAASGSFVFVAPDPNTDTG SSQCESESGSRGCSMGHQRS QHYYHHHHHHHHHHHHHHHH HLDTGWRGE*SRHSAGLCPPSQ RRLHSCQTSPSCSPSGHRCI*LT GIEAA*/WS*PLTLSKRCVSP RAQSSSVTSTSAQASSAPPEKK *L*PERPYSSHPASVADLQMC LPLNRITGQTNRLHRAILLRW MRSCNLLTCTVLSNVFSFSELS YSRNTMCRG
5183	35551	A	5224	3	407	SVGLILPSSLQHYYHHHHHHHH QHYYHHHHHHHHHHHHHHHH ADLPTCAPHQGIRPFGGFPQTS GSPGLPVYAEQGTERTLSLQGT CGCGQAGLLCWGPPVASTSVG FSLESSVSPQVPLSPGAGTDA
5184	35552	A	5225	1	1287	
5185	35553	A	5226	3	1315	STMALLHSGRVLPGIAAFAHPG LAAAASARASSWTHVEMGPP DPILGVTEAFKRDNTSKKMNLG VGAYRDDNGKPYVLPSVRKAE AQIAAKNLDKEYLPIGGLAEFC KASAEALGENSEVLKSGRFVT VQTISGTGALRIGASFLQRFKF SRDVLFPKPTWGNHTPIFRDAG MQLQGYRYDPKTCGFDFGTGA VEDISKIPEQSVLLHACAHNPT GVDPRPEQWKEIATVVKKRNL FAFFDMAYQGFASGDGDKDA WAVRHFIQGINVCLCQSYAK NMGLYGERVGAFTMVCKDAD EAKRVESQLKILIRPMYSNPPLN GARIAAAILNTPDLRKQWLQEV KGMADRINIGHAGLQLVSNLQG REGISTH\N\WATHSPKLGMF FHRG*KLEQVERLIKEFSIYMTK DGRISVAGVTSSNVGYLAHAH
5186	35554	B	5227	57	386	
5187	35555	A	5228	1485	1883	
5188	35556	B	5229	117	641	
5189	35557	C	5230	1	552	
5190	35558	B	5231	250	378	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5191	35559	A	5232	3	1117	TPDPGQGCSEGGIVHETRPSPQP LCQGSCAVGCSPGLLLR*RMM ALGKIPPGHRRGPAFLPAVESAH VVPGLPGLTRETLPAPLGPHRPP QPPQGPLSTAPPAPLVSLGPHV PGLPGPPPGCPSPLPLRPCPPPS WLRPHRPVQPWWT*GSGWRP RCRPGAAGRNPGLPRACCRGL CRGPH*RPGGPRPGHSGPRTSS WGRMTGNRPRPSASAG**PRHR R* TSAERPSPQQSASRTGGRS PLSHPGSWWGVMPGLWAG APSMWG*GPGSRVAGSGRRP TSRPPHYPPHPPGTWPSGAQS GRR*QAQTPGAATEG*GGWGL PPKPWCPQDQFLGVQDWVLP NGARVGGTAWKRESVLVPG
5192	35560	C	5233	229	522	
5193	35561	A	5234	1	972	MTAEYYKLKQVVTPIAAAVPD VVSLLLEQINISLCTWYAVIDL NACFYIPVHKAHQKQFAISRHG QQYTFTVLLQRRDLDFLSLQ DITLVHYVDGIMLIGSSEQEVA STL.DLLVRHLHARGWEINLTKI QGLATSVKFLGVQWYGACRDI PSKVCDKLLHLAPPTTKKEAQH LAASFEWGPEQKGLQVQVAV QAALPLGLYDPAADPMVLEVS ADRDVWVSLWQAPIGESQWRP LGFQNKALPSADNYSPPERQLL ACYWALVETEATPVITQRAHE QSGHGGRDGGYAWAQQHGLP LNKADLAVATAKCPISQQQRPI
5194	35562	A	5235	3	246	
5195	35563	A	5236	3	841	
5196	35564	A	5237	1	746	RDLDFLSLPQDITLVHYVDGIM LIGSSEQEVA STL.DLLVRHLH RGWEINLTKI QGLATSVKFLGV QWYGACRDI PSKVCDKLLHLA PPTTKKEAQHLAASFEWGPEQ KGLQVQVAVQAALPLGLYDPA ADPMVLEVS VADRDVWVSLW QAPIGESQWRPLGFQNKALPSA DNYSPPERQLLACYWALVETE ATPVITQRAHEQSGHGGRDGG YAWAQQHGLPLNKADLAVAT AKCPISQQQRPI LSS
5197	35565	A	5238	1	483	
5198	35566	A	5239	1	1908	
5199	35567	B	5240	1	2718	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5200	35568	A	5241	522	693	LDFFLVFLQQFLPRPSSSEI*MLP GFPAAYAGPVAAAAVAAARGSGRKYVGTGDSQA
5201	35569	A	5242	1	225	MGRNQSRKAENSKHESTYSPP KDHSSSQAMEQSWTENGFEKL GFRKKEALYYLDLTASCQSQEL FQKWVSLCCPD*SYSPPKDH SSSQAMEQSWTENGFEKLGFR RKEALYYLDLTASCQSQELFQK WVSLCCPD
5202	35570	A	5243	1	1129	PWISAPVPVDVVEGAMDSVT LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRN YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRHTVS SSGGNRLPNPGDRSCDNLKTC HTSHGVSMAETAVINHKKRKN SPRIVQSNLDTEAAAYSLSRDQK RMLYLFVDQIRKSDGTLQEH D GICEIHVAKYAEIFGLTSAEASK DIRQALKSFGAKVEVFFRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYKSL CQYRAFVNGGEEKARGKPIL CRYGVGM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5203	35571	A	5244	1	1753	MVDSLIA RVGVGMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLTGGQTPAFGRRVSGVIEI ADGSRRRKAAALTESDYRVLV GELHDEQMAALYRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISHLIIHAEDTFLPFY LGKKDDVITYAIKPTCWPLDII PSCIALHGIEIELMGKFDEGKLP TDPHMLGLAIETVAHDYDVIV IDSAPNLGIGTINVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDIKGFEPDVRILLTKYSNS NGSQSPWMEEQIRDAWGSMLV KNVRETDEVGKAVINHKKGK NSPRMVQSNDLTAAAYLSRD QKRMLYLFDVQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSLAGKEVVFYRPE EDAGDEKGYESFPWFQKQSEE/P QSGNFYTDTLGMAEFRGGGLR ATAGPRLSRTDCQGTKEKVVH KTVFDKTP/VWPKRLKSPSCK NRWP*KMQKLSVCTASSPGQ LSTVRVTQREICFPVVRREVL IGTLTQTRKGQISVRA
5204	35572	A	5245	337	1977	

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5205	35573	A	5246	145	1929	VSGVIEIADGSRKKAAALTES DYRVLVGELDDQMAALSRLG NDYRPTSA YERGQRYASRLQN EFAGNISALADAECNLIKTCHT SHGSMVMAETAVINHHKRNKNSP RIVQSNLDTEAAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPPDFRRRLQGFCFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHYDVVIDISAPNLGIGTIN VVCAADVLI VPTPAELFDY TSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGNSVLRK
5206	35574	A	5247	1	1383	
5207	35575	A	5248	1	1731	
5208	35576	B	5249	1	1290	
5209	35577	B	5250	1	3345	
5210	35578	A	5251	1	1959	
5211	35579	A	5252	3	2356	
5212	35580	B	5253	334	1710	

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5213	35581	A	5254	1	1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRRLRRAEDVFPV NVSKSDDTLKINGVEDHKITFD GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHHKRNKNSPRIV QSNDLTEAAYSLSRDQKRM LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPPLYESLCQYS
5214	35582	B	5255	1	1452	
5215	35583	A	5256	1	1323	
5216	35584	A	5257	1	1557	
5217	35585	A	5258	1	2259	
5218	35586	A	5259	1	2418	
5219	35587	A	5260	1	1218	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQVRVGYTIEQI NHMRDVFGRRLRRAEDVFPV GVAAHKERNQNSIRYISNRLAR RECHDSPEEGTGNTSRKERLQG RLPSRGLTESQEHLLDTRKQFW FEDFKDGLGPIKCDNLKTCHT SHGSVMAETAVINHHKRNKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGICEI HIVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIKRAHSPSRGL YSVHINPYLIPFFIGLQNRFTQFR LSETKEITNPYAMRLYESLSAS NYQRMPDFRRRLQV/CVMEIN KQTSMLRSYI
5220	35588	A	5261	1	2028	
5221	35589	B	5262	1	1653	
5222	35590	A	5263	1	1446	
5223	35591	A	5264	1	1788	
5224	35592	A	5265	22	1893	

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5225	35593	A	5266	1	2144	MEKKITGYTTVDISQWHRKEHF EAFQSAVQCTYNQTVQLDITAF LKTVKKNKHKFYPAFIHILARL MNAHPEFRMAMKDGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYTTQGDVLMPL LAIQFFDMLRDLLKNVDLKGFE PDVRIILLTKYSNSNGSQSPWME EQIRDAWGSMLKNVVRTEDE VGKDTGVRKISGVKIMPMGV AVVNCCTYGSDYRVLASWM MSQWLHYPEWYRKENKHKFY PAFIHILARLMNAHPEFRMAMK DGELVIWDSVHPCTYTFHEQTE TFSSLWSEYHDDFRQLHIYSQ DVACYGENLAYFPKGFIENMFF VSANPWVSFTSFDLNVANMDN FFAPVFTMGKYTTQGDVLMPL LAIQFFDMLRDLLKNVDLKGFE PDVRIILLTKYSNSNGSQSPWME EQIRDAWGSMLKNVVRTEDE VGKQIRMGTELEFFRLSETKEI TNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRM PDFRRRLQCDNLKTCHTSHGS VMAETAVINHMKRKNSPRIVQ SNDLTEAAYSLSRDQKRMLYL FVDQIRKSDGTLQEHGDGICEIHV AKYAEIFGLTSAEASMDIQHAL KSFSGKEVVYRPEEDAGDEK/ GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFLSE
5226	35594	A	5267	1	1167	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYV VFALAGSPEDADDTIYMFYQK CDNLKTCHTSHGSMVMAETA V1NHKKRKNSPRIVQSNLDTEAAY SLSRDQKRMLYLFDVQIRKSDG TLQEHGDGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGFYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAMR LYESLCQYRKPDGSGIVSLK/ID WIIKRSQLPQSAFYQFMGLRR ESFYFRWERTLGPLKSFVSKR GTEAGKFRLAALLVRL
5227	35595	A	5268	1	1395	

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5228	35596	A	5269	1	1375	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNAAGTVAEYNGYHV VFALAGSPKADDDTSIYMFYQ KIRRKNGPVSAFTSDGKIRLFY TDYSGKHYGKQSLTTAQCDNL KTCHTSHGVSMAETAVINHKK RKNSPRIVQSNDLTEAAYSLR DQKRMLYLFVDQIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDPGSGIVSL/KIDW/IIIE/ RYQLPKVPSPEARKITRRWRJ/V KQRI*LGFLRLSEMPRKQGDY RTRIWKFEGLSNVLVIQLNKLII ICVMCLVRDCDVLKTYFHR
5229	35597	B	5270	1	1668	
5230	35598	A	5271	1458	2675	CDNLKTCHTSHGVSMAETAVI NHKKRKNSPRIVQSNDLTEAAY SLSRDQKRMLYLFVDQIRKSDG TLQEHGICEIHVAKYAEIFGLT SAEASKDIRQALKSFAGKEVVF YRPEEDAGDEKGYESFPWFIKR AHSPSRGLYSVHINPYLIPFFIGL QNRFTQFRLSETKEITNPYAM/R IPLH*LFR*TLRQTKPDNSAGKC VKI**HTQNRQSRGSRQND*RR GI
5231	35599	B	5272	1	1317	
5232	35600	A	5273	1	987	
5233	35601	A	5274	1	571	
5234	35602	A	5275	1	4161	
5235	35603	A	5276	1	1228	
5236	35604	A	5277	387	3466	
5237	35605	A	5278	1	6721	
5238	35606	A	5279	1	1651	
5239	35607	A	5280	5082	5879	
5240	35608	A	5281	1	231	NHLAVRRLTELSGGQRQRAFL AMVLAQNTPVLLDEPTTYLDI NHQVDLMRLMGLRTOGKTV VD*VRDLNQVSRYC
5241	35609	A	5282	1	303	CLRILCPYPYIPLTEKTLA*PAL YTLTLTADMAETCKQFLPEFSL TFSFQGWKEKETEYAEVLERNF ERDRQLTYTAHGPBKADLRIQE SGVPYNEILVTL

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5242	35610	A	5283	1	273	TNSSVGPGRLL*QTAAPHRGK LKVFFGACAGVGKTWAMLAE AQRLLRAQGLDIVGVGVETHGR KDTAAMLEGLAVLPLKRQAYR GRHISEF
5243	35611	A	5284	66	1200	HILPAGHPTLRHSLFPHQQGRSS VQSALGAASGNGLKLVGRFEW GPSRRARSQYPDATGYDQPKPI SAAVKEFFGSSQLSQFMDQNNP LSEITHKRRISALGPGGLTRERA GFEVRDVHPHYGRVCPITPE GPNIGLINSLSVYAQTNEYGFLE TPYRKVTDGVVTDIHYLSAIE EGNYVIAQANSNLDEEGHFVE DLVTCRSKGESSLFSRDQVDY MDYSTQQVVSVGASLIPFLEHD DANRALMGANMQRQAVPTLR ADKPLVGTGMERAVAVDSGVS GGVVQYVDASRIGIKVTKTRCI RVKQVSTSTLPLFLMESNPLF WMAVLVSAGILGQWPIGRLAD KFGRLLVLRVQVVFVILGSIAM
5244	35612	B	5285	1	862	
5245	35613	A	5286	1	579	DPRD*RLKVAK*MVTLFGPQFV RELQQRGFDFLDLKFHDIPNTA AHAVAAAADLGVMVMNVHAS GGARMMTAAREALVPRPDAP LLIAVPV*RSIKASDLVDLGMTL SPADYAERLAALTQKCGLDGV VCSAQEA VRFKQVFGQEFKLV TPGIRPQGSAGDQRRIMTPEQ ALSAGVEYMEGRPGTQSVK
5246	35614	A	5287	484	978	GIVRIPIRLADIKCWRAVLVNY THYSYQANLCCANLE*ADLSGS VLDCANLQGVKMLCSNAEGAS LKLCNFEDPSGLKANLEGANLK GVDMEGSQMTGINLRVATLKN AKLKNCNLRGATLAGTDLENC DLSGCDLQEANLRGSNVKGAIF EEMLTPLHMSQSVR
5247	35615	A	5288	3	504	YRLSQSSSKSLVSRSLNMRFIS SVMFMFEPTSSSENRFSPSCSE MSSSEATLRSFFLGTTSPCRSM VGLQLVKSSQSSSVSSSSHVRL SQSSSKSKVSRLAGT*EGSEKRS FREEKVPCLRLGLPESTLYAHC SV*SRTHVFSGTSHHSSKVAVG MSIVQMRKL

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5248	35616	A	5289	2	442	HVIWHMPRKTSKCRQLLCSGA SRNADTAARQSTCSSHRPPGKIP SLGPRRPVPGCSSVPSSRGEQSTG SPAAPRCQDVTHTTEASQEEQP* LRGTHGPASTPEQGTAKAKVR DRRAVVPKGKTGIPSAAG*KGR GRPEPPGAAVQVE
5249	35617	A	5290	151	1185	YVDQVTHITESPLPSVSYSAFAG SLISAVDPVATIAIFNALHVEED TEKGHVRLTPASPSTFFFFSTE EKYAPGSCCRKA AVL*LLHISH QLSLDSPSLTVVIYVLKHIDLRK TPSCRHCEI*VGDHTAVLSVLFS PSLGIMAILFSGIVMSHYTPREA SP*SCCLFTVSSHVTVCCHPGLRG AIPYALSLHLDLEPMEKRQLIGT TTIVIVLFTILLGGSTMLIRLM GLPGGAPRWQQLVAVGPPFLP AQGNTVESEHSELTEEEYEAH YIRRQDQLSLFN*N*SCLWPSPC LPPPP*TPHTKHPVASPPFHGPA PDALTAWLCLSTQDLHHGRIQ MKTLT
5250	35618	A	5291	5	198	VCGRQQSLEAGL*GAATPFAVF PRPWSAVRVKEYGYTRLHLIN GTHIHQQVSDDQAFACHP
5251	35619	A	5292	137	308	HLERTGPNLPPGARLATRPTTR LPAASPRGRDTPLPIPIFYSETE AKGEAPYIEPE
5252	35620	A	5293	612	1078	RPPEKKERGRVRGRRRGGGGK RRRRKRRKKRSGKGREDAAAA AAAAQSPRTAPAPD*ERRPQP APSARAPPRLLPAPRRSRPAQV PPDSASPWAAAAGLALPPQCP GGGARPLRLLPQPPAPGGTAR WEPRRPRPAAAAGLLQSPGFLP RQS
5253	35621	A	5294	515	817	LALPHLPSNLLKGLKWLKA*S RPSRTPSFG*LSQWKHALKRLK PVITCLLQHGLKPINSPYNSLIL PVLKPKPKYKLVQDLRLINQIV LPIHPMVSAQA
5254	35622	A	5295	1	951	
5255	35623	A	5296	1	1077	
5256	35624	B	5297	87	1423	
5257	35625	A	5298	29	234	
5258	35626	B	5299	77	327	
5259	35627	B	5300	1	235	
5260	35628	A	5301	2	2144	
5261	35629	A	5302	1	855	
5262	35630	A	5303	845	1057	

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5263	35631	A	5304	1	933	
5264	35632	A	5305	1	954	
5265	35633	A	5306	1	1603	MEAEKFHQMPVSRRTRKASG VIQSKSENLRTRGANSALRKL KPVITRLLQHGLLKPINSPYNSPI LPVLKPKPKPYKRFLAFYGWSPR SLIVDSCSKLEQHSTLSRVILVIY KGFCFRNHHQTGFSPAGANQ RGPLAATLSGPGGEGQSAVACL TGEKKNHGAQYANRLSPRVG RFINAAGTTGFTGTGKRAVSATQ LMDFAFGTITITQDFRLLGQTS VDRLQLSQGQAVKGNQLLPV SLVKRKTTLPANTQTASPRALA DSLMLQARQVSRLESGQSSQLS SLRLTLPDLRSLPDHHRGRAS GNSHSGSPKPPCLPLISPHLNP QVWDISTPSLATDHMPITILKS NVTLPNLKCCQYPIQHAKRL KPVITRVLQHGVLKPTNSPYNS PILPVLKPKPKPYKLVDRLINIH IVLLPIHPMVPNPYTLSSIPSTI HYSVLDLKHAFITPIPHSSQPL LAFTWTDPDHQAQQITWAVL PQRFPRTGPHYFNQAQISSSV TYLGIIILIKTYVLSLPIVSD
5266	35634	B	5307	1	874	
5267	35635	A	5308	144	539	
5268	35636	A	5309	1165	1639	PHPAVASRRGRAGPGGLSAPER TPSSELSPLSKGDLRKTHRTFSP Q*GDLRKTHRTFSTR*GDLRK HRTFCTR*GDLRKTHRTFSTR* GDLRKTHRTFSTR*GDLRKTHR TFSTR*GDLRKTHRTFSTR*GDL RKTHRTFCTR*GDLQKTHRTFS TR*GDLRKTHRTFSTR*GDLRK THRTFSTR*GDLRKTHRTFCTR* GDLRKTHRTFSTR*GDLRKTHR TFCTR*GDLRKTHRTFSTR*GD LRKTHRTFSTR*GDLRKTHRTF CTR*GDLQKTHRTFSTR
5269	35637	A	5310	235	453	SHWPWLCSSSTCSSQRSIVSSG MARGPFLRKRDLLFPFPPPGSH GLELLEIIFHQGISQVHLLHLQ VWL*NLNVDPSSSLPAENATGP GFVPPPLAPVRGPLFPVDAARGP FLRKRDLLFPFPPPGAMFGASR DYFPFGDFPGPPAPFASMAFL N

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5270	35638	A	5311	2	2333	TGRGYCGDHESFSGAMEEPGA TPQPYLGLLLEELRRVVAALPE GMRPDSNLVGFPPWELVICA VGFFAVLFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSLL EKFSLVQKEYEGYEVESLKD SFEKEATEAQSLAETCEKLNRS NSELEDEILCLEKELKEEKSKHS EQDELMA DISKRIQSLEDESKSL KSQVAEAKMTFQIFQMNFERL KIAIKDALNENSQ LQESQKQLL QEA EVWKEQVSELNKQKVTFE DSKVHAEQVLNDKESHIKLTLE RLKMKDWAAMLGEDITDDD NLELEMNSESENGAYLDNPPK GALKKLIHAAKLNASKTLEGE RNQIYIQLSEVDKTKEELTEHIK NLQTQQASLQSENFHFNENQ KLQKQLKVMTELYQENEMKL HRKLTVEENYRLEKEEKLKSV DEKISHATELETYRKRAKDLE EELERTIHSYQGQIISHEKKAHD NWLAA RNAERNLNDLRKENA HNRQKLTETELKFELKDPYA LDVPNTAFGRGSRGPGNPLDH QITNERGESSCDRLTDPHRAPS DTGSLSPWDQDRRMFPPPPG QSYPDALPPQRQDRFCNSGR LSGPAELRSFNMPSLDKMDGS MPSEMESSRNDTKDDLGNLNV PDSSFPVAKKEATGPGFVPPLA PVRGLFPVDARGPFLRRGPPFP

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5271	35639	A	5312	141	2788	GLRVLPSPSSPRSLRSGPLRLP GADSGSGPKAVCSPPFIVAPTG RGYCGDHESFGAMEEPGATP QPYLGLLLEELRRVVAALPEG MRPDSNLYGFPWELVICAADV GFFAVLFFLWRSFRSVRSRLVY GREKKLALMLSGLIEEKSLLLE KFSLVQKEYEGYEVESLKDAS FEKEATEAQSLEATCEKLNRSN SELEDEILCLEKELKEEKSKHSE QDELMADISKRIQSLDESKSL KSQVAEAKMTFQIFPMNEERLK IAIKDALNENSQLESQKQLLQ EAEVWKEQVSELNKQKVTFFED SKVHAEQVLNDKESHIKTLTER LLKMKDWAAMLGEDITDDDN LELMNSESENGAYLDNPPKG ALKKLIHAAKLNASKLTLEGER NQIYIQLSEVDKTEELTEHIKN LQTEQASLQSENTHFENENQKL QKKLVMTELYQENEMKLHR KLTVENYRLEKEEKLKSVDEK ISHATELETYRKRAKDLEEL ERTIHSYQGQIISHEKKAHDNW LAARNAERNLNDLRKENAHNR QKLTETELKFELLEKDPYALDV PNTAFGREHSPYGPSPLGWSS ETRAFLSPPTLLEGPLTSLPLL GGGGRGSRGPGNPLDHQITNER GESSCDRLTDPHRA LSDTGFLS PPWDQDRRMMFPFGQSYDPS ALPQRQDRFCNSGRLSGPAE
5272	35640	A	5313	217	447	FORMSGL*GYSPPLGGQPAL*E CQGAADSAGGIRGLDSERSLGR PAASGPNTALGWQAQPS*Q AGPELPRAEFLQA
5273	35641	A	5314	3	287	TLRNRHRELRTCLSGPGLGLPT QVSVVAGGCCVCPSSSQSPVPR PPALSAAPWHSRAGCPPSGGL *PQRPLILWNQPLSNTLLEKELA PPPAH
5274	35642	A	5315	3	468	ALARSPAG*PQSPDGLCFRHR KGERRPAAPAGQCPAGRQRHY PAAGRDKPGRAPGADR*AGPI LHLHYLPA PCGGGTPGDSNPRR APAQRSE*CTPPPPQ*RNNRKPS TRAGLLPS*HVQLSGGLTLC GDRVS*WPGVLAAPGPGPCT HL
5275	35643	B	5316	64	288	

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5276	35644	A	5317	73	265	NGRTSRCSFSPGKH*EYCSGTFH PLQVVVGKIYSNLDKIL*ASRAR WGLCSRKPGYWSCTQPTSS
5277	35645	A	5318	125	461	
5278	35646	A	5319	298	593	LGVEVEPVTGGDAVIGASHDAF LQVNIESIVPEHSTRCKLLGKFI RIWIKYFRHLVHGGGSAPVSLV TGPVHGDSLLGFPVAPEPPRVVE PARQVRAHAVVVAGPLRRGRG LGRHRLRARG*GMPQSVRGA CGAQGHGPAGEDQRLPRERG PAGQVQPGVVPGLQDPEGCL RVQDQ*PGLREQSPHRADA*S ILSKFE*IFPTTCSGWNVPEQYS QCLPGEKHRDWPR*LHHLI*PA QI.PPPVTTSTGHPSAIEGLETP RSPLTPGPPGKSIIPHPQSPDCD GTDCAAFPENIIRLSRKICKRG
5279	35647	A	5320	1124	1835	HSLHFPKFPFSLFLTLITLGLLM AVPPGLITTHQQRQAML*YKPL ARLLEPLISFSPWSKILKEITSQC SICYSTTPQRLFRPPFPETHQTR GFAPPR/HWQIDITHMPQVRKL KYLVLVDVTGSKKATVVISLL SDIIPRFGLPTSIQSDNGPAFISQI TQAISLALGIQRTHGLLKTHLT NLSHQLKKDWTLLPLSLRLQ ACPRNATGLHSDG/VGPKLLPG SPFQLHHTWDSP
5280	35648	A	5321	1	1758	
5281	35649	A	5322	1	1967	
5282	35650	A	5323	76	1908	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
5283	35651	A	5324	524	2144	QSDLSASQHGFLPLATEVRSRG AASCPDSDSICPAPIAPGRATP PQANCWASEGTLRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLSNLTQGP RSRPVAFSLKQLDLTVLWGPSC LRAAAAAAALIVLEALKITNYAQ LTLVSSHNFQNLFSSSHLLTHILF CSPGFSFCTHSLLSLPQLPIVPGP DFSPASHIILDTTPDPHDCISLIH LTFTFPFHISFFPAHPDHA*FIN GSSTRPNRHTPAKAGYAIQVQT SPPLKTSHFSLSIVEIYPQGNFS VFHLLFFYSSGIIQAPLLSLHIKL RDLPPRPTGKSALLNMPVRKRL KYLVLVDTGSKKATVVISSLL SDIIPRFLPTSQSDNGPAFISQI TQAISLALGIQRTGHLKTHLT NLSHQLKKDWTILLPLSLRIQ ACPRNATGLHSDGEARSSFAQH HFNFIHTGTVPDVFVPIQLLNE DFEDPCLGYLPSPEISICLEPTS W SKDRSCSSGEGSAGQTVTGD L HKAQTPELDQPASLNCPLD
5284	35652	A	5325	1	420	RTRGGEKE*EEKQRSRR*RIK*E EEEE*RRSRGAGDKG*NERRRR NRGEPVEKEEDRRRRKQWRR GEEKRRRRGRNCGGGGEEKE DGRRRRLPCFLLPSLLVSLW LVSFPCVFGFGAPAVVFARF RGLRAFCRF
5285	35653	A	5326	2	467	
5286	35654	A	5327	269	777	
5287	35655	A	5328	2443	2627	VGFFFFFWGGERGTGSYSVTQ ARVQ*YDLGSLQLPPSFKGFS CLSLPGSWYYRHGPPRLG
5288	35656	A	5329	57	394	
5289	35657	A	5330	33	311	HNTLPKTKPWQEPGDEEPQOE EPPTESRDPAPRLPRSP* SADPP WRSQRPGQLTRPPPEPLRPHGS PPAHLSLFCQRSCPGPQERPHPS TM
5290	35658	A	5331	226	406	
5291	35659	B	5332	51	90	
5292	35660	A	5333	1	348	PPSQRV*GWHEMRQGGGRQHAQ PVLSSQGLTAGCHHHQCRRP LACDVRPVVYVEKVSRDHGLVS GQHN/PAPESQGGQSTSPRHTGR KQARAGGEKKVTS DPANTAQH NPNTGSRGRP
5293	35661	A	5334	109	380	

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5294	35662	A	5335	448	724	WPSRSALAAAGGRTAPTSPRSRAG PPAR*RGAGRESARGTS*GIRPRS QPARRPCPPAPVGRGLPPGPAP PPPRAAPREPPRCRAAAHTSRP AGS
5295	35663	B	5336	1	1554	
5296	35664	B	5337	99	366	
5297	35665	A	5338	1	714	
5298	35666	C	5339	391	689	
5299	35667	A	5340	2	614	
5300	35668	A	5341	2	461	
5301	35669	B	5342	45	1148	
5302	35670	A	5343	215	849	IKRLPLMKRMWL*LQPESLEIA GILVQ*MIE*QPKKGTNSIPVSK PSP/VVQKPNGQWRQVQDLRLI SDAVIPLYPVSNPYTLLSQILE EAEWFTVLDLKDFAFCPLRSD SQFLLAFEDPTDHTSQLTWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5303	35671	A	5344	1	1035	MGQVWALVRSTLELFTDDEE EGEYDEVTEEVTEQVYLPAKA KVAQEEVHPYPSAPPHYFYEE KEWPDPPDLSFLEDTRKVVAP VTEQHLERLLSVLFRQEFSLRD ERDDAVEQLRGVCIRAWKIT GGEQYPSFSAVKQGPKEYADF IAWNLLRQESLKKVISDSAAQD IVLQLLAFGNVNLDCQAALRPI RGKAHLVDYIKACDGIGAKQD SERFAFTIPVNNLQPAKHFHY FTDGSSNGKASYSKGQGNQ PIWILSRHLKPYHEPDAKEEIPG G/CPRTPLWQPCRD*C*GGP*/P VTSNTR*TPPTWGQIKLSQM VEENLRKAGQLVTMTVYWN
5304	35672	A	5345	1566	1767	KGGSWSQRHSQACGYTCRKS GHWAKECPQPGIPKPRPCVGP H*KSDCSTHLAANPRAPGTLAG SGL
5305	35673	B	5346	1	3429	
5306	35674	A	5347	1	1776	
5307	35675	A	5348	1	933	

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5308	35676	A	5349	1	1743	MGKVVAVVRSTLELFHTDDEE EGEYNEVTEITEQVYLPAAKAK AVKEREQRGNITATFEPPFKLL KEFKQAINQYGPESHFVGMGLL KNVAVSSQMIPTDWDALTOAC LTPAQFLQFKTWWAHEASIQ ACNAQAQPNITITGQLLGVG WAGLDAQVVMQDDAIEQLRG VCIRAWEKIPLCGEQYASFS QGPKEPYVDIAWLQESLKKVI ADSAAQDIVQLSADFNDANPDC QAAL*PIRGNAHLVDYIKACDG IRGNMHKATLLVQAMAGLRVD KGNPLLPAGACFNCGKHGHTKQ ERRKKSVSQAARWGKRKTADP EICPKCKKGKYWANQCHSKFD KDGTLSIGNAMRAEQDCEWFT FTIPAVNNLQPAKHFRHRTDVS SNGKASYSGSKGGQARVQLFE NASVRATNSDLPQSSLWCRRT SVSVAVLVSATIPISRVQGPSQV LGQGEKQTNQNVVPNPYTL QIPEEAKWFTALDKDAFFCIPL HSDSQFLFAFEDLTDHTSQT LWTLPGQFRDSPHLFGQALADL GHFSSPGTLVLQYVDDLLATS SEASCQATLDLFLSFLAN
5309	35677	A	5350	1	1085	
5310	35678	A	5351	1	3105	
5311	35679	A	5352	1	5172	
5312	35680	A	5353	41	324	
5313	35681	A	5354	18	270	KLSQVCIDLL*IREGERDMYPG WAKFPSPYSLKGT*PIAQVLW SFGDFFYC/IPSTLPTPKS WRLFESPFESLTPVSLVWWPC
5314	35682	A	5355	80	384	SNRRTGAWGKCOLMSS/PLTE PQVTLTIDSQEIFLLDTGA AFSLVISCPEQLSSRSVTI* GILGQPVTRYFSHLLSCN WETLLFSHAFLVMPESTPL LGR
5315	35683	C	5356	99	317	
5316	35684	A	5357	388	476	KVCPRPCRTSM/LPIRII* KLPQVCLDLL*IEGEGDMYPG* AKFPSPYCLKGT*PGTIAGS WARGVSAASPSYSSPSY

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5317	35685	A	5358	254	849	LQPESLEIAGILVQ*MIE*QPKK GTNSIPVSKPS/GVQKPNGQW RQVQDLRLISDAVIPLYPVSNP YTLLSQILEEAEWFTVLDLKD FFCIPLRSDSQFLAFEDPTDHT SQLTWTWFTQGFMDTPHFGG SLAQDLGHFSSPGTLVLQYVDD LLAKQQAATLDLLNFLANQGY KLSKLKAQLCELLVFSSCARMH
5318	35686	A	5359	1	909	
5319	35687	A	5360	153	436	CFCCCVEGKNPRNLQRTTKTPR LSVMSPPSSCRGRGIWPNPQTC/R PSPSLI*SRSRQTWRITTPCQQG NKTGQRMNLN*QEQAEGG* *QTPLS
5320	35688	A	5361	1	1632	
5321	35689	C	5362	1	675	
5322	35690	A	5363	604	1047	SNNRTDNPTSVAYLSKETDVV AKGWPHCLWVVVAAILVLEA IKIIQKGDFVTWVSHDVNGILG AKGNSWLSDKRLRYQALLLE GPVLQIHCTCVALNPAIFLPEDGE PIKHDYQQIVAAQTVVT*EDLLE VPLANPDNLNLTNGSSFV
5323	35691	A	5364	749	1002	QLKKGTSNLLVSKPSVWIPPTG TLTQIMGTGVANIC*PVF*KD*G ELGKMNYAMMSTITQKEENP AFLKWLWEALRKYTPLSP
5324	35692	B	5365	114	2309	
5325	35693	A	5366	413	1157	
5326	35694	A	5367	105	478	YGHCCYDHRICFFPATEQKVC PCAAQG*PL*LRGDDPEMSVYI *QLPLYSSDLLSAANEVQILAF FQGDVSFFPVATTTDLTSVTFN FPFNQGVNDFDFDKQFLHSS RDFCFGRVFSNFE
5327	35695	A	5368	531	1087	RLQPPGAPVEDTRPVS AKPRD ADRNSTGCYLV*LQHQRQTES GRQLSGL*GPGCNGVH/ASLYR TSAMFAERFGSYRRSTTAGIPS LLRLKSTIRSDRSRRKAQRKR CGQVMPQHRRSIRPLLPITPPL NRNLHRSRPHRSRNRWSRLNRR LKHHLRRSQNRSSRWKKKLHR RVKPMCLNWR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5328	35696	A	5369	544	1381	VNPALQVLVVAITPPSPSPSCI RVLTRVSNIAIAKPLCLAVCAV VEGGRIRALVAVAAWAGAVTG GPAGLIACGPVSPSVIRGQFRHA GISFFLYAIGGEMVPAVRRQNH TPA*HKRFKAFQLAHNAV AEHFAGGDRHLFSLNQCQCVV KHHVRRDITFIGYRFTQFA
5329	35697	A	5370	81	863	AYGNPVEIAGGARQAGVNF VFRPRFSRRWRRISETCKLWW RRWRSAAWASINQTFASWSTLIF RAISNPIIRKPDAPGVMACPRKR CCFTIRLIWRGCAVWKRSE GQLQDIERHKLNAMGAFAEAQ TCRRLVLLNYF/GRRASGAVRE LRYLPRSAETVRRFNRCSDCPF HHWSCSAVWDGLCGGSDSCC GVSRARLFASPVNLPITGEIPER GFHPFCGRRTTENGKNHPRNLFI WRSNCSVLPVKVMSCSSTPCP
5330	35698	B	5371	12	273	
5331	35699	A	5373	145	336	SEEEEEEEEEEEEEEEEEEE E*EEGESAIICAKVCISVFP NELNMAITPNTIPKLNHW
5332	35700	A	5374	294	657	VAPGDRHAFHGGGSLSP PQTQCCAQATVQGLEGRSWS QSGTSSLSPSWHTSLACPQKEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEAKTQ*KSG QK1*TDSPQKK
5333	35701	A	5375	2	588	SRPGITGSTISYGDPGHGAGPPG ADLGPASRLKPERAAGAQLAA GEARQSGDPLPGPGHSLGTA PC*VDKGWGHVPSTVHHQRQP QPGGLRAPGTALLAGTQPSHPA AGWPWPQQRGVRVLGGRRDS *VGGG*GQHNKALWGPR*PHT EQKPRKLSRIPLRAAGGEKRG CGCDRAGCLVLGPPQLPAQGL
5334	35702	A	5376	1	445	SLSHRAGGGGVGGGAVCLFS PPRTKRESAPESPSRLVGHSPVP S*GAPSTRGSVSRILTSGGTHER SNGLTCHRNQAGTGPSALRSGR P*CLSRANPPGSKRSAGPVHEE RT*PCRLSGSAGITQ*DGN*KAG PRVPEAPERGCATC

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5335	35703	A	5377	3	313	QNDEVAFRKLKLIHEDVQGKSY LTFNHGMNLTNDKMCMSVKK WQTVIEAHVDVKTNGYLLCL FCVGFTKKCNQIWKTSLF*QQ SNMEDFFVLTTGIIHSHLEPFLV VTDDQ
5336	35704	A	5378	45	764	TSFLTGGGKGS/KKKVVDPFS KKD/WL*YVKHRAMFNIRNIGK DVGSPRTQGTKIAS/DGLKG/RV FEVSLADLQNDEVAFRKFKLIIT VEDVQGK\NCLTNFHGMMDLTP* QKCCSMVKKM/WQTMl*SSPL MVKT\TDGLLASVSCVGF TKK VRNNQIRKTSY AQHQVQRQIRK KMMEIMTREVQTNDLKEVYNK LIPDSIGKDIEKACQSIYPLHDVF VRKVMLKKPKFELGKLMELH GEGS
5337	35705	A	5379	3	501	SSARFVSSSSGGYGGGYGGVL TASDGLLAGNEKLTMQNLNDR LASYLKVRALAAKILSDMRS QYEVMAEQNRKDAEAWFTSRT EELNREVAHGTEQLQMSRSEV TDLRRTLQGLEIELQSLSMKA ALEDTLAET/EGDVRADSERQN QEYORLMDIKSRLEQE
5338	35706	A	5380	1	716	AQLKVKFWYWPEAGAGGLRR FKHY\YTPFKDCRDKILGATIKN SRIVLQIDNAGLAADDFTKFE TEQALRMSV*ADITGLRRVLDE LTARTDLEMQIEGLKEELAYL KKNHEEEISTLRQVGGQVSVE VDSAPGTDLAKILSDMRSQYEV MAEQNRKDAEAWFTSRTTELT REVAGHGTEQLQMSRSEVTDLR RTLQGLEIELQSLSRLWGFCC PLEGVFWVEGWEGRDPYPRLF
5339	35707	A	5381	3	832	
5340	35708	B	5382	141	1067	

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5341	35709	A	5383	3	1316	GVAPSVLRAMTSYSYRQSSAT SSFGLGGGSYRFGPGVAFRAP SIHGGSGGRGVSVSSARFVSSSS SGAYGGGYGGVLTASDGLIAG NEKLTMQNLNDRLASVLDKVR ALEAANGELEVKIRDWYQKQG PGPSRDYSHYYTTIQELRDKIL GATIENSRIVLQIDNARLAADDF RTKFETEALRMSVEADINGFR RVLE*S*TLAQEPNLEDARIEG LKEELAYLKKNHHEEISTLKG KCEAQVSVVEVD/SA/PGTRSSPK ILSDMRSYQYEVMAEQ/NRKDVA EA/WFTSR/TERIETREVA WPHR SSFQMSQAPRLLDLAAATPQGS *DLSCQSQLEPLKAALGKTPLA ENRKA/RFGNPQLAPYPQALDS AVI*KPQLG/DIVAKLDSSTGRI QEYQ/RLMDIKFARLEQEIHP NRSLA/LEGQEDHYNNLFAASK
5342	35710	A	5384	23	279	GCLRGSLERCGLTKLNLHEISG PESRVQQLSSREEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEERKK ECSKAQCKHFPLSEVL
5343	35711	A	5385	1	507	MEKNEKEEEEEKKEKSKKK EEEEEEEGGEEEEEGEGGEE EEEEEEEEEEEEEEEEEEEE EEEE/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKKKK KKKKKKKKKKKKKKKKKKKK RKKKKKEEEEKVVEEDEFIWF LGNSLYFPFSHFAWSQIPSRD EGERRLRVNSMIMDFTSNTNH
5344	35712	A	5386	3	259	
5345	35713	A	5387	53	387	LEEEKEEEKEEEKEEEEEE KE/DEEGEEGGEGEGEGEGE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEMIVLKIIVAKQLF
5346	35714	B	5388	1	1446	
5347	35715	A	5389	3	122	
5348	35716	A	5390	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEKI FLGHRVGI
5349	35717	B	5391	1	1269	
5350	35718	B	5392	44	244	

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5351	35719	A	5393	1	626	EEGEVEEEEEEEEEEGEGEE EEEEEGEGEGEGEGEGEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEQEEEEEEEEEE EEFFAAAAAASRDSHTSL TYWPPCPALROTLVSNCS CTSGDSFW*ETTIPAMSSCSH QHSLSHQLGIIPQILMRMASLM RRICEDHPATAEQ**HV*GPPD
5352	35720	A	5394	2	506	
5353	35721	A	5395	1	480	
5354	35722	A	5396	1	492	
5355	35723	A	5397	1	870	
5356	35724	A	5398	111	407	
5357	35725	A	5399	1	651	
5358	35726	B	5400	1	2427	
5359	35727	A	5401	571	966	SPFTNSRLTIFISFECGQIAEIYI LSQPFMVRIMATEPPINLQPGN FTL DIVSRDHTAL*PGRQEQNS VSKKKEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEKKKK
5360	35728	A	5402	1	1674	
5361	35729	A	5403	1	306	
5362	35730	A	5404	2	431	
5363	35731	A	5405	1	585	
5364	35732	A	5406	1	708	
5365	35733	A	5407	3	595	
5366	35734	A	5408	287	659	
5367	35735	A	5409	1	633	
5368	35736	A	5411	3	634	
5369	35737	A	5412	344	481	
5370	35738	A	5413	1	525	
5371	35739	A	5414	1	501	
5372	35740	A	5415	1	461	
5373	35741	A	5416	302	567	MLCCLEISSTRYPKSLSSSKFH KSLGQGGQNAASLFAKT**RESPL LQFPASSSSPSETTSAWTLFLISL SAFLTAKAFNKSLGGSKLSH
5374	35742	A	5417	251	844	NLGRGQSITLDFCAPAGLIPCG SCQGLGLPHSEATARAVYWPL SAMAGVAGTQGTSLDSSLFA KT*QESPLLRFPTSSSSPSETTSA FILLFISLSEFLSKPFNKSLGGSK LSHIFVSSSEPSKLSQPLHMPQ ARISSFTSGHTDDSTVLFSVLLK LPLPVPSQAFSLKPGSIVMLLS WSDNFNIPSISDSDA
5375	35743	A	5418	1	1113	
5376	35744	A	5421	1	337	

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5377	35745	A	5422	2	680	
5378	35746	A	5423	144	373	
5379	35747	A	5424	1	597	
5380	35748	A	5425	3	3319	
5381	35749	A	5426	1	612	
5382	35750	C	5427	46	168	
5383	35751	A	5428	1	663	
5384	35752	A	5429	10	417	IAIMNDTVAIRTRKFMNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTTPDVIFFVGFRTTH CGGGKTTGFGMIYDSLDAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
5385	35753	A	5430	67	263	GKTTGFGMIYDCLDYAKKNE PKHRRARHGLYEKKKTSRKQR KERKNRMKKVRGTAKANVGA GKK
5386	35754	A	5431	2	537	TPGSTTTTKFPTASTSEDRSPIM NDVTVTIPH*EKFMQTPTYFRGN QMVIDVLSPPGKGDQCCKHRK FGKKLAQNVPRPTPD/VIFVFWI QNFIFFGGKTTGFGMIYGFPGI YAKEKMNPDRHLCCKDMGLVL RKEKGPSRKANGKGTARNRIG RKVPGGTGKGPNVGCWAKRR NEVSSS

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5387	35755	A	5432	1	2195	ARGLSMGH*FP/PHFQCALA*M PAPGRGPPPLP/CPDAPPACA ATMERPEAGLRVAPRSPVQPGC TSVLPAKRFNARILWLKRPQR QLWSLWRAQATVSLGGFHV LSLQVHRINARVKEAWQLPPRF QMMYQKAWVLRQKPAAAVEP SQRNSPRAMLGNGVLEPPPRV STRALPSGAVGRGLPPSRPKND TATGSLHPELGKAAIDQFHPVR AATGASPCCKSIGTELPKALGAH VLLQCALDVGHGVEGELWSFK TRQPSDFSIFSPFPFYSTKPPLS SWPIPNEPLGTPPRRGRGGAEG LLTSQCSHILNGLCTGGINSNE CENVSRKKKMSEEFANTMDS LVDMPFATVDIQDDCGIFDVW KL RVNQCQILANRHPGRAMRK VVLTKTSWEGESLAVGKLPLK RLVSLDCQLRCLQCECGILIRQ HVVWLERTTGHWHPRSSQSCR LNTTSTALEHCNAFIYNTVCSH KLKDHSHDNGKSSGLNPVAA PHSCIVMGHILTLITTSYTPLT KPDTPDLTKKEGLISQSSSLEV LLHTDPLGKRGTPDPRVDDDSL GKFPVTNSQARKRILEPDDFLD DLDEYCEDAPKHRGKCGSA HKELDASNLEDQDKPYACDIC GKRYKNRPGLSVHYAHSHLAE EGEDKEDSQPTPVSQRSEEQK SKKGDPGFALPNNYCNFCLGNS
5388	35756	A	5433	1	580	FSPLIHILSGHSTCFRHRVGG KVTDQQDPKAEFFLVQNKMK SLPCLLLSTQTRQPSDFSIFSPF PPFYSTKPPLSSWPVLNELLGTP PRRGGGRAEG/PHFPVVGPGPR GAPSPRRGGWPGGGLTPQPPS RTGRLAARGADPPTSLPDGAA GRAGG*PHHLPPGRGGWPGRG APHFPVGVAGQRRLLFC
5389	35757	A	5434	405	685	KVSHVYFYPHRPRNHPSQFFPH PSRLSIPQNRHCHHGGS/RNEPL GTPPR/PGSWPGRGAPHFPETFN HGRRWKGSRHVFTWPEQERE WGSATHF
5390	35758	A	5435	1	654	
5391	35759	A	5436	1	426	
5392	35760	A	5437	1	548	
5393	35761	A	5438	1	459	
5394	35762	A	5439	1	346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,440,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5395	35763	A	5440	1	1248	
5396	35764	A	5441	1	1257	
5397	35765	A	5442	1	1659	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRSLH AKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRKIKNLQNRSTTWKLN NLLNDYWIHDEMKAIEKMF ETNENKDTTYQNLWDAFKATA SKTNKEKEKNQDITKNDKGD TTDPTEIQTIREYKHLANK LENLEEMDKFLDTYTLPRLNQ EVESLNRPTGAEIVAIHNSLPTK KSPGPDGFTAIFYQRYKEELHI NRAKDKNHMISIDAFAKAFDKI QQPFMLKTLNKLGDGTGFKIIR AIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLFNIVLEVLR AIRQEKEIKGQLGKEEVKLSIF ADDMTVYLENPIVSAQNLLKI SNFSKVSQYKINQKSAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKINPCSWVGRIN IMKMAILPKVIYRFNAIPKLP TFFTELEKTTLKFIWNQK/RARI AKAILSQKNEAGGITLP
5398	35766	A	5443	1007	1719	TEPKTKT*LSQ*MQKKPLTKF NNPSC*KLSIN/IVLEVLRARIR EKEIKGQLGKEEVKLSLFA MIVYLENPIVSAQNLLKLSNFS KVSQYKINQKSAFLYTNNR QTESQIMSELPFTIASKRIKYL QLTRDVKHLFKENYKPLLKEIK EDTNKWKINPCSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKFIWNQKACIAXSI LSQKNKAGGITLP
5399	35767	B	5444	1	1020	

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5400	35768	A	5445	1	1576	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSK VSGYRIN VQES/QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKF1WNQKRARIASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNYLIFDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPLTPYTRINSRWIKDLHV RRKTIKTLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYA AKKHKMKCSSLA IREMQIKTTMRYHLTPVRMAII KKS GNN/R/CAPGTPERQNHSL WKG S*SQEP SGLAQWIPLPWSP AS*DPLA*NSCCQH SCLKSTWD AQACARKLRTLIGYRNCQLE
5401	35769	A	5446	1	984	
5402	35770	A	5447	1	1563	
5403	35771	A	5448	1	1449	
5404	35772	B	5449	1	1605	
5405	35773	B	5450	1	1569	
5406	35774	A	5451	1	690	MSELPTIASKRIKYLGIQLTRD VKDLFKENYNPLLNEIKEDTNE WKNIPCSWVGRINIVKMAILPK ATVTKIAWYWYQNRDIDQWN RTERSEIMPHIYNYLIFKKPEKN KQWKGDSLFDKWCSENWLAIC RKLKLDPLTPYTKINSRWIKD LNVRPKTIKLEENLGITQDIGI GKDFMSKTPKAMATKAKIDK WDLIKLK/FCTAKETTIRVNRQS TKWEIISLSD
5407	35775	A	5452	1	1919	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5408	35776	A	5453	1	1416	MIILIDA EKAFDKIQQPFMLKTL SKLGT DGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTTRQGCPL SPLLFNIGLEDLARAIRQEK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQ MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQWNRTEPSEIMPHTYNYLI FDKPEKNQWQKDSLFFHKWC WENWLA VCRKLKLDPLTPYT KINSRWKDLNIRPKTIKLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNROPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL
5409	35777	B	5454	1	810	
5410	35778	B	5455	1	1277	
5411	35779	B	5456	130	1701	
5412	35780	A	5457	1	1395	
5413	35781	A	5458	3	1646	
5414	35782	A	5459	1	759	
5415	35783	A	5460	2821	5781	
5416	35784	B	5461	1	2025	
5417	35785	A	5462	1	3663	
5418	35786	B	5463	1	2265	
5419	35787	A	5464	1	2241	
5420	35788	A	5465	1	2478	
5421	35789	A	5466	1	2067	
5422	35790	A	5467	1	2988	
5423	35791	B	5468	1	2061	
5424	35792	A	5469	1	2141	
5425	35793	A	5470	1	400	
5426	35794	A	5471	2	2507	
5427	35795	A	5472	1	768	
5428	35796	A	5473	1	1527	
5429	35797	A	5474	1	1293	
5430	35798	A	5475	1	1038	
5431	35799	A	5476	1	1572	
5432	35800	A	5477	1	1290	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5433	35801	A	5478	1	524	MSELPFRIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTNK WKNISCSWVGRINIVKMAILPK/ VKHR/FSACIQLGRSGTTGLE ALAM*PIWPQVEV*VKFPALPS GASSTKGGCVP*QIQVEERLLS WKL*QA*TSWYQRRRSDSSL RERK*PKSIQRNVRLSYYP
5434	35802	A	5479	2	1547	
5435	35803	A	5480	1	2376	
5436	35804	A	5481	1	1824	
5437	35805	A	5482	1	1071	
5438	35806	B	5483	1	1839	
5439	35807	B	5484	1	1368	
5440	35808	A	5485	1	1884	
5441	35809	A	5486	1	1053	
5442	35810	B	5487	1	2532	
5443	35811	A	5488	1	2373	
5444	35812	A	5489	1	2361	
5445	35813	A	5490	1	2274	
5446	35814	A	5491	1	1686	MASPGAPTASPPIHSELLTATR EAQRHHPVPRGQDLVTSEFSL SFCFSAAFIFELLGSNSEGVTDL RLWLCQPAPRCGEWTYNPLEQ CCDDGVILDNLQTRLGSSSTCF WPCFQHCCLLELGSQNTVVRV KVPGMKPDCKSSPITRICAQAG VQISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASQ RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA LIAKSILSQKNKAGGITLPDFKL YYKATVTKTAWYQNRDID QWNRTEPSEITPHIYNLIFDKP EKNKQWKGDSLGNKWCWENW LAICRKLKLDPFLTPYTKINSRW IKDLNVRPKTIKLEENLGITIQ DIGMSKDFMSKTPKAMATKDK IDKWDLIKLSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSLSLAIREMQIKTTNQNHM RYHLTPGHG
5447	35815	A	5492	1	1872	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5448	35816	A	5493	195	1494	PPGQHLQRRCLLRVSGFSENAK KGMLEVLARAI\RQEKKIKGIQS GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKALGYKISV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYGF NAIPKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQDKAGGI TLPDFKLYYKATVTKTACNSN GSQSPWMEEQIRDAWGSMLVK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTD\TSLTPAAPMVD SLIARVGMARGNAITLPVCGR DVKFTLEVLRGDSVEKTSRVW SGNERDQELLTEDALDDLIPSFL LTGQQTAPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLGGEI DDEQMAALSRLGNDY
5449	35817	A	5494	1	1845	
5450	35818	A	5495	1	2109	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,400,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, ~-possible nucleotide insertion)
5451	35819	A	5496	1	2535	MKSGHPEKEQDNDVQETREIT IRGLLCTALMRHSTGAIAIYLG VLSGSASLLKLAGVPLRCCEGDKD AGHPLETQTALCERGRGARSLV GNTIMTSQPVPNETHIVLPSNVIN FSQAEKPEPTNQGDLSKKHLH AEIKVIGVNLIQNVLERGWGKC QEMIVYVLGLDICRPFVSRVSEE GRMGQRGEEDANSDFPPASLL CLICQEQGVNGESCSPVGMYYH REIVPVYEVLSVITGLQIQVFSG KEADSVIKRSIGWGPFFKPRTK DKNHMIISIDAEKAFDKIQQHF MLKTLTKSLGIDGTYLKIIATYD KPTANILNGQKLEAFPLKTGTR QGCPSPPLFNIVLEVLAIRAIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSDQNLKLSNFS KVSGYKINVKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPICSWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELEKTTLKFIWYQKRARITKSI LSQRNKAGDITLPDFKLYYKAT VNKTAWYWHQNRHIDQWNRT KPSEITLHIYNLYFFDNPDKNKK WGKDSLFFNKWCWENWLAICR KLKLDPLTPYTKINSRWIKDL NIRPKTIKLEENLGITIQDIGMG KYFMTKTPKAMATKAKIDKW DLIKLSFCTGKETTRVNRQPT
5452	35820	A	5497	3	2284	
5453	35821	A	5498	1	1245	
5454	35822	A	5499	1	1140	
5455	35823	A	5500	383	1185	
5456	35824	A	5501	1	3159	MLEVLAWAVRQEKIKGIQLG KEEVKLSLFADNMTVYLENPIV SAQNLKLSNFSKVSGYKVS GKQSQUALLYTNNRQTESQIMSEL PFTIASKRIKYLGIHLTRDVKDL FKENYKPLLKEIKKDTNWKWNI PCSWVGRINIVKMAILPKDIIQE NFPNLARQANIQIEIRKTPORY SSRRATPRHIVRFTKVEMKEK MLRAAREKASHHTYSKIDPILG SKPLLKSKCRTEIITNYLSHSAI KLEFRIKNL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
5457	35825	A	5502	583	2515	MQKKPLTKFNPPSC*KLSIN*LI SNFSEVSGYKISVQKSQAFLYT NNR/QESQIMSELPFTIASKRIKY LGQLTRDVKDLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKAIYRFNAIPIKLPM FFTELEKTTLKFIWNQKRARIA KSILS QKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSL FNKWCWENWLA ICRKLKLDPF LTPYTKINSRWIK DLNVGPNTIKTLEENLGITIQDI GTGKDFMSKTPKAMATKAKID KRDLIKLSNFC TAKETTIRVNR QPTKWEKIFTTYSDDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEHIYAAKHKMKCS PSLAIREMQIKT TMYHLTPVR MAIHKSENNSLLAAGGGNRR ANVVAHG FANLLTLDKKT LQEI LVHYDPSEIRILMKKARVLLKQ KAKTAEATPPRKDLALLFPPKE ETPKLFKTLGGTGKASLARLL KLKREQAQK KENSEGGE KENEDKQK ENEDKQK ENEDK KENEDKDKGREPEEKPLDRPEC TASPIA VEEEPHSVRRTVLP SRQSLISM APSAEGGEEVLTIE
5458	35826	A	5503	1	2463	
5459	35827	B	5504	1	1221	
5460	35828	A	5505	1	4494	
5461	35829	A	5506	1	2825	MARTSYGQHFFPTLISMNIDSG RQNGIPKLSYSYSLKPMNTLC YL VKRDLEGLVKRLITWESSL DYPGGPSVITKVLIRQKEGQSQ RTRYDNGSRGWSDAIAVKRPQ AKECGWPLEAGKGKEWILRKE CIPANTLM LAQCPTLRVGGVS CSAWRMIONSDGERKKRNRIQL QAVRLSKV IHD TFRNFRFVHS RELSKGA EKSSSLKKGLEQVII WTKRCQCGESRCTKKVEERKV LHNTFISTSTITTLTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
5462	35830	A	5508	1184	4791	TSMQKSSIKYVQTESSTSKSLSTMIKWASSLGCKAGSVYANQ*M*SSI*TEPKTKTI*LSQ*MQKPL/YKIQQPFMLKTLNKLQAQLLKLISNFSKVSQYKINVQKSQAFLYTNNRQTESQIMSELPFTIASKRKIKYLGQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVGRINIVKMAILPQVIYRFNAIPIKLPMFTFFTELEKTTFKFIWNQKRIAKSILSQKNKAGGITLPDFKLYYKATVT
5463	35831	A	5509	516	2233	
5464	35832	B	5510	286	4131	
5465	35833	B	5511	1	4911	
5466	35834	A	5512	1080	3119	SSGLHPWDARLVQYTQINKCNPAYKQSQRQKPHDYLNCRKKAFDKIQQPFMLQTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFPLKTGTRQGCPLSLLFNIVLEVLARAIHQEKEIKGQLGKEEVKLSLFADDMIVYLENPIISAQNLKLLISNFSKVSQYKINVQKSQTF LYNNNRQTESQIMSELPFTIALKRIKYLGIQLTRDVKDLFKENYKPLLKEIKEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIVNQKRA RIAKSILSQKNKAGGITLPDFKLYYKATVTKTAWYVYQNRDIDQWNRTEPSEIMPHIYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPFTRYTKINSRWIKDLNVRPKTIKTEENLGITIQDIGVGKDFMSKTPKAMAAKAKIDKWDLIKLSFCTAKETTRVNRQPTTWKIFATYSSDKGLISR IYNLEQQIYKKKTNNPIKKWAKDMNRHFSKEDIYAAKHKMKK\ CSSSLAIRVEMQIKTMMRYHLTPVRMAIHKSGNNRIRRHQPRSAMFFCCCPGEGSGLQWELLAAWTVLPYPYCPAA TVGRFLKQAQTADHSFLGHVVRVPSSRSWTDKEILSLVNNRQNEVVLQILGCGTHTISPTQHPATG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \-possible nucleotide insertion)
5467	35835	A	5513	2494	4549	LQTLQGYSNSKQHGTTGKTFA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPDKNKKWGKDS LFNKWCWENWLVICIKLLDP FLTPVYTKINSRWIKDLNVRPKTI KTIEENLGNTIQDIGMGKDFMS ETLKARATKAKIDKWDLIKLS ECTAKETTIRVNRQPTKWEKIF AIYSSDKGLIPRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEDI YAAKKHMKCCSSLAIREMQI KTAMRYHLTPVRMAI
5468	35836	A	5514	1	5582	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQAADLIDIYQLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTQIITNYLSDHS AIKLELRKLNLTQNHSTTWKLN NLLLN DYWVYNEMKAEIKMFF ETNENEDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFERINKIDRLARLIKKKRE KNQIDTIKNDK
5469	35837	A	5515	3371	5375	TDTSQKKTTFMQPKKHMKCSP SLAIREMQIKTTMRYHLTPVRM AIHKSGNNRSWYFEKINKIDRL LARLIKKKREKNQIDAINKDKG DITTDPTIEIQTTR EYKHL YA NKLENLEEMDKFLDTYNLPRL KQEEVESLNRPGRSEIVAIINSL PTKKSPGPDGFTA EFYHRYKEE LVPLLLKLFQSIEKEVILPNSFYE ASIIIPKPRDRTAKKENFRPISL MNIDAKILNKILANRIQQHIKKL IHHDQVG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5470	35838	A	5516	314	2695	GSACRDPDPDPLRLVGGGAAA PPCSSVSPSAWRQSRPREYYEG GRGLHAPDRETALGLGIATSER MLGICRGRRKFLAASLSLLCIPA ITWIYLFSGSFEDGKPVSLSPLE SQAHSPTYASSQRERESLEVR MREVEEENRALRRQLSLAQGR APSHRRGNHSKTYSMEETGD SENLRAGIVAGNSSECGQPVV EKCRRNPLHFHLIADSLAEQILA TLFQTWMVPAVRVDFYNADEL KSEVSWIPNKHYSIGYGLMKLV LTKTLPANLERVIVLDTITFAT DIAELWAVFHKFKGQVVLGLV ENQSDWYLGNLWKNHRPWPA LGRGYNTGVILLLLDKLRKMK WEQMWRLLTAERELMGMMLSTS LADQDIFNAVIKQNPFLVYQLP CFWNVQLSDHTRSEQCYRDVS DLKVIHWNSPKKLVRVKNKHVE FFRNLYLTFLEYDGNLLRREL GCPSEADVNSENLQKQLSELDE DDLCEYFRFRERFTVHRTHL YFL HYEYEPADSTDVTLVAQLSM DRLQMLEAICKHWEGPISLALY LSDAEAQQFLRYAQGSEVLMS RHNVGYHIVYKEGQFPVNNLL RNVAMKHISTPYMFLSDIDFLP MYGLYEYLRKSVIQLDLANTK KAMIVPAFETLRYRLSFPKSKA ELLSMLDMGTLFTFRYHVWTK GHAPTNFAKWRTATTPYRVEW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5471	35839	A	5517	3	2079	GKPVSLSPLESQAHSPTYTASS QRERESLEVRMREVEEENRALR RQLSLAQGRAPSHRRGNHST YSMEEGTGDSNLRAGIVAGNS SECGQQPVVVEKCRRNPLHFHLI ADSIAEQILATLFTWMVPAVR VDFYNADLKEVSWIPNKHYS GIYGLMKLVLTPLPANLRLVI VLDTDITFATDIAELWAVFHKF KGQQVLGLVENQSDWYLGNL WKNHRPWPALGRGTYGTGVI LLDKLRKMKWEQMWRLTAER ELMGMLSTSLADQDIFNAVIVQ NPFLVYQLPCFWNVQLSDHTRS EQCYRDVSDLKVIHWNPSKKL RVKNKHVEFFRNLYLTFLFYD GNLLRRELFGCPSEADVNSNL QKQSELDEDDLCEFRERERT VHRTLHYFLHYEYEPADSTD VTLVAQLSMDRLQMLEAICKH WEGPISLALYLSDAEAQQLRY AQGSEVLMRSHNVGYHIVYKE GQFYPPVNLRLNVAMKHISTPY MFLSDIDFLPMYGLYELRKSV IQLDLANTKKAMIVPAFETLRY RLSFPKSKAELSLMDMGLFT FRYHVWTKGHAPTNFAKWRT ATTPYRVEWEADFEPPYVVR DCPEYDRRFVGFVGNKVAHIM ELDVQYEFIVLPNAYMIHMPH APSFIDITKFRSNKQYRICLTKL EEFQDMSRRYGAALKYLTA
5472	35840	A	5518	403	2757	
5473	35841	B	5519	128	353	
5474	35842	A	5520	2	333	
5475	35843	B	5521	25	1359	
5476	35844	B	5522	1	1113	
5477	35845	A	5523	1	2526	
5478	35846	A	5524	3	555	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,420,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5479	35847	A	5525	1	1710	MSQGTTPWGPTPAGTTPSEVH RPFPPVPVPVPEPVSERSFPVRG VCGQAKSGLRRGAARLAPAAAY LFTRQQTRELIHSACVSISVNTM HGLSVAINSRRCCTYYRKYVIDF SKSEIIGIPISKNIDLTVGTTVTQ LQNLNTVGIHGRGGRGQVAAL NCDRQGHLLWLFTRTVHWRM GNDRTFWGLLDTVSELMFIPGN PKHHCGPPVKVGAYGVTFGLV HWCAGACQDTPCKMKDKLLHL APPTTKKKAQYVVGLLGFWRPI YRVTQKAASFEGPEQDKALP QVQAAVQPALLFGPYDSADPM VLEASVADRDAVWSLWQAP/IS HKMGHAQQHSIIKW*YICDW ARAGPKGTTAPMASWGVLYD QLTEEEKTRAFTDGSARYAG TTQKWTAALQPLSRTSLKGS GEGKSSQWAEQLQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDKWIGDKKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
5480	35848	A	5526	1	438	
5481	35849	A	5527	1	612	
5482	35850	A	5528	2	736	EKCAMTALSSKLISQQKAFFAK MVVDVAVMMLDDLQKLMIGI KKVQGGALEDSQLVAGVAFKK TFSYAGFEMQPKKYHNPKIALL NVELELKAEDNAEIRVHTVED YQAIVDAEWNILYDQKLEKIH SGAKVVLKSLPIGDVATQYFA DRDMFCAGRVPEDLKRTMM ACGGSIQTSVNALSDVLRGRCQ VFEETQIGGERYNFTGCPKAK TCTFILRGGAEQFMEETERSLH DAIMIVRRA
5483	35851	A	5529	3	474	
5484	35852	A	5530	374	968	
5485	35853	A	5531	1	568	
5486	35854	A	5532	1	2136	
5487	35855	A	5533	1	240	
5488	35856	A	5534	248	1034	
5489	35857	A	5535	1	1602	
5490	35858	A	5536	120	340	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5491	35859	A	5537	2	408	DEDDDDDEEDDEDDDDDDF DDEEAEEKAPVKKSIRDTPAK NAQKSNQNGRDSKPSSTPRSK GQESFKKQEKTPKTPKGPSSVE DIKAKMQASIEKGGSLPKVEAK FINYVKDCFRMTDQEAHQDLW QWRKSL
5492	35860	A	5538	194	1027	WSFISIHLLSYLSACHLMEDS/ MDMGMRLRPQNYLFSCELKA NKDYHFKVDNNEHQPLPLTTI NLGAGAMDELDIVEAEAMNYE GSPKIVILATLKMSVQPTVSLG GAFETPPVVLRLKCGSGPVHIS GQHLVAVEEDAEEDEEEDV KLLSISGKRSAPGGGSKVPQKK VKLADEDDDDDEEDDDDED DDDDDFDDEEAEEKAPVKKSIR DTPAKNAQKSNQNGKDSKPSS TPRSKGQESFKKQKTPKTPKG PSSVEDIKAKMQASIEKAH
5493	35861	C	5539	212	367	
5494	35862	A	5540	14	1515	
5495	35863	A	5541	1	540	
5496	35864	A	5542	1	1881	MDAALDDLIDTGGPEETEEEN TTYTGPEVSDPMSTYIEELGK REVITPPKYRELLAKPIGDDAI DALSSDFTCGSP*LYPSQVFHLL DLLPFPSPGYQRLQLQHILA/AVP FKVAGSGGADCILHMEVRDTA SDTGAGAAALDSSVFSVGLDGF SLHSDRSKSSSSSSMSDSLRLG LFSSGSGNSGFPPLSVAGFNLYS DGI VSSSPHFSFSSLAFASSTS LIERSSSGSACRPVSEADRASS
5497	35865	A	5543	1	930	
5498	35866	A	5544	1	183	
5499	35867	A	5545	1	555	
5500	35868	A	5546	162	499	FPGSGNMAKDAGLIEANGELK VFIDQNLSPGKGVVSLVAVHPS TVNPLGKQLLPKTFGQSNVNIA QQVVIGTPQRPAASNTLVWVG SPHTPSTHFASQINQPSDSSPW/S AGKR
5501	35869	A	5547	2	451	LVAEFAADNHILPNESA YDQK NIRRRVYDALNVLMAMNIISKE KKEIKWIGI.PTNSAQECQNLEV ERQRRLEIRIKQKQSLQELILQ QIAFKNLVQRNRHAEQQASRP PPPNVSIHLFPFIIVNTSKKTVIDC SISNDKFEYLFNFNDNT
5502	35870	A	5548	37	162	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5503	35871	A	5549	205	616	RKLHGSQSSITIAVFGKQNTYIR LEPFKINVLQITKHIEKLQCGG VVKQLSRGNNQHISSTYDINR ADAQVRRRAVNNYDIHMSNSF NGQSEHQVWIGGQFTFIKFPIN SVSIRCARQEGIMSSPGQVQG
5504	35872	B	5550	1	1407	
5505	35873	A	5551	3	416	MLPARMC GGIVSG*OFITGNSY DHDYEFELGTRSA*KLKLFST LPD*QLPAGSGEGPYHLEGQLS YCHRGGEKALALLSSPTSKTR SPSEPDEQDEQKLRFCRHLV GQQRSPVEIRLQHVIAIAYQTH HAYD
5506	35874	A	5552	1988	2137	LVITLLPLACGTAK*E*VNVTS FGSRPICSTSPVLFSL*GPVKEF DT
5507	35875	B	5553	1	561	
5508	35876	A	5554	1	492	
5509	35877	A	5555	3	1055	
5510	35878	A	5556	1	634	
5511	35879	A	5557	1	723	
5512	35880	A	5558	1	384	
5513	35881	A	5559	1	792	
5514	35882	A	5560	3	1607	HCTRM SVK WTSVILLIQLSFCFS SGNCGKVLVWAAEYSHWMNI KTILDELIQRGHEVTVLASSASI LFDPNSSALKIEIYPTSLTKTEL ENFIMQOIKRWSDLPKDTFWLY FSQVQEIMSFIDITRKFCCKDVV SNKKFMKKVQESRFDVIFADAI FPCSELLAEI.FNIPFVYLSFSPG YTFEKHSGGFIFPPSYVPVMSE LTDQMTFMERVKNMIVLYFD FWFEIFDMKKWDQFYSEVLGR PTTLSETMGKADVWLIRNSWN FQFPHLLPNVDVFGGLHCKPA KLPKEMEDFVQSSGENGVVV FSLGSMVSNMTEERANVIASAL AQIPQKVLWRFDGD/KPDTLGL NTRLYKWIQNDLLGHPKTRA FITHGANGIYEAHYHGPVVG PLFADQPDNIAHMKARGAAR VDFTMSSTDLLNALKRVINDP SYKENVMKLSRIQHDQPVKPI. DRAVFWIEFVMRHKGAKHLRV AAHDLTFWQYHSLDVIGFLLV CVATVIFIVTKCLFCFWKFAR KAKKGKND
5515	35883	A	5561	2	1600	

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5516	35884	A	5562	2	1624	AATGKQALHCIRMSMKWTSAL LLIQLSCYFSSGSCGKVLVWPT EFSHWMNKLTILDELVQRGHEV TVLASSASISFDPNPSTLKFEV YPVSLTKTEFEDIKQLVKRWA ELPKDIFWSYFSQVEIMWTFN DILRKCKCDIVSNKKLMKKLQE SRFDVVLADAVFPFGELLAELL KIPFVYRPRFSPGYAIEKHSGLL LFPPSYVPVMSSELSDQMTFIE RVKNMIYVLYFEFWFQIFDMK KWDQFYSEVLGRPTTLSETMA KADIWLIRNYWDFQFPHLLPN VEFVGGLHCKPAKPLPKEME/E FVQSSGNGVVFSLGSMVSN SEERANVIASALAKIPQKVLWR FDGNKPDTLGLNTRYLYKWIPQ NDLLGHPKTRAFITHGGANGIY EAIYHGIPMVGVPLLADQPDNI AHMKAKGAAVSLDFHTMSSTD LLNALKTVINDPLYKENAMKLS RIHHDQPVKPLDRAVFWIEFVM RHKGAKHLRVAADHDLTWFOY HSLDVTGFLACVATVIFITKC LFCVWKVVRTGKKGKRD
5517	35885	A	5563	1	225	
5518	35886	A	5564	1	3210	
5519	35887	A	5565	1	835	
5520	35888	A	5566	222	477	HPRCLSPKGILKYLTKKYLKKN NLRDWLRVVANSKESYELRYF QINQDEEEDEED*ISFIWKILYE FLNKTWDPKKKKTKKKKK
5521	35889	A	5567	1	778	MAAAAAAGDSDSWDADAFS VEDPVYKVGGGTAGGDRWG GEDEDEDVDNWDDEDEKK EEAEVKPEVKISEKKIAEKIE KERQKKRQEEIKKRLEPEEP KVLTPEEQLADKILRLKKLQEE DLELAKETFGVNNNAVYGDAM NPSSRDDFEFGKLLKDINTQYE ESLYYARFLEVLVRDVCISLEID DLKKITNSLTVLCEKQKQEKQ SKAKKKKGGVVPGGGLKATM KDDLADYGGYDGGYVQDYED
5522	35890	A	5568	1	897	
5523	35891	A	5569	1	2658	
5524	35892	A	5570	1	441	
5525	35893	A	5571	3	427	

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5526	35894	A	5572	1	952	PRLVLLKMAPI.LLDKYVEIARL CKYLPENDLKR.LCDYVCDLL EESNVQPVSTPVTVCGDHGGQF YDLCELFRITGGQVPDTNYIFMG DFVDRGYYSLETFTYLLALKAK WPDRIITLLRGNHESRQITQVYG FYDDCLTKYGNANAWRYCTK VFDMLTVAALIDEQILCVHGG SPDIKTLADQIRTIERNQEPHKG AFCDLVWSIDPEDVDTWAIN PRGAGWLFGAKVTNEFGS*ST NLKLCIRAHQLVHEGYKFMFD EKLVTVWSAPNYCYRCGNIA MVFKDVNTREPKLFRAPDSE RVIPRTTTTPYFL
5527	35895	A	5573	54	588	
5528	35896	A	5574	1	4287	
5529	35897	A	5575	1	507	
5530	35898	A	5576	1	1416	
5531	35899	A	5577	1	841	ILLWDVGGGLTQIDKYLYSSED YIKSGALLACGIVNSGVRNECD PALALLSDYVLHNSNTMRIGSI FGLGLAYAGSNREDVLTLLLPV MGDSKSSMEVAGVTALACGMI AVGSCNGDVTSTILQTIMEKSE TELKDTYARWLPLGLGLNHLG KGEAIEAILAALEVSEPFRSFA NTLVDDVCA YAGSGNVLKVQQL LHICSEHFD/SKEEEDKDKKEK KDKDKKEAPADMGAHQGVAV LGIALIAMGEEIGAEMALRTFG HLLRYGEPTLRRVPLALAL
5532	35900	A	5578	2	391	AFGVTEPGCYGVIDVDTGKSTL FVPRLPASHATWMGKL/HSVLT SQKPSVLLTLRGVNTDSGSVCR EASFDGISKFEVNTILHPEIVE CRVFKTDMLEVLRYTNKISSE AHREVMKAVKVGMEYELER

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5533	35901	A	5579	18	1541	RRCRANMAAATGPSFWLGNET LKVPLALFALNRQRLCERLRKN PAVQAGSIVVLQGGREETQRYCT DTGVLFRRQSEFFHWAFGVTEPG CYGVVDVDTGKSTLFVPRLPAS IIATWMGKIHSKEHFKEKYAVD DVQYVDEIASVLTSQKPSVLLT LRGVNTDSGSVCREASFDGISK FEVNNITLHPEIVECRVFKTMDM ELAEVLRYSNKISS\EAHREV\MK AVKSGEWKEYGVGKASFEHY\ CYSRG\GMRH\TSYT\CILRAVG *GTSAVLTFTHAGAPNDRTIQ NGDMCLFDMGGEYYSVADIT CSFPRNGKFTADQ\KAVYEAVL LSSRAVMGAMKPGDW\WPDMA HRLAYRIHLEELAHMGILSGSV DAMVQAHLGAVFMPHGLGHF LGIDVHDVGGYPEGVERIDEPG LRSLRTARHLQPGMVLTVEPGI YFIDHLLDEALADPARASFLNR EVLQRFRFGGVRIEDVVVID SGIELLTCVPRTVEEIEACMAGC DKAFTPFSGPK
5534	35902	A	5580	1	98	
5535	35903	A	5581	1	810	

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5536	35904	A	5582	1	861	MLKEIIDDTNKWKHIPCSWMGRISIVKMTILPKAIYKFNAVLIKIPPSFFTELEKTILKFLCNEKRAKAKARLNKKNKSGGITLLDFKRYYSIAIVTKTVWYWKYKRNRIHQRRNRIENPEINPNTYSQLIFNKANKNIKWGNDFSKWCWDNWLATCRRMKLDPHLSPHTKINSRWIKDLILRPETTKILEDNIGKTLDDVGLGKDFMTKNPKANARKAKINIWDLIKLSFFTAGKGTVSRVNRQPTWEKIFIHTSDEGLLISRIYNELKQISKKKITNNPIKKWAKDMNRQFSKEDVQMANKYMKKCTSTLIANLICREMQUIKTTMQYHLTPARMAIIKSKISRCWHGCGDQGTLLHCWWECKLVQPLWKTVWRFLKELKVELPFDPAIPLGTHPEEKSLCKDCTCMLLAAQFTIAKSWNQPKCPSVNEWIKKLCPRWLLSKWASA*NKWKHIPCSWMGRISIVKMTILPKAIYKFNAVLIKIPPSFFTELEKTILKFLCNEKRASRAKARNKKNKSGGITLLDFKRYYSIAIVTKTVWYWKYKRNRIHQRRNRIENPEINPNTYSQLIFNKANKNIKWGNDFSKWCWDNWLATCRRMKLDPHLSPHTKINSRWIKDLILRPETTKILEDNIGKTLDDVGLGKDFMTKNPKANARKAKINIWDLIKLSFFTAGKGTVSRVNRQPTWEKIFIH
5537	35905	B	5583	473	1694	
5538	35906	A	5584	1	429	
5539	35907	A	5585	572	1149	PPVSHSMTLGNSYLFAPNWTITPAW/CNTLDPSEFGWQASLSLPSHQQFEHTCPEWLPTYSWPCKVGPDYLSICQPECKQHFQESLLESSKQNIYETCAIYVSSPGERILNQRFGPHGAFILVREYDDIRFHSQGPPSTCPNFGPSYYTARESAYALKLRALEIIQISQSTKMQRNLGNPILPAIHQQPPQ
5540	35908	A	5586	1	804	
5541	35909	B	5587	1	1995	

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5542	35910	A	5588	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTLKKNYLSFLVYISRL *NRVKAIM/VGKA EWKTIELPL PRKTVNQKQYRIPGGIAEIST11 KELNNAGMVIPTTSPFNSPIWP VQKIDGSRWMTVDYCKLNQV VTPIAATVPYVVSSELEQIN/TSPG T/WNRKRFNCNRSRLHLKLLCHL GHMTQQI*CFLRQCWHIGMLF GPEICGCTLSGQKL/WKIFVSH AASFWSPEQEKALQQVQAVV QAALPLGPYDPADPVLLEMSV ADRDVWILWQAPISEQWRPP GFWSKALPSSADNYSFPERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
5543	35911	A	5589	1	1337	MIISIDA EKA FDKIQPFMLKTL SKLEETASPSPVVATYTPQPM PSAFPPLSEEINPVL PETTVMAS PEAVTRQDNVDSPOKPPPTPMF ASRPITRLKPRRAPSEEGIQLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGAKWKPLEQPP PRKIVIQKQYHIPGAITEISATIE DLKETGVVILTTSPFKSSIWPLQ KTDGSRWMTVNYHKLNQVET PIAAVDPDVSLLEQINTSPGT WYAAIDLNVVFSIPVYKAHQK QFAFSWQGGQYTFFTLPQGYIN SPDITLVHYIDIMLIGSSEQEV ANTDLLPARVASWGVYPDQL T/GGRED*GLLHRWSCRICRHH
5544	35912	A	5590	2	693	KIVN/QKQYHRIHGGIAEISATIKD SKDTGVVIPTTSPFNSPIWPVW KTDGSRWMTVDYHKLQDVVTPI AAAVPDVVSLEQINTSPGTWY AAINLENAFFSIPVHKANQ/KQF AFSWQGGQYTIAPVQ/VKFLG IHWFVACQDIPSKIKDKLLHLA PPTNKKEAQCLVGLFGFWRQH PHLRVLLQPIYQVTLKAAIFEW GPEQEKALQQVQAAVQAAALPL GPYDPTDPMVLE

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5545	35913	A	5591	1	1011	MVSTPATLPSLPKALMASWG VPYDQLTKEEKTRVWFTDGS RYAGTTQKWTAVLQPLSR TKDSSEKSSQWAEQAVYLV VHFAWKEKWPDPVGLYTD SWAVANGLAGWSETWEKQ DWKIGDKEIWGRGMWMDL SEWSKAVKIFVSHVSAHQ RVTSAAEEFNQVDRPL/P VFTQWAHEQSGHSGRD GGYSWAQQTGLPFTKADL AMATAECPIQQQRPTLSPL YS TIPQGDQPA TWQIDYIGLP LS WKGQKFVLTVIDTYSRYF AY PAHNASAKTTIHGLIECLH CYG IPHSIASDQSIH/TTKEVQ* WAH AHGIHWSYHVSHHPEAA AGL
5546	35914	A	5592	7	278	SASCTAAFHQMEVVYTRSG SRS*R/PTIPVIAQWDYDHN GHGGRDGGYPWAQQHELPL TKADL ATATAECPIQQQRPSLSP RCGT IPR
5547	35915	A	5593	1	237	
5548	35916	C	5594	63	116	
5549	35917	A	5595	2	739	HKMGHAQQHSIIKWK*YIC DW ARAGPKGTTAPMASWGVLY D QLTEEEKTRAWFTDGSARY AG TTQKWTAAALQPLSRITSL KSGS GEGKSSQWAEQAVHLVVH FS WKDKWPDVRLYIDSWAVAN G LAGWSGTWKKHDKWIGDKEI WGRGMWMDLSEWPKPVKIF G SHVSAHQWVISAEEEDFNQ VD KMTCSVDITQPLSPATPVIT QW AHKQSGHGGRRDGGYTWAQ QH GLPLTKTGLAMATAECPI
5550	35918	A	5596	1	354	
5551	35919	A	5597	3	592	
5552	35920	A	5598	126	365	QLAEPHPWLDP*KAGFEWGP EQKKALQ*VQAAVQAALPL G YDPADPMVLVSVADKDAVW I FHLSGSDRWRTYRCL
5553	35921	A	5599	1	483	
5554	35922	A	5600	1	1908	
5555	35923	B	5601	141	1569	
5556	35924	B	5602	46	1533	
5557	35925	A	5603	61	448	WRFLGPWRIVSCWFCGWE ERR EGSAFFVGIPARMSAARESH PH GVKRSASPDDDLGSNNWEA AY LGNEERKQKFLRLMGA/GK GEE DQKINEELESQYQHSMDSK LSG RYRRHCGGLGFSEVEDHDG EGD

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5558	35926	A	5604	1	404	PWRIVSCWFCGWEEERREGSAFF VGIPARMSAARESHPHGVKRS SPDDDLGSSNWEAADLGNEER KQKFLRLMGAGKKKEHTGRLVI GDHKSTSHFRTGVEDHDGEGDV AGDDDDDDDDSPDP*SPDDSES DSESE
5559	35927	A	5605	2	434	LG PWRIVSCWFCGWEEERREGS AFFVGIPARMSAARESHPHGVK RSASPD DDFLFAIMNGK*KIV NSHRCSVKAKSRQQLGSSNWE AADLGNEERKQKFLRLMGAGK KEHTGRLVIGDHKSTSHFRTGE ED*KINEELESQYQH
5560	35928	C	5606	909	1096	
5561	35929	A	5607	1	309	PQPAAMAAYIWLIRHGESAW NLETFSFGWYDATLSLAGHKE AKRGGQALRGLFQVPLAPEAV GTVWCWSWRTPCALKQL*PRPL KRRLRILADRHATQPRPQQ
5562	35930	A	5608	93	914	SQSVPHQPAPAMAAYKLVLG/ RHGESAWNLENRFSGWDDADL SPAGQRGGERFAAQLQDAGY EFDICFTSVQKRAIRTLWTVL/ DAFDQMWLASGEGWGFNER HYWGS*PGLN*KQKLAAKIG*G PRLKIWRRSYD/VPPPPMEPDH PFYSNISKDRRYADLTEDQLPS C/ESLKDITARALPFWN EIVPQI KEGKRVLIAAHGNSLRGIVKHL EGLSEEAIMELNLPTGIPIVYEL DKNLKP KPMQFLGDEETVRKA MEAVAAQ GKAKK
5563	35931	A	5609	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLKLHDERVLVAF GQRDGI RGVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANY VSIRFGRPRLTSNEKLM LASM FHSIKFVVLADP/RQAGIDSLRK IYEIYSDFALKNPFSYLEMP
5564	35932	A	5610	1	663	
5565	35933	A	5611	1	2034	

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5566	35934	A	5612	374	1106	IPVSRQGSQDWRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTF YPLDLAGSS*HDERVLVAFGQR GRHPEWGHAVLAINGMDVNG RYTADGKVEVLEYLG*PLLNY VSIRFGRPRL/TSNEKLMGLP CFHSLFAIGSQACLPGTREASR HLKILGRQDTFKLHICYQTLTG IKFVVLADPRQAGIDSLRRI YEVYISDFALKNPFIYSLEMP IR CELFDQNLKLALEVAEKAGTF
5567	35935	A	5613	1	336	
5568	35936	B	5614	60	2175	
5569	35937	A	5615	2	198	
5570	35938	A	5616	1	449	
5571	35939	A	5617	1	771	
5572	35940	A	5618	18	736	EAMSSKVSRDTLYEAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGT/VQVGTVLIPPS PQCPRACPSAGSR*AGGGHVG TDVLG*FRPPAPGRRGWTDPHP GS*NMRRGGVGRPPSPASLRS QAGCW*M*TLRVRLGWLLRSQ TLHRLGTPGLGVTWCWCCPPK RRLKSTPRPKFSVCVLGDQQHC DEAKAVDIPHMDIEALKKLNK NKKLVKKLAKKYDAFLASESLI
5573	35941	A	5619	24	698	EAMSSKVSRDTLYDAVREVLH GNQRKRRKFLETVELQISLKNY DPQKDKRFSGTVRLKSTPRPKF SVCVLGDQQHCDEAKAVDIPH MDIEALKKLNKNGKTGSRSWP KKYDAFLA/SQSPLIQADSPKSL GPISLNGKRSKSSPLLTHNKNM VAKVDEVKSTIKFPNWRRCCL CL AVAVGVHVKMTDDELVYNIHLA VNFVSLKKNNWQNVRLYIK SPMGKPQRLY
5574	35942	A	5620	1	843	

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5575	35943	A	5621	3	1215	LLIMADPRDKALQDYRKLLLE HKEIDGRLKELREQLKELTKQY EKSENDLKALQSVGGQIVGEVL KQLTEEKFIVKATNGPRVYVVG CRRQL*QKVSLKPGTRIVALAD MTTLTIMEDILPRIEVDPLVYN MSIHEDPGNVSYSEIGGLSEIQI RGI*GEVIGLPLYKPQSYFQRVG IIPPKIGCLLYGPPGTGKNT/LLA RAVASQLDCNFLKVVSSIVDK YIGESARLIREFNYARDHQPCI IFMDEIDAIGGRRFSEGTSADRE IQRTLMELLNQMDGFDTLHRV KMTMATNRPDTLDPALLRPGR LDRKIHIDLPNEQARLDILKIHA GPITKHGVEIDYEIVKLSDG/FN GADLRNVCTEAGMFAIRADHD FVSTGKTSLKAVRKVADSKKL ESKLDYKPV
5576	35944	A	5622	104	173	
5577	35945	A	5623	1	1140	
5578	35946	A	5624	1	528	
5579	35947	A	5625	1	1083	
5580	35948	A	5626	1	471	
5581	35949	A	5627	1	2322	
5582	35950	A	5628	1	678	
5583	35951	B	5629	213	1477	
5584	35952	A	5630	2	339	FGLHKWGLGLEASSPCGPLTPS YLGFP RPHPGTLGLGRFWPFLA LQSLSETPSHARMPRTVARTS PETLEISPLRAAT*NHRSSGHTC FRERMLRVSCRLSLDLSSSWVR
5585	35953	A	5631	1	783	

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5586	35954	A	5632	92	2746	ASRMTVLQEPVQAAIWQALNH YAYRDAVFLAERLYAEVHSEE ALFLLATCYRSGKAYKAYRL LKGHSCCTPQCKYLLAKCCVD LSKLAEGEQLSGGVFNKQKSH DDIVTEFGDSACFTLSLLGHGII VQTERAAKGTAFSKRLCLHTF PWTPLPLEVEIGERPLPHQTFN FTS*RNFANCLHTSGTKQVTN HVFHRQPETVLTETPQDTIEL NRLNLESSNSKYSLNTDSSVSYI DSA VISPDVTPLGTGTSILSKP VQNKPKTGRSLGGPAALSPL TPKFWGFLPIRKPPSPGDSY LQNYTNTPPVIDVPSTGAPSKK TFRVLQSVARIGQTGTSVFSQ SGNSREVTPIAQTQSSGPQTST TPQVLSPTITSPNALPRSSRLF TSDSSTTKENSKKLKMKFPPKIP NRKTKSKTNKGGITQPNINDSL EITKLDSSIIEGKISTITPQIAF NLQKAAAEGLMSLLREMKGK YLALCSYNCKEAINILSHLPSHH YNTGWVLCQIGRAYFELSEYM QAERJFSEVRRIENYRVEGMEIY STTLWHLQKDVALSLSKDLT DMDKNPESGTQRGRESRPMC GADSQIEKSQSSYFIQDLRSFDY VKFAVVTKIRAWCAAGNCFSL QREHDAIKFFQRAIQVDPNYA YAYTLGHEFVLTEELDKALAC FRNAIRVNPRIYNAWYGLGMI
5587	35955	A	5633	260	678	GEFSIFFWVWN*LLLWHQETFS I*NLFSSH*TSITYQATEEGDFDII QMKLIHFGDSIFIYLLKLLINRK P**EAAISI*V*TWRSRFSHFQLR *HQTQVTNHSWFTEAR*LTDLV KKSPTIPCSRFKANTLF**SDP
5588	35956	A	5634	1	1452	
5589	35957	A	5635	2	1563	
5590	35958	A	5636	1	444	
5591	35959	A	5637	2	345	

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5592	35960	A	5638	2	1721	RSREAAA VAAAAATTAFCGR1 WNPCAALTMKQSSNVPAFLSK LWTLVEETHTNEFTWVSQNGQS FLVLDEQRFakeILPKYFKHNN MASFVRQLNMYGFRKVVHIDS GIVKQERDGPVEFQHPYFKQGG DDLLENIKRKVSSSKPEENKIRQ EDLTKIISAAQKVQIKQETIESRL SELKSENFSLWKEVSELRAKHA QQQQVIRKIVQFIVTLVQNNQL VSLKRRRPLLLNTNGAQKKNL FQHIVKEPTDNHHHKVPHSRTE GLKPRERISDIIIVDVTDDNAD EENIPVIPETNEDVISDPNSCSQY PDIVIVEDDNEDEYAPVIQSGEQ NEPARESLSSGSDGSSPLMSSA VQLNGSSSLTS:EDPVMTMDGFP FGMDNIQSFWGRVELLDYLDLS IDCSLEDFQAMLGRQFSIDPDL LVDLFTSSVQMNPTDYINNTKS ENKGLETTKINN VQPVSEEGK ENLKS(KPDK)QLIQYTAFFLLAF LDG\NPASSV*TRGTTASFRKF CPL*DKPIEVDELDDSLDPEPT QSKLVRLPLEL TEAEASEATLFY LCELAPALDSDMPLDLS
5593	35961	A	5639	2	251	QLRSPLKWKKAQRQPLAIAHV LLLRPRKKRONGFTVRYARLL STLPRSWRRKQWY*AQNHVRS PEWKWHYQSL
5594	35962	A	5640	70	297	
5595	35963	A	5641	3	985	
5596	35964	A	5642	1	3501	
5597	35965	A	5643	1	1752	
5598	35966	C	5644	1	879	
5599	35967	A	5645	21	519	LHHPVRTLSCRFVGVWCWRSTPG PVCGLISSGGCRTVDIAALQLW LRGLALPEQLLRVDPHPQACRR LPREPPGPGQTFTGREPPQAVS TKEASSNHLHAPERTVAGLTFT TEQVRALEGVFRHHQYLGPLE RNWLAREMQLSRSR*KPGFKI AG*NTNGKCRTPS
5600	35968	A	5646	90	2401	
5601	35969	A	5647	776	1018	
5602	35970	B	5648	1	1296	
5603	35971	A	5649	1	1257	
5604	35972	A	5650	731	4841	
5605	35973	A	5651	325	9497	
5606	35974	A	5652	1	322	
5607	35975	A	5653	1	819	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
5608	35976	A	5654	56	251	
5609	35977	A	5655	149	701	
5610	35978	A	5656	3	415	
5611	35979	A	5657	3	467	AIASPRAGIRHELTSTMAAGK NKRLTKGGKKGAKKKAV/DNII NIGKTLVTRTQRTKIASDGLKG RVFEESLADLQNDVTDGYLLRVI *VAFTTERTNQ/REVFNKLIPDS IGKDIEKACQSIYPLHDDFARK VKMLKKPKFELRKLMEHGG
5612	35980	A	5658	2	418	PRVRADGKNFRLTKGGELGAR NKVVDPFSKKDWYDVKAPAM FNIRNIGKTLVSRTOGTIASDG LKGRVFEARLADLQNDVAFIK CKLITDDVHGKNCLTIFHGMDL TRDKM/CSLGKKWQTMIEAHV DVKTDDGYLL
5613	35981	A	5659	3	121	
5614	35982	A	5660	1	237	
5615	35983	A	5661	25	967	FSPAAGIRHEGLTSTMAVGNK KRLTKG/GKKGS/KKKVVDPPF R/KDWY*RRKHPLMFHYKNIG KTLVLTQDPKPKIA/SDGLQGF VCLKVSLADLQNDVSRKF RLITEVCFRGNLP*LTSHGAW DLYPVTMCSHGQKNWQTM DSSR*MFKTNPNGYLALRLFLC /VGFT*KNRNQFRLRKAPPYAS ATQQVPPKSRKKM/MEIMTPR GARQNDLEKKWVNKLIPRQAL GKDIRKGAQSYFIPLHDVLR EKLKLEGSFKF*IGESSLGASM GGRAVVPGKSHLGTGTGAKVG TSLMGYEPPVPRILV

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5616	35984	A	5662	1	2142	MIILIDAEKAFDKIQPFMLKTL NKLIGDGTLYKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLSISVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNTWTQEGEHHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLAIRAQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DPIKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWWYQ NRDIDQWNRTEASEVTSIYNNH LIFYKPDKNKKWGNDSL FNKW CWENWLAICRKLKLDPFLTPYT KIHRSWIKDLNVRPKTIKLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIYKELQIYRKK/TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSLVIREMQIKTTM

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5617	35985	A	5663	1391	2742	KKRESSLTHVMRPA SF*YQSQAE ETQKKRILDQY P**TL MQKSSI K/YLAKRIQGHKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHHIISIDA EKA FDKIQPPF MLKTLNKL ELET TV KFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWY WYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDSL FNKWC WENWLAICRKLKLD PFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFS EEDIYAAK KH MKKCSSLAIREMQIKTTMRYH LTPVRMAIIKSGNNRHAPFSIH THIMFGSLYLIQKDL SILGF WYPRGILEPIY
5618	35986	A	5664	1	1910	MTIIHIIIIIIITIIHVIITINIVIT TTILTTVIISSTIIHITFVFETGAI KLEIRIKLTLQNRSATWKLNNL LLNDYVWHNEMKAEIKMFFET NENKDTTCQNLWDTFKAINKID RPLARLIKKKREKNQIDA IKND KGDITTDITGIQT TIREYYKHLY ANKLENREEMDKFFDTYTL PRL NQEEVESLNRPI TGSKIEEINSL SIKSPGPDGFTA EFYQRYKEE LVPFLLKLFQSIEKEGILNSCCE ASHILIPKGRD TT KENFRPISL MNIDAKILNKT LANRIQQHITK LIHHIVQVGFI PGMGWFNIRKS INNWKKTTLKLIWNQKRACITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWY WYQN RDIDQWN RTEASEIIPHTYNYLSFDKPDKN KKWGNNSLFNKWCWENWLAIC RKLKLD PFLTYTKINSRWIK DLNFGTETIKTLEENLGNIHDI GMGKDFMSKTPKAKATKAKID KWDLIKLSFCTAKETTIRVNR QPTWEKIFAIYPSDKGLISRIY KELKQVYKKKTNNPIKKWAKD TNRHFSNEDIY AANRHMKKCS SSLAIREMQIKTTMRYHLAPVR MTIIKSGSNRQ/W*ASGHVRC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
5619	35987	A	5665	1	2460	MPHAGHARSPGHTLIKLAEWWM MSRWMEWNPFGPLSIDAKCHK DLPRDIQDFSEKGVDFVLNYSK ALNQEEVESLNRPIITGSEIEAII SLPTQKSSGPDGFTAIFYQRYK EELVPFLLKLFQSEKEGILPNSF YEASILIPKPGRYTHKKNFRPI SLMNIDAKILNKILANRIQQHIK KLIHQDQVGIIPGMQSWFNHKK SINVQIHINRTKDKNHMIIISDAE KAFDKIQPFMLKTLNKLGIK YLRIQLTRDVKDLFENYKSL NEIKEDTNKWNIPCSWIGRMN IHKMAI/LPKVIYRFNVIPIKLPMT FFSELEKSTLKIWNQKRARIK TILSQKNKAGGIMLPDFKLYYK ATVTKTAWYQYQNRDIDQWN RTEPSEMTPHYNHLIFDKPDKN KQWGKDSL FNKWCWENWLAI GRQLKLDPLTPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI SMGKDFMSKTPKAMATKAKM DKWDLIKLSFCTAKETTIRVN RQPTWEKNFAIYSSDKGLISRI YKQLKQIYKKKTNNPIKKWAK DMNRHFSKEDVYAANRHMKK CSSSLAIREMQIKTIMIYHLTPV TMAIIKKSGNNRCWRGCGEMG TLLYCWWDCKLVQPLWKTW QFLRDLGLGIPDPAIPLGIYPK DYKSCCYKDTCTPKLARDQI HILKQHRKLETRQKQYRAW
5620	35988	A	5666	689	1909	LIA YQPKKSRTRWIHNQILPERI KYLGIQLTRDVKDLKEKYKPL LNEIKEDINKWNIPCSWIGRIN LVKMAIL/PQAICRKLKLDPLT TYTKINSRWIKDLHVRPKTTKT LEENLGNTIQDIGMGKDFMSKT PKAMATEAKIDKWDLIKRRKSFC AAKETTRVNRQPTDWEKMF IYSSDKGLISRIYEELKQIYKKK TNNPINKWAKDMNRHFSKEDI YAANRHMKKCSSSLAIREMQIK TTVSPFAAQWVSQRYGK WQEA HPSNNDDGKYRGKPRFQSLSD VHGPQDQKKIIESALPPTPTFI NILMNAKTIENGQFPYLLNALK QQQPHDAENLFTWGKENAIV SPCIEVSAALSQWK VPAWPQRS GIPNRILRSPIGLGSWVAFDL VWVRGDPTALK

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5621	35989	B	5667	1	1962	
5622	35990	B	5668	1	1851	
5623	35991	A	5669	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNCKSN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGDGTY FKIIRAIYDKPTANILNGKKLEA FPLKTGTRQGCPSPLLFNIVLE VLARAIQKEIKEIGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLEKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTPQSEITPHIYNLIFD KPDKNKQWKGKSLFNKWCWE NWLAICRKLKLDPLTPYTKIN SRWIKDLNVRPKTTKLTLEENLG ITIQDIGMGDMFSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIHKSGNNRCWRGC GEIGTLLHCWAWINWMKKTWH IYTMEEYASIKKNFMSFAGA* MKLETII
5624	35992	A	5670	2	1967	

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5625	35993	A	5671	1039	2272	KKRESSLTHVMRPASF*YQSQA ETQKKRILDQYP**TLMQKSSI K/YLAKRIQGHKKLIHHDQVGF IPGMQGWFNIRKSSINVIQHINRA KDKNHMIIISIDA EKAFDKIQPPF MLKTLNKELEETT VKFIWNQ KRAHIAKSILSQKNKACGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDLSLFNKWC WENWLAICRKLKLPFLTPYTK INSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKHH MKKCSSLAIREMQIKTTMRVH LTPVRMAIHKSGNN
5626	35994	A	5672	1	3477	
5627	35995	A	5673	1	2814	
5628	35996	A	5674	1	2093	
5629	35997	A	5675	1	2724	
5630	35998	A	5676	1	4680	MDKFLDITYLPRLNQEEVESLN RPITGSEIVAIINSLPTKDDPGPD GFTAIFYQRIKYLGIQTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWYGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARITKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNR AEPSEIML PIYNYLIFDKPDKNKQWGKDSL FNKWCWENWLAICRKLKLPFL LTPYTKINSRWIK
5631	35999	B	5677	1	1989	
5632	36000	A	5678	1	2784	
5633	36001	B	5679	1	3573	
5634	36002	B	5680	1	2630	
5635	36003	A	5681	5339	10577	
5636	36004	A	5682	1	873	
5637	36005	A	5683	1	672	
5638	36006	A	5684	1	435	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5639	36007	A	5685	I	1011	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGGGLQPGQR VLYKQSIQARARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMLATIIANC IVLALQHLDPGDKTPMSERLD DTEPYFIGIFCFEAGIKIALGFV FHKGSYLRNGWNVMDFFVVVL TGRKAGLGCCSGVSEGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKE/DVRIHRK EAKNLEKRLDKM/VNRSNVEK TLNDPMELKTMARELCDACTS FSS*FNQVEEKVSVIEDQMDEM K*EEKFREKRVKRNEQSLQEIW DYVKRPNLRL
5640	36008	A	5686	I	1539	
5641	36009	A	5687	I	756	MDDPRLNVKPLTESLETYSKGS KGLEGDVITDSKLNDCRCPST KLPEEGLGSNCCSAIFAVLQPL LVIPRQTGSGVDHQQPTPTDLRM TVRRKMNMKQGIASSTKRTK KDIHTKTPSVCHQHQRPKDCSP SPATEQSWMENDLEELTEIGFR RSVITNFSELKEDVRIHHKKAK NLGKRLDEWLTRINSVEKTLND LMELKTMARELHDSCTSFNSRS NQAEKVSVIDQFNEIKREEK FREKRVKRN
5642	36010	A	5688	I	1008	MVRFGDELGGRYGGPGGGERA RGGGAGGAGGPGGGLQPGQR VLYKQSIQARARTMALYNPIPV KQNCFTVNRSLFVFSEDNVVRK YAKRITEWPPFEYMLATIIANC IVLALQHLDPGDKTPMSERLD DTEPYFIGIFCFEAGIKIALGFV FHKGSYLRNGWNVMDFFVVVL TGRKAGLGCCSGVSEGGWGD RSSSPAMEQSRMENDFDELTEV GFRKSVITNFSELKEDVRIHRK EAKNLEKRLDEWLTRMNSVEK TLNDLMELKTMARELDACTS FSSQFDQVQEMVSVIQDQISEM KREEKFREKRVKRNE/QLQ*I WDYVERPNLRL
5643	36011	A	5689	I	672	
5644	36012	A	5690	I	807	
5645	36013	A	5691	I	1617	

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5646	36014	A	5692	1064	1893	LLEGSININKKDIYTKTQSVGRQ HQRPKVDKTTKMRNQNRKA ENSKNQSASSPPKDCSSSPAME QSWMENNFDELTEIGFRSSVIT NFSCLKEDVQTHCKEAKNLKK RLDECLTRINSVEKKTLNLDLME LKTMAQELHDTCTSFNTQFDQ VEERSVIEDQINEIK*EEKFRE KRVKINE*SCQEIWD*VKRPNI HLITVPESDGEKGTLENTLQDI IQENFHNIAEQANIQIEIQRTA QRYSSRTATPRHIVRFKAVEM KEKVLRAARKKG
5647	36015	A	5693	3	620	EAGWLLSSVDEVKMKENDEL DSISLQKQILSLKSAKIALTESL ISFRERAIEVEKQTQALIM*VAD LQQGNDQTFQGLDGTSELTLI PGDPKHHC GPPGPKVRAYGDO VINGVLAQVQLIVGPVGPWTHP VVISPVPECVIGAILNSWQNP HIGSLTGRVRAIMVGISWQGGQY TFTVLPRQYINFPALCHKTAKR HTARR
5648	36016	A	5694	1	1098	
5649	36017	A	5695	2	563	IIRRAVFRWFVG*RSWGLNMIR PQNTKDSNSNCKLEKTDSPWC ELFKELYKINAFDTPDSSLMRGNE FSDPIHHTFDHMRWRTKEHNEA GWLLSSVDKVMKENDELGDS ISLQKQILSLKSAKIALSESUS CRERAIEVEK*T*ALIMLVADL Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTD
5650	36018	A	5696	1	499	FVLVDVNNMWHRYASMLYER RLLIICSKLSTLTACIHGAAML YPMYWQHVVYTPVLPPHLLDYC CAPMPYLIGIHLSLMEKVRNMA LDDVVILNVDNTNTLETPTFDDQ SLPNDVISSLKNRLKKVSTTTG DGVARAFKKAQAFFGSYRNA LKIEPEEPTFCEEA
5651	36019	A	5697	1	795	
5652	36020	A	5698	103	3531	
5653	36021	A	5699	1	2073	
5654	36022	A	5700	1	901	
5655	36023	A	5701	148	639	
5656	36024	A	5702	1	318	REYGTPEQELNALLTLNFLSL PKGQMLSAAEQHLQKPAKTE A/GRMIWQRDPITKIWEIGKIT WGRGYACVSPGQNHQSVWIPS RHLKSCGHGDAKEEIPGGS

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5657	36025	A	5703	1	612	PTRPKIHITDIPYNSEGOAIVER MNLSLKQQLQKHKKGGK/SKD YGTPHMQLNLALLTLNLSLPLK GQILSVAEQHLQKPAKTEAEQ LVWWRDPITKS*EIGKIITWGK GYACVSPGLTQQPIWIPSRHLK PYHEPDAAEEIIPGSGRGPPPPV/ DSHVETDAEEPHCHEQHLNST ATHLGTDDQEA VTAGGRKPEES KTTSHNK
5658	36026	A	5704	2	791	
5659	36027	A	5705	2301	2620	DGQQLIALHRLALRELQQAGH AGLPQQA KILFDGGSEIGKIRGL QRPRAKNRLSGRGPLREPSPK*F FGVQGRKTLNRTLKGAPH*NL AAKAGKPLSPCTSGRIRM
5660	36028	A	5706	1	1010	MDDIPQEA GRYRHNQAYAYS QGDGAEDDDERIVRFHTRVT DSDTLASDAARLTCRHGLGNQ GSDLVLYGTSTPKNLIWVRVH VVGHRPDRRFFAFDVWSPRLI VDSCSKLEQHSTLSRAILLIYKG FCRFRNHHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGFPTGKRAVSATQLMD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQANVQQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLV FEANTGTENGYQGEESLFNKA YYGGGTNFRKESQKLQQSAK KRDAELANGALGHIELNNDYTL KKVMKPLITSNTVTDEIERANV FKMNGKWYLFDTDSRGSKMTID GINSNDIYMLGYVSNLSLTGPYK PLNKTGLVLQMGDPNDVTF YSHFAPVPAKGNVVTSYMT RGSSR*RQRP*IPCIRSQHGNRK RIPR/SKNLYLTKRTTAAARTSS VKKARSFSLRALKNAMLS*RTAP
5661	36029	B	5707	1	1149	
5662	36030	B	5708	55	3947	
5663	36031	B	5709	4	885	

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5664	36032	A	5710	461	1560	SLQTRDLPISEPPSNRIFACWGK PAWTACCNLSLRARR*RAISCCP SH*KRIPRRRIFI*PKRTTAAART SSVKKARSFSRALKNAMS*RT APSVS*S*IMITH*KK*SR*SLQ TRDLPISSEPPSNRIFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGIPDWKAGSERNAI NGAIALIEGFRPLTLEPSSLIVNS CSKLEQHSTLSRAILLIYKGFCR FRNHQTGFSPAGPNQRGPLAA TLGPGGEGQSAVARLTGEKK NHIPGAQYANRLSPRVGRFINAA GTTGFTGKRAVSATQLM
5665	36033	B	5711	1	1458	
5666	36034	B	5712	1	3573	
5667	36035	A	5713	606	1005	GGMLCGTLSPDGEQGSAAVAR LTGEKKHPRGDQ*QKAPLLAR W/RNPLMQLAQ/PDFTGKRRAI DTHRSVSHAHIIIHSSSTLSSDIS HTDAPNTSSNNYVIAITSPSDTA PSTRPLHRIHHHTPIPIATLARP
5668	36036	B	5714	1	1566	
5669	36037	C	5715	29	2314	
5670	36038	A	5716	597	1384	ISYTVPEALSARSNPAACQHAS CRPAACPVASVGSPPQAPGGA GGHRHWPRRRWRLRQRPSPA PGRPRRRPRPRRHRRRPRPH HHAPPPRPSCAETRSRRGGGRR PLPRPLPPGAAGAGHREVGDK AGAAGCGRRVVALAA/PVSPPS SPSSPSPLLSAAVGVAGCFSAE LSDSRLLAPGGEGPLARSPAR CDPAAGSACPAWSSRQRRC ELMCAAGISCWHTGHCTWCSL SFMPPLVLMILAASFRPVAVSSH
5671	36039	B	5717	1	3873	
5672	36040	C	5718	356	784	
5673	36041	A	5719	1303	1664	KRRDEIIPCVLKQLLVTFITCR ASCINESANARGEAVCVLGAR VV/SSFHQ*DGQQLIALHRLALR ELQQAVHAGLPQQA KILFDGGS EIGKIPYKSKE*PENRLSVVPVW EQUESTLASV

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5674	36042	A	5720	453	915	TVSRWAMLEHILLFSREPSNKE PET*AHSM*ADDKRFAAYKKK TKGGTERWDKYGRPPANGIRT GENNAKTEHLRDRDQKR/PRER ERAR*TTTEITEQEGSG*GEPVEQ MRKKRAQAWSRRKSTGSGQTET RSVRVTRVGLKTASESRRTM EQN
5675	36043	B	5721	319	1469	
5676	36044	B	5722	164	3112	
5677	36045	A	5723	1	1102	MRWTPGHEITKALQTFQRYTGI QHVHRIGMAERMWCDNRNR HTVSSSGGNRLPNPEHFEAFQS VAQCTYNQTVQLDITAFKKT KKNKHKFYPAFIHILARLMNAH PEFRMAMKQDVSCSKLEQHST LSRAILLIYKGFCFRFNHHQTGF SPAGANQRGPLAATLSGPGGEG QSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPTGK RAVSATQLIYRELFPPQLVQLD PCSVPQMPPSPKSRRAWVSDI ALLEFQKKKEMEKKKEKERKK ELQGGRRRRGGGWGKGRER GGRGKKRRGGGEAIRDAEKAG RLPHPDMEIRGRVEQRVGYTIE QINHMARDVFGTRLRLRAEDVFPP VIGVAAHKGGVYKTSVSVHLA QDLALKGLRVLLVEGNDPQGT ASMYHGWVPLHIHAEDTLLP FYLGEKDDVTYAIKPTCWPLG DIIPSCALHRIETELMGKFDG KLPTDPLMLRLAIETVAHDYD VIVIDSAPNLGIGTINVHPAWGS AISLLEYSPGHLAGFVASIPAPL QLVPRWDTKPVLEDASASSRFS IPQRNPTHILHPTTSFPCNDPTV DAWMRFLITWCLYTSPYSTLM GELFPFYQGMLESTKQGSQVR KVFVWTLVPNWNNTQPSRAI LLIYKGFCFRFNHHQTGFSPAG ANQRGPLAATLSGPGGEGQSA
5678	36046	B	5724	90	6258	
5679	36047	A	5725	837	1485	
5680	36048	A	5726	1	2993	
5681	36049	A	5727	1	123	
5682	36050	A	5728	1	960	
5683	36051	A	5729	507	755	NKRGYKQMEEHSLMLGRKNQ YRKNGHTAQNL*IQCHPHQA TNDFLHRIKGNDFQVHMEPKK SPHRQVNPKEQSWRHAT

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5684	36052	A	5730	274	882	PDQVDRGGAHWQTDADDPWL ADHLQHCQRCGEILRHYSGGIR GNVSAYKCAEHVPAFARLRN PQCGDFQLRDYRLFDSPGVKRR EL*TA YRFCHVAP*LMDLRSG WAAGAVYRYQSH*FTADRLRSV VDMDEAGNHHSQQT\SQDQKI KQRTFSLISGS*TTTRTHGHREGN ITHRGLSRPNTARILCASKAHLG LPLRSSLP
5685	36053	A	5731	114	329	
5686	36054	C	5732	1	1983	
5687	36055	C	5733	1	588	
5688	36056	A	5734	1	597	
5689	36057	A	5735	1	721	MTSYNEQNKKPVTDPNEMAIH EDSNQEFKIAVVNETQSRSSP TEHLMTPPLPTREQPPLT VIF HYLPKSYKTAPPLSPFDSLFGL SQPAPRDMDEAGNHHSQQT K QEOKTKHCMFSLTSGS*TMRT H GHREGTVIHRGLLGQFSQQLN KSEFNTVCREKSGRVLQVNM ESPL*MIQDALQDQTPPKGPITV FL*LFYLDHLLRSSHKVASYLST ESRSRGSITVLFIRCSEP
5690	36058	A	5736	417	696	DRNRKANTACFQHSQVGEQ* EHMDTGKV*SI*YGNYEHTSTC ERMEIQKATTEHLNL*S*SGSFL RFTWKMLQFSKISR SFYQVLKH QQKIM
5691	36059	A	5737	325	1489	RSPTLLMHVHYIKVISWRELLLI WLRAANASINPGVEQSPSGDPK TVTGPFPLRLEAADWVEEASVP KGVHIALSSQEQRAGDPRDLEA PSNLVISERTHRFRVSWTPPSD SVDRYKVEYYPVSGGKRQEVV RTPGVDPDLRLPAIIPQAAWLI.A HLPAPSA PPTLEPTKHTEAQSQ RCWSLLCSVTEVAAPSQVVK EAPPSFHTGTENGYQGEESLFN KAYYGGGTNFFRKESQKLQQS AKKRDAELANGALGIELNNDY TLKKVMKPLITSNTVTD EIERA NVFKMNGKWYLF TDSRGSKM TIDENKIPRNPTYKGREGPLQGE LQTTAQGNKRGYKQMEEHSM LMDRKNQYRENGLT AQAPQPP PSGI*GYTAPCFPWENLI
5692	36060	B	5738	1	873	

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5693	36061	A	5739	274	716	QACYIYTTEYYAAIKNDEF/TVL CRDMDEAGNHHSQQTVTRTKN QTPHVLTHRWELNNENTWTQE GEHHTPGPVMLDSAPPTLGHQT PGSSAFGLWDLHQRRLRPRPQT KGSTVGFPGSEAFKLGLGHYW LSFFPSLQTA YRGTL PFNH
5694	36062	B	5740	134	2283	
5695	36063	A	5741	3	872	
5696	36064	A	5742	1	480	SKLNSGDGCSWGARRGSAHSR SPLPSPLRPRAKMA TEGLHENE TLASLKSEAESLKGLKEERAK LHDVELHQVAERV/VGPGAVC HEDQKDPQRPREQSPVHGLVQ R*EEDRELVTGWEGDRVGFH HKQGARGHHALHVGDMCLC PIGMCHCLWWFG
5697	36065	A	5743	3	387	AKMATEGLHENETLASLKSEA ESLKGLKEERAKLHDVELHQ VAERV/VGPGAVCHEDQKDPQ RPREQSPVHGLVQR*EEDREL VTGWEGDRVGFH HKQDPDSER RWHMCPVGRGERAAAAELPRT
5698	36066	A	5744	1	1575	
5699	36067	A	5745	20	510	
5700	36068	A	5746	1	1392	
5701	36069	A	5747	1	1560	
5702	36070	A	5748	3	325	
5703	36071	C	5749	206	409	
5704	36072	A	5750	1	855	
5705	36073	C	5751	233	571	
5706	36074	A	5752	1	3600	
5707	36075	A	5753	1	4137	
5708	36076	A	5754	3	1357	
5709	36077	A	5755	3	194	
5710	36078	A	5756	3	269	
5711	36079	A	5757	1	1770	
5712	36080	A	5758	164	411	RKNRKPNTAFLTHKWELNNEN TWTQGGNITHQG/CWGVQG*R RDSIRRN1*CKCRVPGCSKPPW HVVYTYTNLHILHMPRT

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5713	36081	A	5759	1	3095	MKMADAKQKRNEQLKRWIGS ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLLKLLHR GADINYNVDGLTALHQACID DNVDMVKFLVENGANINQPDN EGWIPLHAAAACGYLDIAEFLIG QGAHVGA NVNSEGDTPLDIAEEE AMEELLQNEVNRQGV DIEAAR KEEERIMLRDARQWLNNSGHIN DVRHAKSGGTALHVAACKGY TEVLLKLLIQAGYDVNIKDYDG WTP.LHAAAHWGKEEACRILVD
5714	36082	A	5760	1	591	FTVTRCYAVAQEGTYFDGSGY AALVKEGYKVQSDVNITLVS NIPRRNGVFLGISTAIVHAI GLEL VDGKVL FHVNNAGRITAAYE PKTATVLCDGK WHTLQANKSK HRITLIVDGN AVGAESPTQSTS VDTNNPIYVGGYPAGVKQKCL RSQTSFRGCLRKALIKSPQVQS FDFSRAFELHGVFLHSCPGTES
5715	36083	A	5761	340	739	
5716	36084	A	5762	1234	1897	
5717	36085	A	5763	1	4070	VTPRAAWLGLGFRGSAVLGLC WQPRSPPSRAAGMMNRTPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQLQFESQQ TISRTHEIKKQVDGLIRETKATD CRLHN VFNDFLMLNTOFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVEILILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
5718	36086	A	5764	1	972	

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5719	36087	A	5765	1	2193	MVPYSLLVTWLQKALGVRQY HVASVLCQRAK VAMRPFEPKY IHVDLLEKNINIVCK*LNRLTL SEKIVYRHPDDPTSQEIERGGTY LQQWPDSVTMQD/ATAQMAM LQFISSRL/SKVTMPSTIHC DHLI EAQLGSEKDLHQAKDINHEVY NFLATGSVKYGLSFWKPGSGII HQHILENYEYPGVLLIGTDSHTP NGGSLGGICIGVGA/DAVDVM TGIPWELCKCPKVIQVGLMGSLS GWTSPKDVILK VAGILTMKGG TGAIVEYHGPVVDISCTGMVT VCNMGLEIGTTSVFHYNLRM KKYMSKTCQADIANLADEFKD HLVPDPGCHYDQLIEVNPSELK LHNGPFTPDLAHPVAEVGKVA EKEEWPLDI*VGLWGCTNSSY EDMGCSAGVAKQALAHGLKC KSQFTITPCSEQIRASIEQDGYA QTLRDVGGIVLANACGPCIGQL HRKDINKQEKNIIVTSYNRNF GHNDTNPETHAFITSPETVTAL AIVGTLKFPNETNYLTGKDGGK FKLEAPDADELQAEPGPQDQT YQHP*PWGTTDHI SAAGP*LKFR GHLDTISNNLLSGAINIENGKAN SVHDAVTHEFGPPD TARYKK YGISWVWIGD*NYGKGSSWEH AALEPHRLGGRAITKSFARIHE TNLRRQGLLPLTFADPADNKIH LVDKLTIQSLKDLT/PGKPLKYI
5720	36088	B	5766	3	1205	
5721	36089	A	5767	435	1428	
5722	36090	A	5768	1	615	
5723	36091	A	5769	79	381	DKPOPHLQHTRTSKRLNRSSQA FLQNLPLQELATSAGNLAIRP NACSLGFLVSRVPSLAATPRAP WNSGPRLSD*LLPRSSRLSS*RL TLPDRLGSPVDH
5724	36092	A	5770	38	452	
5725	36093	A	5771	435	524	
5726	36094	A	5772	284	411	
5727	36095	A	5773	1	354	
5728	36096	B	5774	1	942	
5729	36097	A	5775	1	417	
5730	36098	A	5776	88	279	EDLGRSQSESLGPEFG*VVAIE TIWPTPEKIFTICLSGSHSQSPW NSGPRLSD*LLPRSSQLSS*RLT LPNRLRSLQDHHRCR

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5731	36099	A	5777	206	816	FIDSMSPSRVQ*LSSQNWKKL L*ISYGTKNPEA*PKQS*AQRTK LEASH*LTSNCTTSLH*SKQHGT GTKTEKT*AIPFT*AWAKTS* LKHHQKWQQKPK*TKKIKYLG IQLTTDVKDLFKENYKPLLNEI KEDTNKWNIPCSWIGGINIMK MAILPKVIYRFNALPIKIPMTFF TELEKTTLNFIWNQKRARIAT LSTKNKAGGITLADFKLYYKPT LVKTAWYWYQNREENLGNTIQ DIGMGKNFMTKTPKAMATKA KIDKRDLIKPKSFCIAKETTRM NRQPTWEWELFAIYPSDKALIS GIYKDLKQIYKKNNPIKKWA KEMNRHFSKEDIYAANRHVKKN AHHHWSSEKCKSKPQ
5732	36100	A	5778	502	600	
5733	36101	A	5779	51	452	ADKQLQQLRQNGCTKITSILI HQQTNRPNHE*TPHNCFK NKIPRNPTYKGCEGLQGLQT TAQGNKKGYQMEEHSMMLG RKNQYRENGHTAQELEKTKVH MEPKSPHRQVNPKEQSWR HHIT
5734	36102	A	5780	381	528	LPPPLPAGLC**DQQQNSNAPLI H*EKERPDDSYRIFLPRYHFHD DRI
5735	36103	A	5781	1	477	
5736	36104	A	5782	180	496	TPHNCYKENKIPGNPTYKGCE GPLQGLQTTAQ*NRGQKQM EEHSMMLMDRKNKYHEN/EPYSP R*FIDSMSPSNYQ*LSSQNWK KLL*GPYGTCKEPT*PRQS
5737	36105	A	5783	1	533	MGPEICTDKLSDADVTVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIEHSIKWKNIPSSWVG RISIMKTAIPLKVYIRIKDDEWN IYRRYTEFRSLHHKLQNKYPQV RAYNFPPKKAIGNKEAVLCHG R*HDCISRKPHRLSPKSP*ADKQ LQQLRQNGQCAKITSILYQ*QT NREPHE*TPHNCFKENKIPRN PTYKGCEGLQGLQTTAQGN KRGTFHQMEHSILMGRKNQY HENGHTAQGLHPDKRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
5738	36106	A	5784	599	870	TPANQQHYRRMTLQLKENQTN RKRRQKQHQKRPKNPIQRS ATSKIKGDGSIQ*MLPWGQSP QKALTLATAPEQRKDTPPVRGL SLQD
5739	36107	C	5785	1	1170	
5740	36108	A	5786	317	960	KWPYCPQRQFIDSMSPSSYQRL SSQNWKLL*SSYGTKKEPTSP SQS*AKRTKLEASRYLTSNYTT RLQ*PKQHGTTKTEI*INGTQQ SPQK*/OPHVYNYLIFNKPEKKK QWKGDSLNFKNWDMDEVGNHH SQQTITRTGNQTPHVFTHRWEL NNEITWTQGAGHHTPGPVVGL GAGRGIALREIPNANDELMVQQ TNMAHIYLCIKPARCADVP
5741	36109	A	5787	903	1050	LPPLPAGLC**DQQQNSNAPLI H*EKERPDDSYRIFLPRYHFHD DRI
5742	36110	A	5788	281	491	SFGYIPNSNGMAGSNGISSRSLR NRHTDFHNG*TSLSHQQCKSV PISPHPLQHLLFPDFLMAIALTGV R
5743	36111	A	5789	1	381	
5744	36112	A	5790	1	3231	
5745	36113	A	5791	1312	1463	KGSATCSPQANATTTTALQML GGIPWGNACGIFTRPPPTYLN THLSTR*RPLLLLLKCVR*KGSA TCSPPQANATTTTALQMLGGIP WGNACGIFTRPPPTYLNTHTLS TR
5746	36114	A	5792	811	1065	IS*VSFMSITH**WKKKEQQLLG CWL*A*M*SMLICV*RER*THKL E*LILCI*RMKKILEIQKGMFKL LPY*TKRIMLK/TLNRQLNSTVS SLHSRVDSLEKSNTKLIIEELAIA KNNIIKLQENHQLRSENKLLIL MKTQQHLEVTKVDVETELQTY KHSRQGLDEMYNEARRQLRDE SQLRQDVENELAVQVSMKHEI ELAMKLEKDIHEKQDTLIGLR QQLEEVKAINIEMYQKLQGSSE GLKEKKEIIVRLYWSALCG
5747	36115	A	5793	1	1353	
5748	36116	A	5794	78	503	TKELLHSKRNYHQSEQATYRM GENFCNLLI*QRANIQNLQ*TQT NLQEKKNQPHQKVGEGYQQTL LKRRHLCSQKTHEKMLITGHQ GNTNQNHNEIPSHTS*NGDH*K VRKKQGHG*SWKPSFSANYRK DKKPNSTCSHSQ

SEQ ID NO:	SEQ ID NO: in peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
5749	36117	A	5795	2	200	YGLMIRTIPVDPTRITTSVSLTV RLATMNP RSRPAPVDLTAPGPP HLHKNQKSSQHSQYLDLTSYC
5750	36118	A	5796	76	195	
5751	36119	A	5797	1	2445	
5752	36120	A	5798	207	475	TNLQEKKNQPHQKVGKGYEQT LLKRKHSCSQQTYEKMLITGH QRNANQNHNDIPSHSS*NNDH* KDRKQQMLERM*RNRNAFTLL VGV
5753	36121	B	5799	1	681	
5754	36122	A	5800	1	798	
5755	36123	C	5801	78	245	
5756	36124	A	5802	16	491	EPYPDRPREPKRDPESWSGLW DKGGLVLSLGRTRTEAHTALS RLRASMWIDRSTRASVHFTLY NPPTQLFTSVSLRVEILPTGSLV PSSLVESFSIFRSDALQYHMLML PQLVFLALSLIHLVCVQLYRMMD KGVLSYWRKPRNWLEVASLVS FSFEK
5757	36125	A	5803	3	2791	
5758	36126	A	5804	219	392	
5759	36127	A	5805	1	1044	
5760	36128	A	5806	1	360	
5761	36129	A	5807	1	528	
5762	36130	A	5808	127	360	
5763	36131	A	5809	1	421	GRRSRLAMRPLSMSYFDLSDV TTPESTKNLVESSMVNGGLTSQ TKENGLSTSQQVPAQRKKLLR APTLAELDSSESEETLHKSTSS SSVSPSPFPEEPVLAEAVFTRKKP PKFLPISSTPQPERRQPPQRRHSI EKETP
5764	36132	A	5810	328	1086	
5765	36133	A	5811	1	2076	
5766	36134	A	5812	1	450	
5767	36135	A	5813	901	1506	
5768	36136	C	5814	17	106	
5769	36137	A	5815	24	330	ARDQPI/PKKGTVGEFEPADNK CLLRATDGKKKISTVVSSEKVN KFQAMAYSNLLRANMDGLKKR DKKNKTKTKTSSSSSSSSPA AATAATTAATTAATAAQ
5770	36138	A	5816	1	2247	
5771	36139	A	5817	1	339	
5772	36140	A	5818	3	463	
5773	36141	A	5819	3	83	
5774	36142	A	5820	1	642	
5775	36143	A	5821	2	583	
5776	36144	A	5822	193	409	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5777	36145	A	5823	3	425	
5778	36146	A	5824	1	450	
5779	36147	B	5825	82	2096	
5780	36148	B	5826	1	1554	
5781	36149	A	5827	129	522	LCTDNIEITSKVHLHCSHHGAG LGTCSPLCLSLPPPWAPVQPEP PR*APPPAPQRPVPSTIQGRKRL QLHS*SQ*DH/DAHAKVCSFTPE PARPRTHQKEETPNTSEHQKKQ TPDTPPLRTVTLTARLHGF
5782	36150	A	5828	1	541	
5783	36151	A	5829	1	714	
5784	36152	A	5830	188	287	KELPSGGHYNCRAPSSPHAGS S*SGHQPNSSQ
5785	36153	A	5831	71	689	SPVLDCCPGPLPSEESW/EQPV TRQYPLRPEVHKGLQNVKHLK APGLVRKCSHCNTPILGVQKP NGQWRLVQDLRLINEAVVPLY PVVNPNTLLSQTPEEAEWFMV LDLKDFAFFCIPLHSDSQFLFAFE DPTDHTSQITWMVLPQGFDRSP YLFQALAQDLGHFSSRGTLVL QYADLLFATSEASCQATLD LLNFLANQ
5786	36154	B	5832	45	1148	
5787	36155	C	5833	233	319	
5788	36156	C	5834	11	133	
5789	36157	A	5835	215	849	IKRLPLMKRMWL*LQPESEIA GILVQ*MIE*QPKKGTNSIPVSK PSPVVQKPNQGWQVQDRLRI SDAVIPLYPAVSNPYTLLSQILE EAEWFTVLDLKDFAFFCIPLRSD SQFLAFEDPTDHTSQITWTVF TQGFMDTPHLFGQSLAQDLGH FSSPGTLVLQYVDDLLAKQQA TLDLLNFLANQGYKLSKLKAQ LCELLVFSSCARMHS
5790	36158	A	5836	1	449	MNKELGISSYKFCGMGRKTSVS AAKSVSATIPISRVQGLLQVLG QEVFLLLCQDQEEQAKREKRD QRKATALAMALRQITNLGGSER IENGAGQSPSRACYQCGLQGHF KKDYPTREPAAPCPLC*GNHW KMHCPGRQSCDSHLAITHL
5791	36159	A	5837	1	723	
5792	36160	A	5838	186	602	
5793	36161	A	5839	1	843	
5794	36162	B	5840	1	1779	
5795	36163	A	5841	1	1182	

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5796	36164	A	5842	23	302	LSQWKNRWTRTFLASLSVIANI LEPLLNILHVAVWLM.PN* [*] S* [*] V KKQVIM/FWNWWVLGLTDFKN EATDPRVCSWPCWLRSEADL CGECYSS
5797	36165	B	5843	1	2622	
5798	36166	A	5844	279	1024	
5799	36167	A	5845	3	3619	
5800	36168	B	5846	1	1898	
5801	36169	A	5847	1	420	
5802	36170	A	5848	1	1632	
5803	36171	A	5849	1	597	KYLTKKTQAASVEAVKMLDEI LLQLSASVPVDVMPGEFDPNTY TLPQQPLHPCMFPLATAYSTLQ LVNTNPYQATIDGVRFLGTSGQN VSDIFRYSSMEDHLEILE*LRVR HISPTAPDTLGCYPFYFCGNTPS FGSKIIRGPEDQTVLLVTVPDFS ATQTACL VNLRS/LACQPSISFG FGAEDDDLGGGLGWAPDSKKW
5804	36172	A	5850	1	1490	RDAARRALNLLGLEAVVWTKQ VRSVAMFSEQAAQRAHTLLSP SANNATFARVPVATYTNSQPF RLGERSFSRQYAHYATRLIQM RPFLENRAQQHWGSGVGVKKL CELQPEEKCCVVGTLFKAMPL QPSILREVSEHNLLPQPPRSKY IHPDDEL VLEDELQRIKLKGTID VSKLVTGTVLAVFGSVRDDGK FLVEDYCFADLAPQKPAPPLDT DRFVLLVSGGLGGGGGESLLG TQLLVDTVGTQLGDEGEQCSA AHVSRVILAGNLLSHSTQSRDSI NKAKYLTCKTQAASVEAVKM LDEILLQLSASVPVDVMPGEFD PTNYTLPQQPLHP/CMFPLATA YSTLQLVTNPYQATIDGVRFLG TSGQNVSDIFRYSSMEDHLEILE WTLRVRHISPTAPDTLGCYPFY KTDPFIFPECPHVYFCGNTPSFG SKIIRGPEDQTVLLVTVPDFSAT QTACL VNLRLSLACQPSISFGF AEDDDLGGGLGLGP
5805	36173	B	5851	13	441	
5806	36174	A	5852	3	279	

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5807	36175	A	5853	23	841	EKAKEFRRAEEKKKEVPAPVET LKKK*RNFAELKIKRLRKKFA QKMLQRARRKFIHEKAKH\YH KEYRQMYRTEILMA\RMARKA GNFYVPAEPKLA\FVIRIRGINV SPKVRK\VLQLLRLRQIFNGNLL *SSTKASINMLRDCRSHILAWG VPQILKSVNELIYK\IRGYGKINK KRIA\LTDN\ALIASLGGKYGIL LAWEDLIHEIYTV\GK\RFKEAN NFPVGP\SNLSSPPRWK*KKKTT HFCKKVEDAGNREGRTSRNP YLEGMDLRCLP
5808	36176	C	5854	57	287	
5809	36177	A	5855	1	450	
5810	36178	A	5856	1	549	
5811	36179	A	5857	3	581	EQRKIPLVPENLLKKRKAYQAL KATQAKQALLAKKEQKKGGK LRFKRLESFLHDSWRQKRDKV RLRRLEVKPHALELPDKHSLAF VVRIERIDGVSLLVQRTIARLRL KKI\FSGVFVKVTPQNLM\LRIV EPYVTWGFPNLKSVRELILKRG QA\KVKNKTIPLTDNTVIEEHLG ECYSLGVSWGRKPGSLKL

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5812	36180	A	5858	1	2652	MFGRSRSWVGGGGHGKTSRNIH SLDHLKYLHVLTKNNTTVTEQ NRNLLVETIRSITELIWGDQND SSVDFDFLEKNMFVFFLNILRQK SGRYVCVQLLQTLNILFENISHE TSLYYLLSNVYVNSIIVHKFDFS DEEIMAYYISFLKTLCLKNNH TVHFFYNEHTNDFALYTEAIKF FNHPESMVRIAVRTITLVYVKV DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDDCVQTDDEHR NRGKLSDLVAEHLDDLHLNYND ILIINCEFLNDVLTJILLNRLFLP LYVYSLENQDKVFLIIHAPLV NSLAEVILNGDLEMYAKTEQD IQRSSVLPPTSSLWQGSLSLNQ LQSGHLKCSHLCGAQAADS VTGEIPAIRSLWELISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLQALPSNRLTDVAAV HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPAKPSIRCFIKPTETLER SLEMNKHGKRRVQKRPNYK NVGEEDEEEKPTEDAQEDAE KAKGTEGGSGIKTSGESEIE MVIMERSKLSELAASTSVQEQN TTDEEKSAATCSESTQWSRPF LDMVYHALDSPDDYHALFVL CLLYAMSHNKENLLKKRKAYQ ALKATQAKQELLAKKEQKKGK GLRFLKLESFLHDYWQQKPKD
5813	36181	A	5859	1	405	LEISIMAAISISGYTFSVACFHSA NSNADHEGFLJ.GEVRQEETFSS DSQISNTEFLQVIKVIWYRFR RNTQQQMSYREQVLHKQLTRI LGPVPLVFLFISFISTANNSTHA LEYVLFRRPNRRYNQRISLAIPN
5814	36182	B	5860	1	843	

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5815	36183	A	5861	3	1260	EISIMAASISGYTFSAVCFHSAN SNADHEGFLLGVEVRQEETFSSID SQISNTEFLQVIQIYNHQPCKSL FSFYDYASKVNEESLDRILKDR RKKVIGWYRFRNTQQQMSYR EQVLHKQLTRILGVPLVFLLF SFISTANNSTHALEYVLFPRNRR YNQRISLAIPNLGNTSQQEYKV SSVPNTSQSYAKVIKEHGTDF DKDGVMMKDIRAIYQVYNALQE KVQAVCADVEKSERVVESCQA EVNKLRRQITQRKNEKEQERRL QQAVLSRQMPSCSLDPAFSPRM PSSGFAAEGRSTLGDAEASDPP PPYSDFHPPNQESTLSHSRMER SVFMPRPQAVGSSNYASTSAGL KYPGSGADLPPQRAAGDSGE DSDDSDYENLIDPTEPSNSEYSH SKDSRPMAPHPDEDPRNTQTSQI
5816	36184	A	5862	1	742	
5817	36185	A	5863	1	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPFVQNCLS LARSDSREQGLVLMVESNRNE VVPVGVSYSKDGAKSLKGDVP ASEVTSKDSFQSFPSSAEEC GDDEKIKVDDPLTRTCNQASG SAPQQDYDKLKAFGGENSSTK GLSPSGNMEKNVVKREAEAN SINLSVYEPFKVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
5818	36186	A	5864	2	626	LCQHNRKIKHGIRKVVYACSHCP DSRRTFTKRLMLEKHVQLMHS LKDPDLKE/TDRCHQ*GGNRNK RRH/LSSPVPVSGSWKNQFSR/CA MCGFTTENLLQFHEHIPQHKSD SSSYQCQECGLWYTSHSVLSRH LFIVHKLKEPQPVSKQNGAGED NQQENKPSHEDESPNGITVSDRK CKVCVKTFETEAAALNTHMRIH GMAFIKSKRMSSAKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5819	36187	A	5865	1	765	MQRDVYISHVRKEHGKQMKK QPCQQRDKPFSSSHSLCWHNR1 KHKVIRKVYTCSHCSDSRGTFT KQLMLEKHVQLTHGIKDPDLK E/TDRRHQ*GGNRNRKRPQGPQ SQVEVERTGSGVQASQ\GAITQ PLKCLKINVFVHKCARA\GFT TENLLQFHEHIPQHKSDGSSYQ CREHLFVVHKLKEPQPVSKQN GAGEDNQENKPSHEDESPNG AMSDRCKCKVCAKTFETEALN THMQTHGMAFIKSKRMSSDEK
5820	36188	A	5866	878	1095	AFFLDTLYTQFSRC*SRAVFVFA HPTAMACSSRR/LIRVQEQDAA QVTHQSFKDDL CVVLGDTLHH RFLLIFRH
5821	36189	A	5867	1	1137	
5822	36190	A	5868	1	1380	
5823	36191	A	5869	55	558	
5824	36192	A	5870	1	897	
5825	36193	A	5871	1	565	
5826	36194	B	5872	22	1696	
5827	36195	A	5873	295	522	
5828	36196	A	5874	3	3678	IPAPVSGRPPGLLAEGKLSGPR PMCRTRLGSHTAASAPARMWL FHTLLCIASLALLA AFNV DVAR PWLTPKGGAPFVLSLLHQDPS TNQTWLLVTSPTKRTPGPLHR CSLVQDEILCHPVEHVPIPKGRH RGVTVVRSHHGVLICIQVLVRR PHLSSELGTGCSLLGPDLRPQA QANFFDLENLLDPDARVDTGD CYSNKEGGEDDVNTARQRR LEKEEEEDKEEEDEEEEEAGT EIAHLDGSGSID
5829	36197	A	5875	1	3189	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in US\$N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5830	36198	A	5876	1119	2463	LRAGGPGQGGKGAHPGRRVD ELL.LGHPTAVGCAKGTDCPTPT PGGLWV*GVQEESDLPTAVDS SRPDIRDQAWASVHWELVYVHG SSFINT*GERGAGY/AVITW/STV VEARSMPPQGTSAQKAELIAFIR ALELSEALAKTVRQRCVSCRQ HHARQGPVAVPGIQAYGAAPFE DLQVDFTEMPKCGDIRKIVTGD VNTPAILGVVSSPPSHIGNNITE DPELQPILAGLSMYLVTVLR NLLIILAVSSDPHLHTPMCFFLS NLCWADIGFTLATVPKMIVDM QSHTRVISYEGCLTRISFLVLFA CIEDMLLTVMAYDCFVAICRPL HYPVIVNPHLCVFFLLVYFFLSL LDSQLHSWTVLQFTIKNVEISN FVCDP\$QLLKLACDSVINSIFM YFHSTMF\$FLPISGILLSYKIVP SILRISSSDGKYKAFSTCGSHLA
5831	36199	B	5877	1	1830	
5832	36200	C	5878	109	245	
5833	36201	B	5879	1	801	
5834	36202	B	5880	171	288	
5835	36203	B	5881	49	502	
5836	36204	B	5882	1	639	
5837	36205	A	5883	1	821	MSGQFDFLLWTP\$EDNSDESD AEGEHGDGAEEEEAPPVPRPGP KPAGLGRRPCPYEQAQGGDGP EEQWMSFCWDIPRKS\$APRERI TLRRHLED\$CGCKV\$K\$KKAQICR QKQDPQ\$E\$PAQFYERLCEAYG MYTPFD\$P\$PENQRM\$H\$MALV RQ\$AEDMRRLQKQAGLAGM NPSQLLERASQVFVNRDAV/TP** GKQ\$REWRERG*YDSQYRRGG TQPCDIVPNIRRERR*YHSQYRR RARPPGPH*SERGALRPGSLPRQ AA*RVPSG\$ADGQ
5838	36206	A	5884	1	1860	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5839	36207	A	5885	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKQESWRHHTT*LQTLQG YSNQNSMPGTPQ*PSTPAPGG NLNRNPQSSDLLQVTKQQGQAL AIQREAPLHRIPAPEAIPWYFQP QPAATQLGSPVPDPSSAMM/SR RAHRSRGPDRQGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQAATQHPEEPDAHQPYKH LFQVCAHQGHVPVAQRNR*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRLNLLIS
5840	36208	B	5886	1	2379	
5841	36209	B	5887	1	6741	
5842	36210	B	5888	165	928	
5843	36211	A	5889	56	2028	
5844	36212	B	5890	1335	3804	
5845	36213	A	5891	365	1573	
5846	36214	A	5892	1	1491	
5847	36215	A	5893	25	458	
5848	36216	A	5894	1	1194	MGGNAADKFRAGVELALQSG NKVCVCSPRTTISGDAVAPRSV LPGCRHIPGEISQSHCWAGRS LSSRKRGSLFRMGFIKVVKNK AYFKRYQVKFRRRIRKGTDDY YARKRLVIQDKNKYNTPKYR MIVRVNTNRDNIICQLYA/RRIE GDMIVCAAAYCTPNLPKIWV*RV GLTNYAAAYCTGLLLVARRLL NRFGMDKIYEGQVELTGDEYN VESIDGGQPGAFCTCYLDAGLAR TTTGKNVFGAPEGLWMGGLS IPHSTKVRFGYDSEISKEFNAIE VTSGKHIMGPCKCLQNYMRYL MEVEDIEDAYKKQFSQYIKNS VTPDMMMEEMK/KAHAIRE ESSMEKKAQGGKFKKKRWNR PKMSLAQKKDRVAQKKASFL QSSRSGLLESLETPAIFP
5849	36217	A	5895	1	1191	
5850	36218	A	5896	21	159	PRSSVRPAGGFSSTCPPSWAAS RSCCTSHGCGHQ*CAAGTGQTR L
5851	36219	A	5897	1	1062	
5852	36220	A	5898	1	246	
5853	36221	A	5899	1	642	
5854	36222	A	5900	2	648	
5855	36223	A	5901	1	555	
5856	36224	B	5902	151	513	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5857	36225	A	5903	1	2915	VSLAFCQPLSLSLSPLLPLASSL APERTHLPGGSLLLSPSPFAR PREPRGCVTAAPPDKMDTAE DICRVCSEGTPEKPLYHPCVC TGSIKFIHQECLVQWLKHSRKE YCELCCKHRFAFTPIYSPDMP SRL PIQDIFAGLVTSIGTAIRYWFHY TLVAFARWEVLLPACRIYKCL FLGSVSSLLTLPLDMLSRKNLL ADCLQGC/VVVTCTLCAFISLV WLREQIVHGGAPIWLEHAAPPF NAAGHHQNEA
5858	36226	A	5904	3	907	
5859	36227	B	5905	102	406	
5860	36228	B	5906	1	5241	
5861	36229	A	5907	1	519	
5862	36230	A	5908	1	3067	TRDAAMAEAALEAVRSELREF PAAARELCVPLAVPYLDKPPPT LHFYRDWVCPNRPCHRNALQH WPALQKWSLPYFRATVGS TEV SVAVTPDGYADAVRGDRFMM PAERRLPLSFVLDVLEGRAQHP GVLYVQKQCSNLPSELQLLPD LESHVPWASEALGKMPDAVNF WLGEAAAVTSLHKDHYENLYC VVSGEKHFHPPSDRPFIPYEL YTPATYQLTEEGTFKVVDEEA MEKAEVSRCTLLTVRVLQA
5863	36231	A	5909	1	429	
5864	36232	A	5910	1	690	
5865	36233	A	5911	1	376	
5866	36234	A	5912	1	471	
5867	36235	A	5913	1	606	
5868	36236	A	5914	3	2756	SPGGRTPAARDSIVREVIQNSKE VLSLLQEKNPAPFKPLAIQAG DDNLMQEQINQNLAEEAGLNITH ICLPDSSEAEIIDEILKINEDTRV HGLALQISENLFNKNVNAKLP EKDVGVDINLGLKLVGRDAH ECFVSPVAKAVIELLEKSGVNL DGKKILVVGAGHSLEAALQCLF QRKGSMTMSIQWKTRQLQSKL HEADIVVLGSPKPEEIPLTWQIP GTTVLNCSHDFLSGKVGCGSPR IHFGGLIEED
5869	36237	A	5915	3	404	RLKEKKLVKEVIAVSCGPAQCQ ETIR TALAMGADRGHVEVPPA EAERLGPLQVARV/AVVTADLR LNEPCYATLPNIMKAKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETTEDLVAKLKEIG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5870	36238	A	5916	1	334	
5871	36239	A	5917	88	870	MADVRLVAVKRVIDYAVKIR VKPDRTGVVTDGVKHSMPFC EIAVEEAVRLKEKKLVKEIAV SCGPAQCQETIRTAI\MGAD RGIHVE\VPPAEAEERF/GVPLQV ARVLGQAWQRRRLDLVLLGK QAMACTDCNQ\TGQMTAGFLD WPQGTFAASQVTLEGDKLKVER EIDGGLETLRLLKLPVV\TADLR LNEPRYA\TLNIMKAKKKKIE VIKPGDLGVDLTSKLSVISVEDP PQRTAGVKVETEDLVAKLKEI
5872	36240	A	5918	1	774	
5873	36241	A	5919	1	1557	
5874	36242	A	5920	1	759	
5875	36243	A	5921	305	638	
5876	36244	A	5922	364	540	
5877	36245	A	5923	9	111	
5878	36246	A	5924	1	594	
5879	36247	A	5925	169	594	
5880	36248	A	5926	37	936	
5881	36249	B	5927	91	2043	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
5882	36250	A	5928	1	2298	MSRKGPRAEVCADCSAPDPGW ASISRGVLVCDECCSVHRLGR HISIVKHLRHSAWPTLLQMVH TLASNGANSIWEHSLDDPAQVQ SGRRKANPQDKVHPIKSEFIRA KYQMLAFVHKLSCRD/DDGVT AKDL/SKAN*HSSVR/TGKPWK TCLRLLS/LGA/QANFFHPEKGT TPLHVAAGAGQTLQAE/LVVY GADPGSPDVNGRTPIDYA/RQA GHHELAERLVE/CQYEL/TERLA FYLCGRKPDHKNHGYIIPQMAD SLD/SELAKAAKKKLQALSNRL FEELAMDVYDEVDRREND/AV WLATQNHSTLVTERS/AVFPLPV NPEYSATRNQGRQKLARFNAR EFATLIIDILSEAKRRQGGKSLSS PTDNLELSLR/SQDLDDQHDYD SVASDEDTDQEPLRSTGATRSN RARSMDSSDLDGAVTLQEYL ELKKALATSEAKVQQLMKVNS SLSDELRLRLQREIHKLQAE/LQ LRQPPGPVPTPLPSERA/EHTPM APGGSTHRRDRQAFSMYEPGS ALKPFGGPPGDELTTTLQPFFHS TELEDDAIYSVHVVPAGLYRIRK GVSASAVPFTPSSPLLSCSQEGS RHTSKLSRHGSGADSDYENTQS GDPLLGLEGKRFELGKEEDFH PELES/DGDLDPGLPSTEDVILK TEQVTKNIQEL/LRAAQEFKHDS FVPCSEKIH/LAVTEMAS/LFPKRP
5883	36251	A	5929	1	924	
5884	36252	A	5930	214	387	RRAFHPTPVTSARSTLHSGQL RLPHSM*SGGTLISM/QANQS LSLEFSKWTSP/LD
5885	36253	A	5931	1	1639	
5886	36254	A	5932	1	1098	
5887	36255	A	5933	1	546	NSSQV/LQF*YLWVNEAPFRLLT MPQYPYQINITADQLWGSVAVL V*MH/NGLPGLCI*AWEKTTSG GEQYPSSAIKQGPKEPYADFIA RLQESLKKVIADLAAQDVLWL LAFDNANPECQAALRP/IRGKAH LVYD/YTKVCDGIRD/LHKATLL AQAMAGLRMGKGNT/PPGACF NCGKHGH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *~Stop codon, /~possible nucleotide deletion, ~possible nucleotide insertion)
5888	36256	A	5934	1	648	MGQVWGLVHFTLEV FHTGD EEE EQEYSEVTFDVTEHVYLP KVAKEEEAGIQQARQEGDLEA WQFPVRIHPPDQENITATFEFF PFLLKELKQAINQYGPSPFV MGLLKNVTVSSQMIPDGDPLT RACLTQAQFLQFKTWWADEAS IQAARNAWAQFQINITADQLLG VGGWAGLDAQFVMQDDAIEQ LRGVCIAREKVI*CGEQYPSF
5889	36257	A	5935	120	254	
5890	36258	C	5936	366	479	
5891	36259	A	5937	1	933	
5892	36260	A	5938	1	840	MGKVWGLVIHSTLEL FHTDVEE EGEYNEVTEEVTKHVYLP KAAKEGEVHPYHSAPPHYFFE ENDPPDLSFLEDGTGRLAAAA TTKANA/KQPLLLSPSMHR/PLP TRPLLAGIATALPQGV*PLIAP PTRPHLEHCSTQ*RPQAPTLGE ITPVTVPQAPLHPRVQPV/HST PTRSWLQAVMPGIAPSRSPPW AVQLRLTYLGCLSTTPAAVQS LSQPPASVRQARVPQAPASSLC QEKPPSPPPVAPHGAAAAARPP SYHSSCASVAVVAANVLIG
5893	36261	A	5939	1	134	MGQVW*KSQSPKA*EPGVSCP RAGRREASVPRWYSS
5894	36262	A	5940	1	1158	
5895	36263	A	5941	1	673	MGIALGSPPTTGPKAMKQNL SIG PAGILLPQPVMTPGCPAAAPPV APRCGYVLS EDAWGNLQGLCT GLSCGQPVAPWATDSGGAQDP VALLPPFSPRGLLGPSCMQRSQ VVKGGRQSEISSQNKKVIADLA AQDIVLQLLAFDNPANPDCQAA LRPIRGKAHLVDFIKACDVIGGI PNLLHPRGLRAITIAVFGKQIR TSGSNPLRSTFLSRSRISKNCSEA EV
5896	36264	A	5942	1	1182	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5897	36265	A	5943	1056	2128	TQPPTWGQIKKLSQMVEENLR KAGQLVTMNNLMVAMIVVITT TEEQEYSEVTEEVTEQVYLP AKVAKEGEVHPYPSAPPHYF EKEWPPDPLSFLDTRQKVVA PVTVRAAPRATVLSIQAGIQ AR*EGDLEAWQFVRHPPDQ GNIIVTEFPFPLFKEFKQAVN QYGPSPFVMGLLNVAVSSW MIPTDWDALTRACLTQAFLQ KTCAMKQGPPEPYVDFIARLQ SLKKMIADSAAEIVLQLLAFD NAHPDCQAALRPIRGKAHLVD YVKACDGIGEYTPSTYEKKVN CKTASCRSFRYPPEGIVITGDD SSMRVVVPEDLPVGGQDVEVED RDIDDPDPV
5898	36266	A	5944	1	300	
5899	36267	A	5945	1	373	
5900	36268	A	5946	1	2976	
5901	36269	A	5947	287	544	
5902	36270	A	5948	831	4555	
5903	36271	C	5949	108	434	
5904	36272	C	5950	145	402	
5905	36273	A	5951	3	1104	GSRPGGHTLQSHRGRHAQGLR SPLLA PVCLGCGTWGQRRLFW SLKI*RLLCWF/CRRLQINCKNK PAIPRGPT/GPSEKSGLLLDQDG DTTNTTEENSKLENIFGRVIKE NFQSLVRDLDIQYKKHKEHPG NSSQKDHHLGTLSSGYPKLRQR KES*ELSDRSTRKISQS/YNLYTP NTGAPRFIKQLLTLRNEIDSNT IIVGYSTPLTALDRSSRQKVND ETVDLNYTLEQMDLTIYRTFH PTTTEYTFYSTVHGTFKIDHMI CHKMSLNEFKKTEIISSTLSDHS GKLEINSKMNQLQHANTWKL NNLLLNEHWVWNEIKMEIEKFF KLNDSDNTTYQNLWDMAKAV LRGKFIALNTYIKKMM
5906	36274	B	5952	1	2367	
5907	36275	A	5953	21	132	WREGARQCQEDPAEFLSD*DW ADPGPPHNAPGQNVH
5908	36276	A	5954	1	1461	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
5909	36277	A	5955	31	802	SAWWNSRELLDPQSRSGGCF *EYPTSGTEQESVSGNRALCSS LRMNGDQNSDVYAQEKQDFV QHFSQIVRVLTEDEMGHPEIGD AIARLKEVLEYNAIGGKYNRGL TVVVAFRELVEPRKQDADSLQ RAWTVGWCVLQLQAFLVAD DIMDSSLTRRGQICWYQKPGV GLDAINDANLLEACTYRLKLKY CREQPYLNLIELFLQSSYQIEI GADPGPPHSPPRAMWILSDSLK RGTNLLSSTRQLSTPSTFL
5910	36278	A	5956	1	532	RLNEAEQKYKDIQDKLQIIEET NARAPECMALKADVVAKKRA YNEAEVLYNRSLEYKALKKD DEQLCKRIEELKKR/VL.TN/RLE PERLERQKKISWLKERVAFQ QENSVNQIEIQFQQALEKDKKE HGKIKREKLDVKHALSYNQL LKLKDSKTDRLKRFPGNPVPA LEAIDD
5911	36279	A	5957	121	475	
5912	36280	A	5958	131	2891	
5913	36281	A	5959	131	3101	
5914	36282	A	5960	44	292	CQDYRWLLASSVLCWLY*KTQ QSDTEDLLCSAPTGPPEEDD GKS*PEKCRQMT*KKWSINCKC FFASSHTTSLIGLFLR
5915	36283	B	5961	26	239	
5916	36284	A	5962	131	3121	LVSFLLFDALPEGDASPLGPY LLPSGAPERGSPEGHEPPEERV TAPSSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPPIVASE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTSTIIT TTVITTEQAP
5917	36285	A	5963	1	1185	
5918	36286	A	5964	495	636	PSVVLDDINVSFNHWSAIFLTME PFCHRVRSHAMESR*GSVLP*N KPQ
5919	36287	A	5965	2	376	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5920	36288	A	5966	3	688	GTSAGDGC PHPTVLWPPDIMP PKKDVVKKPAGPSISKPAKAP AAAGAPPAKTKAEPVAPQAPQ KTQEPVVDLSKVVFIEFNKDQLE EFKEAFELFDRVGDGKILYSQC GDVMRALGQNPTNAEVLKVLG NPKSDEMNVKVLDFEHFLPML QTVAKNKDQGTGYEDYVEGLRV FDKEGNGTVMGAEIRHVLVTL GEKMTTEEEVEMLVAGHEDSNG CINYEELVRMVLNG
5921	36289	A	5967	54	540	AVYMCDLTENQTADLIPSTVEF KEAFQLFDRDTGDKILYSQCG DVMRALGQNPTNAEVLKVLGN PKSDEMNVKVLDFEHFLPMLQ TVAKNKDQGTGYEDYVEGLRVF DKEGNGTVMGAEIRHVLVTLG EKMTEEDVHMLVAGHEDSNG CINYEAFVRHILSG
5922	36290	A	5968	1	405	
5923	36291	A	5969	93	506	
5924	36292	B	5970	43	615	
5925	36293	A	5971	2	598	TRTSLHAALFSWDVPGTSLTEFI SHLEVKKGMLVGIVGKVCGCK SLLAAIAGELHRWEQVQCGG HTLH*APEQMLRGHVAVRGLS KGFLATQEPWQFATIRDNLIF GKTFDAQLYKEVLEACALNDD LSILPAGDQTEVGEKGVTLSSG QRARIALARAVYQEKELYLLD DPLAAVDADVNPACTGCNP
5926	36294	B	5972	137	371	
5927	36295	A	5973	1	1398	
5928	36296	A	5974	1	915	
5929	36297	A	5975	40	564	
5930	36298	A	5976	62	280	
5931	36299	A	5977	17	744	
5932	36300	A	5978	1	537	
5933	36301	A	5979	242	576	AANSLYKGSNSAALIILVGP*IS CLTHPVYMK*AP* TICLLYSM VILKALFFPQNINIFLPVKSRRHS
5934	36302	A	5980	924	3473	
5935	36303	A	5981	1	604	
5936	36304	A	5982	288	732	RNCIANYDFLILPTSF*WCSEFFV LLFLFLSLSSSLKLHSDLDKGE GTAKYTLSGDGAGPVFTIDETT GDVHAIRSLDREKPFYTLRA QAVDIETRKPLEPESEFIIKVQ DIANDNEPKFWG WDLMAVATGP QK WSPVG*VGQIKIL
5937	36305	A	5983	1	1510	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5938	36306	A	5984	1	603	
5939	36307	A	5985	250	505	GFSPTWQ*MNTHPSLMCFSPSR TTGSAAN*RGQQKSGVPFWS* SHVKGKDQIPVPCPCTTAPVT MESTCIC*PTHVSKCTLMV
5940	36308	A	5986	3	131	RVLVDPDIRGAI*AVPKSPSIKSY ALPRALFLLPPYPDDLGI
5941	36309	A	5987	1	913	
5942	36310	A	5988	5	177	
5943	36311	A	5989	3	383	
5944	36312	A	5990	1	1323	
5945	36313	A	5991	342	594	
5946	36314	A	5992	1	321	
5947	36315	A	5993	3	601	
5948	36316	A	5994	1	1023	
5949	36317	A	5995	1	606	
5950	36318	A	5996	1	1536	
5951	36319	A	5997	2	1394	
5952	36320	A	5998	371	1045	
5953	36321	A	5999	3	360	
5954	36322	A	6000	1	636	
5955	36323	C	6001	1	861	
5956	36324	A	6002	1	711	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met cod	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5957	36325	A	6003	18	2446	AGSPPRADAAAGLWERGHLLS AAVAAMGKRDRADRDKKKSR KRHYEDEDDEEDAPGNDPQE AVPSAAGKQVDESGTKVDEYG AKDYRLQMPLKDDHTSRPLWV APDGHIFLEAFSPVYKYAQDFL VAIAEPVCRPTHVHEYKLTAYS LYAAVSVGLQTSIDITEYLRKLS KTGVPDGMQFIKLCTVSYGKV KLVLKHNRVYVESCHPDVIQHL LQDPVIRECLRNSEGEATELIT ETFTSKSAISKAESSGGPSTSR VTDPPQKSDIPMDLDFYEQM DKDEEEEEETQTVSFEVKQEMI EELQKRCIHLEYPLLAEDFRN DSVNPMDINIDLKPTAVLRPYQE KSLRKMFNGRARGSVIVLPC GAGKSLVGVTAACTVRKRCLV LGNSAVSVQWKAQFKMWSTI DDSQICRFTSDAKDKPIGCSVAI STYSMLGHTTKRSWEAERVME WLKTQEWGLMILDEVHTIPAK MFRRLVTIVQAHCKLGLTATLV REDDKIVDLNFLIGPKLYEANW MELQNGYIAKVQCAEVWCP MSPEFYREYVAIKTKRILLYT MNPKNFRACQFLIKFHERRNDK IIVFADNVFALKEYAIRLNKPYI YGPTSQGERMQILQNFKNPKI NTIFISKVGDTSFDLPEANVLQI SSHGGRRRQEAQRLGRVLRAK KGMVAEEYN AFFYSLVSQDTQ
5958	36326	A	6004	1	933	
5959	36327	A	6005	1	879	
5960	36328	A	6006	1	727	
5961	36329	A	6007	1	1509	
5962	36330	A	6008	1	1698	

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5963	36331	A	6009	2465	2751	VPTSSAPMPWPSRQWERSRT MTVISSSQLMALGP*RTAQVLA AAPA*LGASSAARGIDPQAGKT QKQETDIATMQLCANKLDKKDF FGKSDPFLVFYRSNEDGTFITICH KTEVVKNLTNPVWQFSPVRA LCNGDYDRTVKIDVYDWDNRD GSHDFIGFITSYRELSKAQNNQ FTVYEVLPNPRKKCKKKYVNS GTVTLSSFSVDSEFTFVDYIKGG TQLNFTVAIDFTASNGETRMSE KVGGNPLQPTSLHYMSPYQLS AYAMALKAVGEIIQDYDSDDL FPAYGFGAKLPPEGRISHQFPLN NNDEDPNCAIEGVLESYFQSL RTVQLYGPITYFAPVINQVASLP
5964	36332	A	6010	1	1059	
5965	36333	A	6011	255	405	
5966	36334	A	6012	251	1199	
5967	36335	A	6013	1	1791	
5968	36336	A	6014	335	984	
5969	36337	A	6015	1	127	LPLRLSYEIVLYFTF*KPEHNKS HFLESHLRNTRSA LNTRK
5970	36338	A	6016	1	774	

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5971	36339	A	6017	186	2699	PRGAKPAVPAGPERPGPGPGPC SPRPMVLPTCPMAEFALPRHSA VMERLRRRIELCRRHHSTCEAR YEA VSPERLELERQHTFALHQR CIQAKAKRAGKHRQPPAATAP APAAPAPRLDAADGPEHGRPA THLHDTVKNRLDSATSPQNGD QQNGYGDLFPGHKKTRREAPL GVAISSNGLPPASPLGQSDKPSG ADALQSSGKHSLGLDSLNNKKR LADSSLHLNGGSSNPSEFPLSLN KELKQEPVEDLPCMITGTVGSIS QSNLMPDLNLNEQEWKELIEEL NRSVPDEDMKDLFNEDFEEKK DPSSSGSATQTPLAQDINIKTEF SPA AFEQQLGSPQVRAGSAGQ TFLGPSSAPVSTDSPSLGGSQTL FHTSGQPRADNPSPLMPASAQ AQNAQRALAGVVLPSQGP GGA SELSSAHQLQQAIAKQKREQML QNPQQATPAPAPGQMSTWQQT GPSHSSLDVPPYMEKPA SPSSY KQDFTNSKL/PHDA*CE*EFP SARRPLPPAQCEPAESPATE*LES ELRE/YTRGLCWIRQYKTPFSL QSGLWARQPGVWPEQASPDGL SSPAAVPYKSRAELPVSDEAKA RKYAFPTGSTWPGAEPFQCPC ASPGYQCWDPAACRVRGQLPQ QLPLSQQPATGRCAEASVAFG PTETKGA AAKAFTATAVPSEAT APSRGTGEATVSPSPDPTTPVP
5972	36340	A	6018	1	1062	ASRPVPTLRLVVPASQCGSLIG KGGCKIKIESTGAQVQVAGD MLPNSTERAITIA GIPQSIIECVK QICVVMLESPPKGVITPYRPKPS SSPVI FAGGQAYTIQQQYAI PQP DLTKLHQLVAMQQC/HFPMTHG \NTGFQWALESS/FPEVKGYWA AGLDASAQTTSHELTIPNDLIGC IIGRQGA KIN
5973	36341	A	6019	3	566	TLRSSWQVVRTGTAQAATVRG FPPHPPRPASSTLTLEGPPLEAY TIQQQYAI PQPDLTKLHQLVAM QQSHFPMH/GDGIHSDYSAG/LD ASA\QTTSHELTISKRLIGLA*S GRSRAPKINGGSRQMSGAQIKI ANPVVEGSTD*GRFTITGSAASIS LAQYLINVRLSSETGGMGSS
5974	36342	A	6020	2	531	TLRSSWQVVRTGTAQAATVRG FPPHPPRPASSTLTLEGPPLEAY TIQQQYAI PQPDLTKLHQLVAM QQSHFPMH/GDGIHSDYSAG/LD ASA\QTTSHELTISKRLIGLA*S GRSRAPKINGGSRQMSGAQIKI ANPVVEGSTD*GRFTITGSAASIS LAQYLINVRLSSETGGMGSS

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5975	36343	A	6021	181	1369	PLKVVQLPRTLDMDTGVIEGGL NVTLTIRLLMHGKEVGSIIIGKK GESVKKMREESGARINISEGNC PERIITLAGTH*LPSFKAFAMII DKLGRRDISSMVTNSTAAQLGP PVTLLKGLAPAS/QCGSLIGKGG CKIKEIRESTGAQVQVAGDMLP NSTEAGHHYLLGIPQSIIECVK QILRGSCWETLFPSSPPKGVTPA YRPK/PSSSPVIFVAGPGQVPA QAATVRAFFTTPRPGSTLTWE GPPLEAYTIQQQYAIQPDALT L/HQLAMQQSHFPMTHGNTGF SGIESSFPEVKGYWAGLDAS AQTTSHELTPNGFDWAGIIGA FKGAKINIEIRQMSGAQIKIANP VEGSTDRQVTITGSAASISLAQ YLINVRLSSETGGMGN
5976	36344	A	6022	1	690	
5977	36345	A	6023	1	399	
5978	36346	A	6024	3	397	
5979	36347	A	6025	3	249	
5980	36348	A	6026	177	477	
5981	36349	A	6027	49	451	
5982	36350	A	6028	1	1305	
5983	36351	A	6029	1	568	
5984	36352	A	6030	207	1053	PLTFGPARWRETPPSLYKEFSG LFGSFFLSSAWGAHNLRALFLL LPSSRIQPTPWVFGDLKSPAGL QVLNDYLADKSYIEGYVPSQA\ DVAVFEAVSSPPADLCHALR WYNHIKSYEKEKASLPGVKKA LGKYGPADEVDTTGSATDSK DDDDIDLFGSDDEEESKPKRL REERLAQYESKKAKKPG/LVA KSSILLVKP/WD/DEDTMAKLE ECVRSIQADGLVWGSSKLVPV GYGIKKLQIQCVVEDDKVGTD MLEEQITAFEDYVQSMDDVAAF
5985	36353	A	6031	1	211	
5986	36354	A	6032	27	241	EVFGSWWQVPHEWLGSVLVV MSEFLFH*LM*ELVLKR*CLS HLSLAPFLAM*YACSSSPSTMI VSFFFF
5987	36355	A	6033	1	588	

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5988	36356	A	6034	279	1333	LIFCGCWLFLASLTVMEEAAHFFE GTEKLLLEVWFSRQQPDANQGS GDLRTIPRSEWDILLKDVQCSII SVTKTDKQEAAYLSESSMFVSK RRFILKTCGTTLTLKALVPLKLI ARDYSGFDSIQSFYSRKNFMK PSHQGYPHRNQEEIEFLNAIFP NGAGYCMGRMNSDCWYLYTL DFPEERVISQPDQTEILMSELD PAVMDQF*HEDGVTAKDVTRE SGIRDLPGSVIDATMFNPGYS \MNGMKS\DGTYWT\IHITPEPEF SYVSFETNLQTSYDDLIRKVV EVFKPGKFVTTLFVNQSSKCR RLGLPQK\IEGFKRLDCQEGWF KDSNFFVTSFAKKQQQQQS
5989	36357	A	6035	1	687	
5990	36358	A	6036	1	894	
5991	36359	B	6037	1	1458	
5992	36360	A	6038	1	1062	
5993	36361	A	6039	1	1218	
5994	36362	A	6040	277	3508	RSGRIAWAQEMDAAGRCHLL PLPAARGPARAPAAAAAAS PPGPCSGAACAPSAAGAGAM NPSSSAGEEKATGGSSSSGSG AGSCCLGAEAGDPRGAGSAA AAGAAALDEPAAGQKEKDEA LEEKLRNLTFRKQVSYRKAISR AGLQHLAPAHPLSLPVANGPA KEPRATLDWSENAVNGEHLWL ETNVSGDLCYLGEENCQVRFA KSALRRKCAVCKIVVHTTACIE ELEKINFRCKPTTFREGIS
5995	36363	A	6041	45	155	
5996	36364	A	6042	1	979	
5997	36365	A	6043	3	1042	
5998	36366	A	6044	2	401	
5999	36367	A	6045	1	5772	
6000	36368	A	6046	16	5678	VTSGRLLFYFRSMGPGCDLLLR TAATITAAIMSDTDSDEDSAG GGPFSLAGFLFGNINGAGQLEG ESVLDECKKHLAAGLGLGLG SLITELTANEELTGTGALVND EGWVRSTEDAVDYSINEVAE DESRRYQQTMGSLQPLCHSDY DEDDYDADCEDIDCKLMPPPPP PPGPMKKDKDQDSITGEKVDFS SSSDSESEMPQEAQTAESEDG KLTLPLAGIMQHDAKLLPSVT ELFPFRPGKVLRLR
6001	36369	A	6047	1	354	

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6002	36370	A	6048	1	666	
6003	36371	A	6049	129	456	TYPAVGESSRRPERSRGVPGPD AAAESHFRPGRI SNPLHRAEQ GHARAEGSGVFRPHRGRGLRL LRVQAPDQVDAPVHG*VAPPAP GARDAQTCRSHECPRTPLDEV
6004	36372	A	6050	1	1095	
6005	36373	A	6051	171	619	
6006	36374	A	6052	1	621	
6007	36375	B	6053	1	181	
6008	36376	A	6054	1	905	
6009	36377	A	6055	1	855	
6010	36378	A	6056	2	244	
6011	36379	A	6057	3	829	LTDCLKDVLIPPFNRMLLEVT FGKLYAWTVQNILNVLMDASA KFKELGIQPVPLQTITSENPLGP SLGSIPQARFLLMMLSLTLQH SANNLDLLNSGTLALTQTALR LIVLPDVELLI*DHLL*MQTSIV* LPVLALLAQHRSFGPSCDNVE EDMNAsAQGASATVLEATRKE TAPVHLPVSGPELAATMKIGTR VMRGVDWKWDG/QEAEQTER NIHPPTMMFTSTINLLQTLCLPA RVHAEIMQSEATKTLGGLLQIL VESGITDKTRME
6012	36380	A	6058	133	5421	IFVFGCPGSPRLQMVENRYTES FFTGQNCNRNEKVTLVRIADLE NHNNDDGFWTVIDGKVYDIKD FQTQSLTENSILAQFAGEDPVV ALEAALQFEDTRESMHAFQV QYLEPDQEGVTIPDLGSLSSPLI DTERNLGLLLGLHASYLAMSTP LSPVEIECAKWWQSSIFSGGLQT SQIHRYNEEKDEDDHCSPPGT PASKSRLCSHRRALGDHSQAFL QAIADNNIQDHNVKDFLCQIER YCRQCHLTTPIMF

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6013	36381	A	6059	1	2607	MMGHSSAIPLTATPGELKGQSP TKMPDPELGCQGAQSGCSR ARHQKARSMPLQDQHLALAIL LELAQVRGTLSQMLSAIILLQ LWDSRAQETDNERSAQGTSTL LLSLQTTFQSIICSKDTPPSEGN MHLISGPLSPSEFLRESFFTQV NCRNNEEVTICKADLENHNK DGGFWIVIDEKVYDIKDFQTS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFVGVQYLEVR LYALSDAEDGRGVTL*WLQSSIF SG/GLQTSQIHYSYNEEKDEDH CS/SPVGTAPASKSR/CSHRWALG DHSQAFLLQAIADNNIQDHNVK HQQGRSYKEVCTPVIERLRF SNELRPVAGNDLSISEFKLLSSL PRWRRIAQKIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAISKPTITSEN LGPSLGSIPQARFLLMMLSMILT LQHSANNLDDLNSGTALTLTQT ALRLIGPSCDNVEEDMNASAQ GVSAATVLEATRKETAPVHLPVS GPELAATMKIGTRVMRGVDW KWGDQDGPPLGRVIGELGE DGWIRVQWGTGSTNSYRMGK EGKYDLKLAELPAAQPSAEDS DTEDDASPNRLVYREQHRSW CMLGFVRSIALTPQVCGALSSP QWITLLMKVMKGHAPFAASL QRQRWVAVSLPHALVKSQTVP
6014	36382	A	6060	1	7297	
6015	36383	A	6061	32	259	SLRVTPGGRNVSSEKKDRKKTG R/PPELERKSHTERLYLEEGSAE PA*VGRRAPESVNDRGGAIQRA QRGQAPPLPR
6016	36384	A	6062	3	437	
6017	36385	A	6063	1	425	MTELTPLWKPLKNSPMFRVIAR AFCVTFILVSTHQEMLTITSEN LGPSLGSIPQARFLLMMLSMILT LQHSANNLDDLNSGTALTLTQT ALRLIGGTPVELPAELAAPAFR AAAA/VDKNPRRRGQKVAVAK SGDGRGKKS

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6018	36386	A	6064	2	14566	RRGGRALRVRPETWEEAGEKM PSEFCLAAQARLDSKWLKTDI QLAFTRDGLCLGNEMVKDG EIVYTGTESTQNGELPPRKDD VEPSGTTKEDLNDKEKKDEET PAPIYRAKSILDSWVWGKQPDV NELKECLSVLWKEQALAVQS ATTLTALRLKQRLVILERYFIA LNRTVFQENVKVWKKSSGISLP PVDKSSRPAGKGVGLARVG SRAALSFAFAFLRRWRSGEDA DLCSELLQESLDALRAL
6019	36387	B	6065	75	581	
6020	36388	A	6066	517	5495	ESFFTQGNCRNNEKVTVFRIAD LENHNNDGGFWTVIDGKYVDI KDFQTSQSLTENSILAQFAGEDP VVALEAALQFEDTRESMHAF VGQYLEPDQEGVTIPDLGSLSP LIDTERNLGLLLGLHASYLAM TPLSPVEIECAKWLQSSIFSGGL QTSQIHYSYEEKDEDHCSSPG GTPASKSRCLSHRRALGDHSQA FLQAIADNNIQDHNKDFLCQI ERYCQCHLTTPIMFPPEHPVEE VGRLLCLCLKH
6021	36389	A	6067	1	1851	
6022	36390	A	6068	53	423	YHLTLIHGTVSATRPGHCSP GKLPSSWVPSLQCTPSSPECRSV *RQL*HGHMHELLYIITKADSVI TASCLISRSEWWDGGTVSLV QRFDYDGSQCQRPHRTGCASS SAPQRASSVAPG
6023	36391	A	6069	1	49	EWSGTRTWWRPWCRT*CRT
6024	36392	A	6070	1	726	
6025	36393	A	6071	368	485	
6026	36394	A	6073	1	414	
6027	36395	A	6074	3	535	RRREFFPAKERESASMSSPEE*P/ DMAKGA PPSQPPNSVPAD/CS RSVRLSSSNFEESLRTEDDEGQ EGQDSMSRAKANWLRANFKV RMQLQEARGEEMSKSLWFKG GPGGGLIIDSMPDIRKRKPIPLV SDLAMSLVQSRKAAITSALASS TLNNEELKNHYKKTQLALYIP ISC
6028	36396	A	6075	1	222	
6029	36397	A	6076	2	284	NGIPDFSNTLLRGLQMPGARG PCCGSQRHINLLMGTGVFLVK MKA/NEFFLDSETRLCIAPEG WREQPQKTSMTNTFTLFLRIKFF VSHYGLL

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6030	36398	A	6077	91	749	
6031	36399	C	6078	1	380	
6032	36400	A	6079	1	877	MPPRDLAPALLVAVLVLLYLL VSAAAAPSSDSTPENVCVET TTNFIWELSSPHNTSAVLLVVF HKGPSKPFVKLKKNANGLGFS FVQMEKFCSCSLKSDLVRIKRL FPGHPAEENGAIAGDIILAVN GSPRKASSRCRGSWAMQLSV QAGPSFASYYPAAVEVLHLLRG APQEVTL LCRPPP GALPELEQE WQQQKYKCAWAIVNEAEVEE VVEVAGTVEFFGDQGA*CHHP ACSGKPLGWHGGLSRKCPRLFF RGATRVGTGAQGLKEVKQQSFR SNMMWLGLRL
6033	36401	A	6080	1	1683	
6034	36402	B	6081	66	1214	
6035	36403	A	6082	1	5694	
6036	36404	A	6083	3	483	SSLTSSMEDPAAPGTGGPPANG NGNIGGGKKGQAAPKGREAFR SQRRESEGSVDCPTLEFEYGDA DGHAAELSELYSYTENLEFTNN RRCFEEDFKTQVQKKEWLELE EDAQKAYIMGLLDRLLEVVSRE RRLKAARAVLYLAQGTGECED SEVDVLHWSRY
6037	36405	A	6084	1	2646	
6038	36406	A	6085	115	1289	FSPLEPRLCSLGGWGAQAGEP CQPSRAGCGREGATMGCTLSA EERAALERSKAIEKNLKEDGIS AAKDVKLLLLGAGESGKSTIVK QMKIIHEDGFGEDVQKYKPV VYVNTIQSLAAIVRAMDTLGIE YGDKERKADAKMVCDDVSRM EDTEPFAELLSAMMRLWGDS GIQECFNRSREYQLNDSAKYYL DSLDRIGAADYQPTQDILRTR VKTTIGIVETHFTFKNLHFLRLD VGGQSRERKKWIHCFEDVTAIL FCVALSGYDQVLHEDETTNRM HESLMLFDSICNNKFFIDTSIILF LNKKDLFGKIKKSPLTICFPEY TGPNTYEDAAAIIQAQFESKNR SPNKEIYCHMTCATDTNNIQVV FDAVTDIIIANNLRCGGLY
6039	36407	A	6086	1	1053	

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6040	36408	A	6087	2	377	IYDGFDFGFAKGQIKGWTVDVG GWTGQGSILGTRVLP GK/Y MEEIATQMRTHSINALLIIGGFE AYLGLLELSVFVTLKLFYQHFM HVLTLIPNRRVPICTSPSACC LWSVSHAFRCAYEQN
6041	36409	A	6088	1	591	
6042	36410	A	6089	1	2391	PGRAAPLGLLAMDADDSRAPK GSLRKFL EHL SGAGK AIGVLT GGDAQGMNAAVRAVVRMGY VGAKVYFYEGYQGMVDGGSN IAEADWESVSSILQVGGTHGSA RCQAFRTREGRLKAACNLLQR GITNLCVIGDGS LTGANLFRK EWSGLLEELARNQIDKEAVQ KYAYLNVVGMVGSIDNDFCGT DMTIGTDSALHRIEVDAIMTT AQSHQRTFVLEVMGRHCGYLA LVSALACGADWVFLPESPPEEG WEEQMCVKLS ENRARKRLNII IVAEGAIDTQNKPTSEKIKELV VTQLGYDTRVTLGHVQRGGTP SAFDRILASRMGVEAVIALLEA TPDTPACVSLNGNHAVRLPL MECVQMTQDVQKAMDERRFQ DAVRLRGRSFAGNLNTYKRLAI KL PDDQIPKTN CNVA VINVGAP AAGMNAAVRS AVR VGIADGH RMLAIYDGFDFGFAKGQIKGWT TDVGGWTGQGSILGTRVLP GKYLEE IATQMRTHSINALLIIG GFEAYLGLLELSAAREKHEEFC VPMVMVPATVSNNVPGSDFSIG ADTALNTITDTCRJKQSASGT KRRVFIIETMGGYCGYLANMG GLAAGADAAYIFEFPDIRD LQ SNVEHLETKMKTTIQRGLVLRN ESCSENYTTDFIYQLYSEEGKG VFDCRKNVLGHMQQGAPSPF
6043	36411	A	6090	1	459	

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6044	36412	A	6091	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLSPIKRHLASWIKSQDP SVCCIQETHLMCRDTHRLLKIG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSLDLQRLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNLYSDHSAIKL ELRIKNLTQSR
6045	36413	A	6092	1	3654	
6046	36414	A	6093	1	5127	
6047	36415	A	6094	1	3663	
6048	36416	A	6095	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKA VCRGK FIALNAHKRKQERSKIDTLTSQ LELEKQEQTHSKASRRQEITKIR AELKEIETQ
6049	36417	A	6096	1	5073	
6050	36418	A	6097	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTTEITNLYSDH SAIKLELRINKPTQSRSTTWKLN NLLNNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIPLNAHKRKQERSKIDTL TSQLELEKQEQTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKTDRPLARLIKKKR EKNQIDTIKNDK
6051	36419	A	6098	1	3235	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6052	36420	A	6099	1	3070	MATLIPLLFHKHPLHTQRYQFN VRGGCPTSTAIAITLDPRTAVFP LMSVFQTSAPWPFWGFTHTQTP VPQPLKVKIHSSADTAADIQAN RVWSGPPANSKRPAEEGKLT NRKDIHTKNPSVRHHHQRPKV DKTTKTGKKQRRKTGNSKKQS ACPPPKERSSTATEQSWTEND FDKLREGFRSSNYSKLQDEIQT KGKEVENLEKSLDECITRITNTE KGLKLENYVKNEETSGANAI NWKKGINKIDRLARL
6053	36421	A	6100	1	3297	MKAIEKMFFETNENKDTTNQN LWDAFKAEEVESLNRPTGAEL GAIINSLPTKSPGPDGFTAEFY QRYKEELVPFLLLKQFSIEKEEL LPNSFYEASILIPKPGRDTTKEE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDA EKAFDKIQQPFMLKTL NKLGDIGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIQKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS GYNKINQKSAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPTYKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIK KSFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYA AKKHKMKCSSLAIREMQI KTTMRYHLTPVRMAIHKSGNN
6054	36422	A	6101	1	2563	
6055	36423	A	6102	1	3417	

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6056	36424	A	6103	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSAPEPPSAIPKAQV SSTEKLRNCIDDLKPFPAALASEL SRRAKALQIAGFPPMKVPRDTI SKVCCLKTVGKLCHSGEESRK CTLICNNKHYPIDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSEDDQGPTRVI AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRALDLK
6057	36425	A	6104	1	4371	
6058	36426	A	6105	1	1825	MVKGSIQEEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTROKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYVWHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKAVCRGK FIPLNAHKRQKERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKREKNQI DAIKNDKGDITTDPEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPIGTAE IVAIINSLPTKKSPPGPDGFTAKF YQRYKEELVPFLKLFQSIIEKE GILPNSFYEAHILIPKPRDRTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDA EKAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNI CSWVGRINIVKMAILPKNILITL QLLLVLPSTLPLWLPALAGO
6059	36427	A	6106	1	4449	

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6060	36428	A	6107	824	3693	AWKGTDDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRKINFTQSRSTTWKLNLLNNDYVWVHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGKFIALNAHKRKKQERSKIDTLTSQLKELEKQEQTTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFFERITKSDRPLARIKKKREKNQIDTIKNDKGDIT
6061	36429	A	6108	1	3297	
6062	36430	B	6109	112	3300	
6063	36431	A	6110	3	3316	
6064	36432	A	6111	1	3457	
6065	36433	A	6112	1	3170	MVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQRLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHILGSKALLSKCKRIEITNYLSDHSAIKLELRKINLTQSRSTTWKLNLLNNDYVWVHNEMKTEIKMFFETNENKDDTTYQNLWDFAKAVCRGKFIALNAYKRKEERSKIDTLTSQLKELEKQEQRHSKPSRRQETKMR AELKEIETQ
6066	36434	B	6113	1	4753	
6067	36435	B	6114	1	3384	
6068	36436	A	6115	1	3345	
6069	36437	A	6116	1	3780	
6070	36438	A	6117	1	3720	
6071	36439	A	6118	1	3894	
6072	36440	A	6119	1	3335	MVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQRLDSHTLIMGDFNTPLSTLDRSTRQKVNKDTQELNSALHQAADLIDYRTLHPKSTETYTFSSAPHHITYSKIDHIVGSKALLSKCKRTEITNYLSDHSAIKLELRKINLTQSRSTTWKLNLLNNDYVWVHNEMKAEIKMFFETNENKDDTTYQNLWDFAKAVCRGKFIALNVYKRKKQERSKIDTLTSQLKELEKQEQTTHSKASRRQETKIR AELKEIETQ
6073	36441	A	6120	1	3780	
6074	36442	A	6121	1	3852	
6075	36443	A	6122	1	3345	
6076	36444	B	6123	1	6136	
6077	36445	B	6124	1	3924	

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6078	36446	B	6125	295	4185	
6079	36447	A	6126	1	405	
6080	36448	A	6127	1	1059	
6081	36449	A	6128	2	518	EKATCDENDSVSNIA TEIKGQ QSVVHVSPQKQSAWKVIFKKKV SLLNIA TRIIGGKSGTVSSQKQ PPSKATSDKTDALNIA TEIKDG LQCGTVSSQKQPALKATTDEED SVSNIA TEIKDGEKSGTVSSQKQ PALKATTDEKDSVSNIA TEIKD GEKSVTVSSQKQPASK
6082	36450	A	6129	1	843	
6083	36451	A	6130	1	432	
6084	36452	A	6131	2	835	CGSAQAAAAAAEEATEKIPAL RP/ASAVGAAGALAVLRDPRA WREAGSKS/PETPFS* CQGA/HG GGQFCPSGTAFPGKMKVMMR KRKKKGQCLPGICRSLKRRKSP RSPGM/IGYSTLSIPPEMLASYQ SYSSTFHSLEEQQVCMA/G*HR QMPGADKPVRAQQRVLAGVW AGFTMRHQSRLY*ECSCIGVIFR HRCVAHLLGRAIGALFVITPA GERGMCCAKILGNARVFPVT TL*NDGQCQACMHAG/TTLED P GKNYISSPSSSSSSPSSPRVPS
6085	36453	C	6133	278	446	
6086	36454	A	6134	1	1152	
6087	36455	A	6135	1	639	
6088	36456	A	6136	12	1436	
6089	36457	A	6137	367	1056	
6090	36458	A	6139	1	4263	
6091	36459	A	6140	1	1311	
6092	36460	A	6141	1093	1358	MQKKPLTKFNNPSC*KLSIN*V LMGRISK*VTTTATTTTITTTT TTTTTTTTTATTTTTTTTTTTT TTTTTTMGPTLPLIPGLGS
6093	36461	A	6142	1	699	
6094	36462	A	6143	1	489	

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6095	36463	A	6144	5	916	ALGGTPMLGKLAMLLWVQQA LLALLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVPRV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNTKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHHGRGLLPAPQQ WREGLFQNYTPPGLLGLPDHFR
6096	36464	A	6145	5	756	
6097	36465	A	6146	1	471	
6098	36466	A	6147	184	1097	ALGGTPMLGKLAMLLWVQQA LLALLPTLLAQGEARRSRNTT RPALLRLSDYLLTNYRKGVPRV RDWRKPTTVSIDVIVYAILNVD EKNQVLTTYIWYRQYWTDEFL QWNPEDFDNTKLSIPTDSIWVP DILINEFVDVGKSPNIPYVYIRH QGEVQNYKPLQVVTACSLDIY NFPFDVQNCSTFTSWLHT/SPG HQHLFVALARKGEIRQECLHEP GRVGVAAGGAALLSGVQHGKQ* LLCRNEVLCGHPPAAPLLCGQP ATAQHLPHGHHGRGLLPAPQQ WREGLFQDYTPPGLLGLPDHFR
6099	36467	A	6148	3	672	
6100	36468	A	6149	3	398	LRKIKIDLGKFSNDPBGYIDVLQ GLRQSFDTWRDIMLLDQSLT PNEKSAAKTAAREFGDLWV/S FQN*SCKTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYPAPIQQA V
6101	36469	A	6150	1	420	

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6102	36470	A	6151	1	878	TLLPPRPGVGS DYPNIPGCPMW GNKDPGEGTLER GKVEDASQR TSRTLKETS GKAHRKKQDGK CSPQGKNALKMYSGEFDPVRV CVPFSLDLKQLKIDLGRFSDNP DGYIDV/LQGLGQSFDTLWRDI MLLLDQTLTPNERNATITAAARE FGDLWCLSQVNDRMTTEERER FPTGQQA VPSADPH*DTSEHG DWCCRHL LTCVLEGLRKRKK AVNFSVMSTVTQGKEENPTAFL ERLREALRKHTSLSPDSIEGQLI LKIKFITRSAADIRKQTSKVHLR PGAKLKTPY
6103	36471	A	6152	1	417	
6104	36472	A	6153	1	415	
6105	36473	A	6154	1	234	
6106	36474	A	6155	1	335	TCPIVPG/QEMIIEISKGRSGLGL SIV*GKDTPLNAIVIHEVVEEGA AAVDGRLWAGDQILEVNGVDL RNS SHEEAITLMTQPKQVRLV VYRDEA HYRDEENLEIFPVDLQ
6107	36475	A	6156	109	4687	
6108	36476	A	6157	109	4991	
6109	36477	A	6158	3	862	
6110	36478	A	6159	1	1857	
6111	36479	A	6160	3	100	
6112	36480	A	6161	1	537	
6113	36481	A	6162	125	1184	
6114	36482	A	6163	875	1506	LSIYLV TQKAA/SSEWGP EQEK ALQEVQAAVQAA LILEPYDPA GPVVLVSLADRD A VWSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQHSIHKWKWYIHD RARAGPEGTNSSARYAATM*K WTASALQPLSRKSLKDSSEK SSQWAE LRAVHLAVHVAWKE KWPDPRLDTDSWAV/ANGLAR WGTWKEHDRKIGDKEVWGR GTRI
6115	36483	A	6164	1	1566	
6116	36484	A	6165	1	1098	
6117	36485	A	6166	1	538	
6118	36486	A	6167	410	625	LTLVPFSFVS VLTPLPKGNTRY *TGIL*GWNLSWKGT LGFSVTA QPSSGTPRTALGSR TT KPLLVSL LQV

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6119	36487	A	6168	821	1428	QVTDVQDFPLCKIQWRRTVR GDLQ/PFTRVTVHWGKGNQDT FQGLDITGSELTLPDGPKRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT GVIPTSPFNSPI*PMQKTDGSW RMTVDYL
6120	36488	A	6169	203	850	DVEHVKGKRRRRWRRRVVAD GNVVKPMSCAGDLQ/PFTRVTV HWGKGNQDTFQDLLDTGSELT LPDGPKRHC GPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VV/I/SPVPECIIGIDILSSWQ/NSH IGSLTVHLSSDPKGCHEWGP QEKALQEVQAAVQAALILEPY DPAGPVVLEVSLADRDVWWSL WQAPIGESQQRPLGFWSKALPS
6121	36489	A	6170	1	864	
6122	36490	A	6171	1	205	VPDFPAKPIQGFHNSRYL/REA VHGAEVHAFIAGQPLT**ELM SIFPQFQFFLYRRLDSHSGSQW I
6123	36491	A	6172	1	3039	
6124	36492	A	6173	1	1364	MIISDAEKAFDKIQPFMLKTL SKLEETASPSVVA TYTPQPMML PSAFPLSEINPVL PETTVMAS PEAVTRQDNVDS PQKPPPTPMF ASRPITRLKPRRAPSEEGIQLRK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTFSQLQN LNTMGIFGSCDRSQVAALNHQ RQVPELIIGIDILSSWQNP HIGSL NGRGYINSLALCHNLIRDLDR FLLPDQITLVHYIDHIMRLDSVK DKWLHLAPPTKKEAQLVGL/ FGFWRQHS/LWROPLACYWAL VETEHLTMGHQV/TMQPELPIM NWLISDPSSYKPAPMASWGV YQQLTEEEKTRAWFTDGSARY TETTRKWTAVAIQPLSRTSLKD SNEGKSSHQA KNGITVLACVI DPDYQDEISL/LTPQWRCHPGSS VWRASSLGISHPP
6125	36493	A	6174	114	1996	

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6126	36494	A	6175	1	475	MGRNQNRKAENSKNWNASSPP KEHNSSPAREQNWRDEFNELT EVGFRRSVITNFSDLKEHVLTH CKEAKILEKRLDKWLTKITSVE KS/CK*PDG/D*KPQYENFMKHT QASIALDLIKRKKRYQ*LKIKLM K*SKKTR*EKKKYKLPSENTTN TSMQIY
6127	36495	A	6176	179	393	NKRGYKQMEEHSLMDKKNQ YYENGHTAQGN*AGEGNKGYS IRKGTGSQIVPLCR*HDCISRKPD CLSPKSP
6128	36496	A	6177	1	710	MARELRDECTSFSSQFHQLEER VSVIEDQMNEMKQEEKFREKGI KRSEQSLQEIWDYMERPNLCLI GVPESDGENGIKLEDTLQDIQK DFPNLGRQANIQIEIQRMPQR YSSRRATPRHIVRFTKEIQTIR EYYKHLANKLENLEEMDKFL DTYTLPRNLQEEVESLNRPTGS EIEAIINSLPTKKSPPRGFTA YQRYKEELVPFLKLFQSIKE GILPNSFYEAHILPKLGRDITTK KENFRPISLMNIDAKILNKILAN QMQQNIKNLIRHDQAGFIPGMQ CWFNIRKSNVVIQHINRTKDKN HMIISIDAFAFYKIQQPFILKTL NKLLENKIPRNPITYKGCEGPLFK ENYKLMLEKEIKEDTSKWKNIP WSWGRNIVKMAILPKVIYRLS AIPKLPIMIFFTELEKTLTKFIWN QKRACIAKSILSQKNKAGGIML PDFKLYYKATVTKAAWYWYQ NRDIDQWNRTEPSETIPHIYSHL IFDKPDKNKKWGDFLFNKWC WENWLAICRKLKLDPLTPYTK INSRWIKDLNVRPKTIKLEENL GNTIQDIGMGKDFMCKTPKAM VTAKIDKWDLIKLSFCTAKE TTVRVNRQPTWEKIFAIYSSD KRLISRIYKELKL*PCSIV*SQVA *CLQLCSFGLGLTWQCRLFFGSI
6129	36497	A	6178	464	724	IGEVLLDNILQRFVQLGSILPTF RYTNQT*IWSWTLFWLVS
6130	36498	A	6179	1	2022	
6131	36499	A	6180	1	882	
6132	36500	C	6181	1	1935	
6133	36501	A	6182	1	672	
6134	36502	B	6183	140	2195	
6135	36503	A	6184	26	354	

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6136	36504	A	6185	86	747	SLEDAMSLKDDDSGDHDQNEE NSTQKDGEKEKTERDKNQSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFASIVEQFWRFYSHMVRPGDL TGHSDHFLKEGKIPMWEDDA NKNKG/KWIRL/RKGFGRCW ENLILAMLGEQFMVGEIECGG CGVCPAFQEDIH/IWNTASDQ ATTARIRDTL\RRVL\NLPANTI MEYKN
6137	36505	A	6186	23	127	
6138	36506	A	6187	2	419	
6139	36507	A	6188	1	714	
6140	36508	A	6189	19	373	AVFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFLL FFFFKLKELRLV*PLNPEN*ESC PLFSPVNLDMPTFKDKRWKV NWARSTSRQQLLESARTKSWA EREGGTRWRAW
6141	36509	A	6190	227	420	KNFLPNCASAKELFFFFFFFFFLL LLLLLLLYFKF/M*WFKHLAF PLLAFILSPITAL*RGVFHH
6142	36510	A	6191	400	582	
6143	36511	A	6192	1202	1678	
6144	36512	A	6193	2	109	FTFWHDFAAAGTGCSFPCLVLP SWW*QNLSAFACL
6145	36513	A	6194	110	377	QWISRQKPYKPEKRGDQYSTFL *EC*ILVPLFWLVGFLPRDPLL V*WAYGCP*HFFLHFNLGESNN YVSWGCS
6146	36514	A	6195	1	381	
6147	36515	A	6196	1	759	
6148	36516	A	6197	1	609	
6149	36517	A	6198	2	1178	
6150	36518	B	6199	159	290	
6151	36519	A	6200	716	1001	SMPASTHLILVGSCSWKMVIVL PLVTHLFTALTVPWNLPWVEL YWNM*TM*LRSMKESLMATIF TLPELKA/VLHEKLQ*LQSTEDL *HGLLGG
6152	36520	A	6201	5772	5971	TANIIMTGSNSHITILTLNVNRL NARIKRHRENCIKSQDPSVCCI *ETHLMCRDITYRLKIKGWSN
6153	36521	A	6202	1	974	
6154	36522	A	6203	1	600	

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6155	36523	A	6204	51	424	MAPKQDPKPKFQEGERVLCFH GPLLYEAKRVKVAIKD/ITREIH SYITVVGIKIGMNGFRRAKYSN TWTPICRNSENFKKPSKFVL* T EY*GEMPVDF*FWTWNQWRSC WLPCLYNDTSDLSAGV
6156	36524	A	6205	1	3827	MQKAIRLNDGHVAPLGLLARK DGTRKGYLSKRSSDNTK WQTK WFALLQNLLFYFESSRPSG LYLLEGVCVCDRAPSPKPA SAK EPLEKQHYFTVNF SHENQKALE LRTEDAKDCDE VAAIAHASY RTLATEHEAL MQKYLHLQIVE TEKTVAKQL RQQIEDGEIEIERL KAEITSL LKDNERIQSTQTVAPN DESDIKKIKKVQSFRLG WLCR RKWKTIIQDI RSPHADSMRKR NQVVFS MLEAEAY
6157	36525	A	6206	1	900	
6158	36526	C	6207	172	501	
6159	36527	A	6208	499	848	KIRVPAA VAGLSPPLGPWSLRS PSQPERCCPWRNSSWWTAPRTS IITAAGKVSAPRLSSISCTTRGS WVKTPPTRARMVIASSNLERP SALSRM*PTSQSMTRKRWWRL WPSTTL
6160	36528	A	6209	3	495	SCAQTFPKLDTFLEHIKSHQEEL SYRCHLCGKDFPSLYDLGVHQ YSHSLLPQHSPKKDNA/CLQVF PCERYLRRHLPTHSGGRFKCQ VCKKFFRREHYLKLHAIHSGE KPYKCSVCESAFNRKDKLKRH MLIQYDEVQRQGLGMVPGTQKV LNKCFCHNVKKKK
6161	36529	A	6210	667	2142	
6162	36530	A	6211	1	396	
6163	36531	A	6212	213	446	
6164	36532	A	6213	101	580	VAGVGS LPRSMEDDAPVIYGLE FQARA/LTPQTAETDAIRFLVG TQSLKYDNQIHIDFDDENNIIN KNVLLHQS/AGEIWHISASPADR GVLTTCCYNRTSDSKVLTCAA V WRMPKELES GSHESPDDSSSTA QTL/ELLCHLDNTAHGNMACV VWEPMGDG
6165	36533	A	6214	1	933	

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6166	36534	A	6215	3	404	RLKEKKLVKEIVASCGPAQCQ ETIR TALAMGADRGHVEVPPA EAERLGPLQVAVR/AVVTADLR LNEPCYATLPNIMKAKKKKIEV IKPGDLGVDLTSKLSVISVEDPP QRTAGVKVETEDLVAKLKEIG
6167	36535	A	6216	1	408	
6168	36536	A	6217	88	871	MADVRLVAVKRVIDYAVKIR VKPDRTGVTVDGVKHSMPFC EIAVEEA VRLKEKKLVKEIVAV SCGPAQCQETIR TALAMGA/D RGIHVEVPPAEAEFR/GVPLQV ARVLGQLAKKEKVDLVLLGK QAMACTDCNQ/TGQMTAGFLD WPQGTFA SQVTLEGDKLVER EIDGGLETIRLKLPAVVTADLR LNEPRYATLPNIMKAKKKKIEV VIKPGDLGVDLTSKLSVISVEDP PORTAGVKVETEDLVAKLKEI
6169	36537	A	6218	1	1023	
6170	36538	A	6219	110	842	
6171	36539	A	6220	1	122	
6172	36540	A	6222	1	1257	MNDATAVQEGSQMYSWQKLT PTGPFIMQPEGMGRLFAINKMA EGFPPEHYEPIETPLGTNPLHPN VVSNPVVRVLYEQDALRMGKKE QFPYVGTTTYRLTEHFHTWTKH ALLNAIAQPEQFVEISETLAAAK GINNGDRVTSSKRGFIRAVAV VTRRLKPLNVNGQQVETVGIPI HWGFEGVARKGYIANTLPNV GDANSQTPEYKAFL/GQHREGV RN*LHHA AFSGA*LQCFQYAH NSRKNN
6173	36541	A	6223	737	941	WLRMMEHRLFPLWKRESKKA HYVQSSVLLCLGMLR*KYKGG KGKKERKKDEKRKGNGKKRI KIHSI
6174	36542	A	6224	1	1072	
6175	36543	A	6225	1	585	
6176	36544	A	6226	1	930	
6177	36545	A	6227	28	392	AGEVPLQLPPAAVCSACLQRP LWNSSFFL*SCLHALFH*VDL QSLIAFLLD*SS*YLCMLHEV LVLCFAPS GHLCSLS*LF*LAI HLTFFQGS*LPCIGLEHASLAQR SLLLP TF
6178	36546	A	6228	1	271	SAIVTFVCFMKFSCCVFQLHQV FHVLFKLVILVSSCNLFSRFLA SLHWVTTCFSFSEEFVITHLLKP APVNSSNSFSVQFCSLAGKEL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6179	36547	A	6229	1	1089	MGWRPRWLPYLYWGFQSDLC PHCKRKAQEEDSLAAQAASHP RLSANSKNNSWKGQYSYALFK AMRHMLCIGYGRQAPAAVSDV WLTMLSMIVGATCYAMFIGH/ ATALIQVLDCSRRQYQEKVVL REHPNIGSSQEGGTWHQTVGL QQTSKDFDANDPILKQDTQEW SGSATFTSDGKIRLFYTDYSGK HYGKQSLTTSANTGTENGYYQ GEESLFNKAYYGGGTNFFRKES QKLQQSATTRDAELANGALGII ELDNDSPKKRGATQRSSEENI TLKAYKRDVRSLLMLTRNEDV ADSLNSSKKRQNYQLPSIRSVT RCKKIGVCAKIGCGQGTHYLS VSILNTADRRRLGFFRTSMY
6180	36548	B	6230	1	1140	
6181	36549	A	6231	3	204	GSDYELGLW*PWLTSATDLH GECYSS*SGASGVVRSWLARG LAGFRSEADLRGRESVAVTN
6182	36550	A	6232	1	1296	
6183	36551	B	6233	1	1686	
6184	36552	A	6234	1	627	
6185	36553	A	6235	570	736	SATFGRSSRSGCSGFPAASRRG RLPLSPPPWPAVRVYPCGMLD NKASAAHPKKK
6186	36554	A	6236	1	103	
6187	36555	A	6237	699	887	GLQPPAPRETRPLY*TLAWNLI FLFVSPLDSCDLVRSVLTCLSP GNSPSFDMHRYQLPCVH
6188	36556	A	6238	2	803	
6189	36557	A	6239	2	1277	YKETYLIHLHFTTGLSIAYFNF GNQLYHSLLCIVQLILRLMG RTITAVLTTCFQMA YLLAGYY YTATGNYDIKWTMPHCVI.TLK LIGLAVDYDFGGKDQNSLSEQ QKYAIRGVPSLLEVAGFSYFYG AFLVGPQFSMNHYMKLVQGEL IDIPGKIPNSIIPALKRLSLGLFYL VGYTLLSPHITEDYLLTEDYDN HPFWFRCMYMLIWGKFVLYKY VTCWLVTGVCIL.TGLGFNGFE EKGKAKWDACANMKVWLFET NPRFTGTIASFNINTNAWVARYI FKRLKFLGNKELSQGLS\MLFLF LWHGLHSGYLVCFQMEFLIVIV ERQAARLIQESPTLSKLAITVL QPFFYLVQQTTHWLFMGYSMT AFCLFTWDKWLKVYKSIYFLG HIFFLSLLFILPYIHK\AMVPRKE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *~Stop codon, /~possible nucleotide deletion, ~possible nucleotide insertion)
6190	36558	A	6240	56	324	
6191	36559	A	6241	68	487	
6192	36560	A	6242	52	457	
6193	36561	A	6243	263	787	SLEV*KWPGVACRLQL*P/MVP APKS*ESKSAGSLNTPSAICRDA SGRGLARPWLRSKSKLACHLV DTRSKTAGGLAPVPSAHLISVR EREPLCAVLVSQLEFRVGVGL VGPTLGARREPCWPQAMGDLA PEPVAALRLISRRLPAFPWGR ARDLQAMPEPPTHSMGSCAPE PPR
6194	36562	A	6244	3	236	
6195	36563	C	6245	1	1608	
6196	36564	B	6246	1	1083	
6197	36565	A	6247	823	1055	KQKDGTPAPWSRGRSSGRLG THRSRRGWAEQAWRAAGPET CPAGRQLRPGEKSSAPG*RSR RKDAYEMDTAKKK
6198	36566	B	6248	1	390	
6199	36567	A	6249	27	363	
6200	36568	B	6250	1132	1268	
6201	36569	A	6251	11	489	
6202	36570	A	6252	356	638	
6203	36571	A	6253	1	507	
6204	36572	A	6254	80	336	
6205	36573	B	6255	100	912	
6206	36574	B	6256	821	2992	
6207	36575	A	6257	2	602	
6208	36576	A	6258	1	519	
6209	36577	A	6259	3	228	STGVVPSQRTCLLEKASVLFNT GALYTQIGTRCDRQTQAGLESA IDAFQRAADMSPGLTRRLGP TRWHQGTPH
6210	36578	A	6260	1	963	
6211	36579	A	6261	1	925	
6212	36580	A	6262	1	397	
6213	36581	A	6263	1	2625	
6214	36582	A	6264	11	241	SLQHLNPATFLPVSKSPVKHNC VEVLDSVYSSGPNHRDHP*TSV DWELYMDGSSFTNPCKVTLKK TTSPAPVTPGS
6215	36583	A	6265	1	1662	
6216	36584	B	6266	1	897	
6217	36585	A	6267	3	258	
6218	36586	A	6268	1	279	
6219	36587	A	6269	1	258	
6220	36588	A	6270	1	639	
6221	36589	B	6271	1	1935	
6222	36590	A	6272	698	1643	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6223	36591	A	6273	91	386	IFDFLLYYVSGCNSIAEPQHFT TTVTRCSPVAFVEFPSSPQLKN DVSEEDQK\KPIENEMSGKGG SWVLFTKGEVQEWRESGLNPT KFNMGPLIYS
6224	36592	A	6274	1	2538	
6225	36593	A	6275	1	471	
6226	36594	A	6276	152	520	CPLTLLPSRGAGLGTCSPPCLS LPPTPWAPVRPEPPRRAPPAPR RPVPSGTKEQTTQGLRNASARR GTGRQLHLSPGVGSGTG*SQGL
6227	36595	A	6277	831	1449	HPGQWLRRVCWVSSGAGLAL CSISCPALAAFPVRVGLGTCSPPC LSLPPTPWAPVRPEPPRRAPPAPR PPSPIDHPRAEEYE/PHGAGL AGSSTCSPSAESTG*SQLGS*VV RVRGFILVSETKNPPIDTFGL PPGSSAASLTVQVTRL*ISAIL PHLLSRPCSNARGPVPAVPG AAVRAPAAGRWCGGARGRG RRGGGH
6228	36596	C	6278	1	426	
6229	36597	A	6279	1	535	MKHSGAQLASPSGS\PLGPQVE LPASPVCACTSQPLGGRWDW APWSRGWCSSGRLGPHRSPWS GWE\LRHGGQLVPSAPREGS* GPARNP/GTAPGRPAAPS\GGPP SPRPRTPAGPQALRAAPVP\LA PLPPLPAS*GSLQWPWA*KE APTVCQCAEGLLKCRQSGSPGR GGAESE
6230	36598	B	6280	1	1743	
6231	36599	A	6281	1	428	GTR EEHLKRSRGRIALPIEACV MLLLETGMKEEGLFRIGAGASK LKKLKALDCS\LTWDEFYSD PHAVAGALKSYLRELPEPLMT FNLYEEWAQVASVQDQGQKT FKDLWRTCQKLPQNFVNFY LIKFLAKLAQTSDV
6232	36600	A	6282	135	512	LPFRGAGLETCSPPCLSLPPPPW APVRPKPPR*APPPAPRRVPST TQSLGPHCFYEL*HSP*RSAAS LLKPARP*AHREERTTP/GRSAL/ TSCNTHREGLO/PSLRKKETPNT SEHQKEQTPDAPP

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6233	36601	A	6283	698	2233	IQAAMQAAAPQFGPSTED*CCPIT SEAPWAIMDAKLRLKPPSHPL VSPHLNPQVWDTSSPSLA TEHA SLTISLKPNIHPYPAQSQYSIPQH ALKGSKPVITRI LEHGLLKPIN PYNPILPVQKLDKSYRLVQHL CLIQVLPIHPMPNPYTLSSSI PFTTHYSVLDLKHAFFTIPLYP SQPLFAFTWTDPDTHQAQQTIL AVLPQCFIDSPHYFSQAQISSSS VTYLGILMKTHIGLGAVEQGV VLVGEARAAQEPMEWVGSG MVGCRSRALPRGKA AKARREI ERSAVTIVPVLDFNPAFHIPDTT PDHHDICSLIHLTFTFPFHSFFP VPHLEHTWFDGSSTRPNCHSP AKAGYAIVSSTSHI EATALPRST TSQQA KLIAYTDSKCAFHILHH HAVIWEERNFLTMQGASIIINAF LIKTLKDLLPKEAGVIHCKGK QKASDPITQDNAYADKVAKKQ LAFQLLSLTA VFLLLIRPLSPTSP LKLPLNLFPHKANDS
6234	36602	A	6284	1	1239	
6235	36603	A	6285	1	477	QRPPHG VFLVGVAGR VHGP ASHKAGPQLGDVGVCAQGG QVGPLVLQPVVEHIQQLPG/AG HCAHQ*QGSPS*SSLPRPERSLQ CRRPQGATA TIRSTWWGPRGP VCTAALVPLCWPGWPVQKDEL QAVRSHSALASAMQTCSLAGP GLGSSHARLTA
6236	36604	A	6286	1	1134	
6237	36605	A	6287	673	836	
6238	36606	A	6288	1	225	
6239	36607	A	6289	1	468	
6240	36608	A	6290	495	1637	ESQVLSNVSPHVKV*NMASWE GKDLTVPPQPDTRKGSVLRISK RGRNASCS*DKRKASVCLSLG NGMSRYKTRLYAPSTEIGKNRL RAGGGTCGQYCFVKH
6241	36609	A	6291	1	507	
6242	36610	A	6292	215	389	
6243	36611	A	6293	1	255	
6244	36612	B	6294	69	1055	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v-possible nucleotide insertion)
6245	36613	A	6295	23	1596	IKPQRWGGETRAEMLKILKTREP FLLQRIASPRQQWKNAGQRRS WFFERL/NKIDRLARLIKKKRE KNQIDAINDKGDITDPTIEQT TIREYYKHLKYANKLENLEEMD KFLDTYTLPRLNQEELESNNRPI TGSEIEAIHSSLRTKKSPGPDGFT AEFYQRYKEELVLFLLKLFQSIE KEGILPNSFYEASIIIPKPGRDT TKKENFRLISLMNIDVKILNKIL ANRIQQHKKLVHHDQVGFIPG MPDWFNICKSINIIHHINRTNGK NHMIIISDAEKAFEKIQCFMLK TLNKLIGDGMYLKIIIRAIFDKPT ANVILNGQKLEAFPLKTGTTQG CPLSPLLFKIVLEVLAIRAIRQEK EIKRIQLGKEEAKLSLFADDMIV YLENPVSAQNLLQLRSNFSKV LGYNKINMQKSQAFLYTKNKQT ESQIMSELPFTIATKRIKYLGIQL TRDVKSLFKENYKPLLSKIKED TNKWKNIPSSWIGRISIAKMAIL PKVIYTFNAIPIKLPMTFTFTELEK
6246	36614	A	6296	1	1488	
6247	36615	A	6297	1	1401	
6248	36616	A	6298	2	1256	
6249	36617	B	6299	84	955	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6250	36618	A	6300	735	2718	RSFPRSRPSPFLLLSRYLRIHMV FSVLPGFLQNPKYLLSGSLQEK FRTPGINSKTLDPNRYHIKVR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDATIEQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNRPIGTGSEIAIINSL PTKRSPGPDGTAEFYQTYKEE LVFPPLKLFQSTEKEGILPNSFY EASIIIPKPGRDTTKKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHYDQVGFIGMQGWFNKRK SINVQIHINTNDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCLSPLLFNI VLEVLARAVRQEKEIEGQLGK EEVKLSLFADDMIVYLENPIVS AQNLKLLISNFSKVSQYKINIQA SQAFLYTNNRQTESQIMSELPFT TASKKKIYLGILTRDVKDLFK ENYKPLLNEIKEDTNKWKNI SWVGRINIMKMAILPKVICRFN AIPKLPMPFFTELETTTLKFIWN QKRARKSILSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTPESEIMPHIYNYLIF DKPEKNKQWGKDSL FNK* CWE NWLAIWRKLLK
6251	36619	B	6301	1	2907	
6252	36620	A	6302	1	2358	
6253	36621	A	6303	1	1866	
6254	36622	A	6304	1	885	
6255	36623	A	6305	1	1059	MKNNSSEFPELLIPRQRSGV DLQQTPTDLQRLVLTVRRTN KQDIHTKTPTVRRHHQRPKNP WDTFKAVCRGKFIALNAHKRK QERSKIDTLTSQLEKEVKEQET QSKASRRQEITKIRGELKEIETQ KTLQKINESRSWFEKINKIDRL LARLIKKKREKNQIDTIKNDKE DITTDSTIEQTTIREYYKHLYAN KLENLEEMDKFLNIYTLPLNLQ EEVESLNRPIGTGSEIAIINSLPT KKSPGPDGTAEFYQSYQEELV PFLKLFQSEIEGILSNSFYKA NIILIPKPGRDTTKKENFRPISLM NIDAKILNKILANRIQQHIKKLI HHDQVGFIGMQGWFNI
6256	36624	A	6306	1	1692	

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6257	36625	B	6307	1	2871	
6258	36626	A	6308	2	2315	
6259	36627	A	6309	1	1210	MMSFHLSVHTAIDGSHSSCS AWCSPIDRDYFEQENNSSSSCC CCCYHCHRRKHCGGKGLSFPGE MPLSPGHFNKMMYSVSELMQG SGSGTFIPLPAELSLWLLVTNTK GQRMKND AEIQT TIREYYKHL YANKLENLEEMDKFLDTYTL P RLNQEEVESLNRPTSSEIVAIIN SLPTKKSPGPHGFTAEFYQRYK EELVPFLKLFLQSIEKEGILPN SF YEASILIPKPGRD TT KKNFRPI SLMNSDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIIIDAE KAFDKIQPPFMLKTLNKL/GIK YLG IQLTW DVKDLFKENYKPL LKEIKEDTNKWNIPCSVWGKI NIMKMAIPPKATSPLESYKREK
6260	36628	A	6310	1	2745	MEGEMNEMKREGKFRKRIKR NEQSLQEIWDYVVKRPNI RLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIEIQRT PQ RYS SR RATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNLLLN DYVWHNKMKA EIKMFFETNEN KDTTYQNLWDTF

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6261	36629	A	6311	1	2052	MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQNRSTTWKLN NLLLN DYWVHNEMKAEIKMFF ETNENKDKTYQNLWDAFNAV CRGKFVALNAHKRQEGSKID TLTSQLEKEKQEQTHSKASRR QEITKVRALKEIETQKTLQKIN ESRSVARLIKKKREKNQI/DAIKN DKRDITDPTEIQTITREYYKHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIITGSEIVAIIN SLPTKKSPGPEGFTAIFYQRYK EELVPFLKLQFQSTEKEGILPNS FYEASIIIPKPGRDTTKKENFRP ISLMNIDAKILNKILAKRIQQHI QKLIHHDQVGFIPGMQGWFNIC KSINVIQHINRTKDKNHMISID AEKVFDKIQQRFMLKTLNKL LEVLA RAVRQEKIKIGIQLGKE ELKLSLFAADDIMIVYLENPVSA QNLLKLISNFSKVSEYKIN VQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDVNWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTSFTLEKTTTFKIWNH KGARIAKSILSQKNKAGGITLPD FKLYYKATVTKTAWY

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6262	36630	A	6312	2	2143	SSDGSWWTGFQWREWRQAGR SVNSWDNPKQEVRASSKDKSR GSIQEAAMRMQSSAKLLCSAWT LAYSIIVRTLSSDSEGQPPVIH RQTGSGEDLQQTPTDLQLRVLT IRRKTNKQKGFPHQNPISRRQ EITKIRAEKKIETQKPFKKINES RSWFFKINKIDRLRLARLIKKKI EKNQIDAINKDKGNITTNPTIEQ TTIREYYKHLANKLEHLEEM DKFLDIYTLPRLNQEEVESVNR PITGSEIEAIIINSLPTKKSPGPRF TAELYQRYKEELVPFLKLQFSI EKEGILPNSFYEAIIILISKPRGR TTKKENFRPISLMNIDAKILNKI LANQIQHHIKKLIHHQVGFIPG MQGWFNILKSINVIHINRTKD KNHMIISIEAEKAFDKIQPFML KTLNKLIGIDGTYLTYLKIIRAIY DKPTANIILNGQLEAFPFTGT RQGCPLSPLLFNIVLEALARAIR QEKEIKGQLGKEDVKLSLFAD DMIVYLENPVSAQNLLKLISNF SEVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLENIK EDTNKWNIPCSWIGRINIVKM AILPKTLNQKFSYWFRVKNHYI HQRTFPLKETEFNTIATLYNGA SP/CTAPKSTGTNGHQASGLPRF *RIAFCSALVKSRRKLYQGYLP GQTDREEGVSWCPGGP
6263	36631	A	6313	1	3018	
6264	36632	A	6314	1	2016	
6265	36633	B	6315	1	1215	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
6266	36634	A	6316	1	2268	MAGYPSETKPPEERSDSNICSSA IFTVLHPPLLIPRQTAFGMDLQQ MPTDLQLRVLTVKRKTNKQKG HPHQNPRTSPSKTEDFQPTKI KRDKEGHYIMVKGSIQQEELTI LNIYAPNTGAPRFIKEVLRLDQ RDLDSHTIMGEFNTRLSTLDRS MRQKVNKDIQELNSALHQADL IDISRNHLPKSTEYTFFSAPHRT YSKIDHIVGSKALLSKCKRTEII TKCLSDHSAIKLELRKLNLTQNC SITWKLNNLLNDYVWHNEM KAEIKMFFETSENKDDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKTDLTSLKELEKQEQT HSKASRRQEITKIRAELEIETQ RTLQKISESRWFFEKINKIDRS LARLIKKKREKNQIEAIKNDKG DITTNPTETQTTIEYYKHLYK NKLLENLEMDKFLNTYTLPRLN QEEVESLNRPI TGSEIVAIINSLP TKKSPGPDGFTA EFYQRCKEEL VTFLKLFQSIEKIGILPNSFYE ASINLIPKPGRDTTKKENFRPISL MNIDAKILNKILANRI/WGN*AE ERNKEYSIRKRGSQIVPVC R*H DCVSRKPHHLS PQSP*ADKQLQ QSLRIQNQCTKITSILIHQ*QTNR EPNHE* TPIHNCFKENKIPRNPT YKGC EGP LQGE LQTTAQ* NKR GHKQMEEHSM LMDRKNQHRE NRHTAQGNL*IQCHSHQATNDF
6267	36635	A	6317	1	1797	
6268	36636	A	6318	2	2063	
6269	36637	A	6319	1	1212	

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6270	36638	A	6320	1	2718	MALFRVGM TTRRLGHANKFTR DLLVKRLLEYFVVEIIPGLRTK TTLVGPLETGYTSSDVNSPHF MLDIALSHNVKSTQLLRPWR NIDCSRNIHNAKKEEQMGDDE INRQQECSSSPAMEQSWTENDF DELREEFVRRSNYSELQEFIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQEITKIRAELEKEIE TQKTLQKINESRSWFFKINKID RPLARLIKKKREKNQDTIKND KGDIIPTDPTIEQTTIREYYKHL TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPIGTGEIEAHNSL PTKKSPGPDGFTAIFYQRYKEE LVPFLLLKLSQIEKERILPNSSYE ASIIILPKPGRDITTKENFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KLISKFSKVSQGHKINVQKSQAF LYTDNRQTESQIMSELPFTIASK RKYLGLQLTRDVKDLFKENYK PLLNEIKEDTNKWKNI PCSWVG RINIVKMALLPIRFSAPIKLPMT FFTELEKTTLKIWNQKEP/CIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNLYLFDKPKD KKEWGGKDSL FNKWCWENWLA ICRKLKLPFLTPYTKMNSRWI
6271	36639	A	6321	1	2307	
6272	36640	A	6322	1	1989	
6273	36641	A	6323	1	3285	
6274	36642	A	6324	3	4732	
6275	36643	B	6325	1	2693	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6276	36644	A	6326	603	2976	DNTARGTIRQQHLLFTNIRCSA ASAAADTQANRVWSGPPANSNR PAAARVLTVRRKTNKQKGHPH QNPICTSFSSKTKETQITIREYY KHLVYANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRITSDIE AIINSLPTKKSPPDGFATAEFYQ RYKEELVPFLLKLFQSIKEGIL PNSFYEAIIILPKLGRDITKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHQDQVGFIPMQG WFNICKSINVIHHMKTDKDKNH MIISIDAFAKAFDKIQPFMLKTL NKLIGDGTLYKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLNFIVLEVLARAIRQEKEIK GFQLGKEEVKLSLVDEMILSL ENPMVSAKNLLKLISNFSKVS YKINVQKSQAFLYTSNRQTESQ IMSELPFTIASKRIKYLGIQLTGD VKDFFKENYKPLLNEIKEDTDK WKNI PCSRVGRINIMKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRARIKSLSQKNK AGGITLPDFKLYYKATVTKTAC HRVGRAQQHSISKWKWYIHDW SQVGPEGTNDSARYPDTTQKW TAAALQPLSRITSLKDSHEGKSS QWAE LRAVHLVLRFAWKEKW PDVQLYTD SWAVASGLAGWS GTWKKHDKWIGDKIEWGRATP VIAQWAHEQRGHGGRDGDYA
6277	36645	A	6327	3193	6107	SMKTGLEKKMKRNEQSLQEIW DYVKRPNLPLIGVPESDGDNAT KLENTLQDIIQENCNPLARQANI QIQEIQRTPORYSRRATPRHIIV RFTKVEMKEKMLRAAREKGRV THKGKPIRLTAALSAETLQARR DRRPIFNILKEKNFQPRISYPAK LSFVSEGEIEYFTDKQMLRDFL MTRPALKELLKEALNMETTGA PRFIKQVRLRELQRDLDTHTIITG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADL
6278	36646	A	6328	1	1808	
6279	36647	A	6329	1	4695	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
6280	36648	A	6330	1	2915	MIMGDFNTPLSTLDRSTRQKVN KDTWELNSALHQADLIDYRTP HPKSTEYTFFLAPHHTYSKIDHI AGNKALLSKCERTEIHTNCLSDH SAIKLQLRIKKLTQNHSTTWKL NNLLNDYWVHNEMKAEIKIF FETNKNKDTTYQNLWDTFKAV CRGKFIALNAHKRQKERSKTD RTSQLKHLENQEQTTHSKARRS WFFEKINKIHRPLARLIKKKREK NQIDAINKDKGDIITNPTEIQTTI REYYKHLTYN
6281	36649	B	6331	1	6730	
6282	36650	A	6332	1	378	
6283	36651	A	6333	3	1700	
6284	36652	A	6334	1	1759	
6285	36653	A	6335	2	409	
6286	36654	A	6336	1	2051	MFGRSRSWVGGGHGKTSRNIH SLDHLKYLYHVLTKNTTVTEQ NRNLLVETIRSITELIWGDQND SSVFDFLEKNMFVFFLNLRQK SGRVVCVQLLQTLNILFENISHE TSLYLLSNVYNSIIVHKFDFS DEEIMAYYISFLKTLCLKNNH TVHFFYNEHTNDFALYTEAIKF FNPESMVRIAVRTITLVYKVV DNQAMLHYIRDKTAVPYFSNL VWFIGSHVIELDDCVQTDDEHR NRGKLSDLVAEHLDDLHYLND LIINCEFLNDVLTDDLNRFLFLP LYVYSLLENQDKVFLIIHHAFLV NSLAEVILNGDSEMYAKTEQD IQRSSVLPTLSSLWQGSLSLNLQ LQSGLHKCSSHLGCAQAAADS VTGEIPAIRSEWLISAGSKART FFFLKMLIGFWEKVDCEYQRR QVLSTRLQALPSNRLTDVAAY HSSCMLGFGSTAPRGSWIGDPA AVHLPLPGELAEHLGSKGTTTV TKHQPPQAKPSIRCFIKPTETLER SLEMNKHGKRRVQKRPNYK NVGEEDEEKGPTEDAQEDAE KAKGTEGGSGIKTSGESEIE MVIMERSKLSLAASTSVQEON TTDEEKSAATCSESTQWSRPF LDMVYHALDSPDDDYHALFVL CLLYAMSHNK/GKSPEKEEGLS GTQSHPGKAGTFGKEGAERK
6287	36655	A	6337	2	2753	
6288	36656	A	6338	1	577	
6289	36657	A	6339	1	849	

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6290	36658	A	6340	1	1293	
6291	36659	A	6341	1	861	
6292	36660	A	6342	154	6208	RRAPGKIPGQASAFGLGRTWSRP CLRTQLCVIVSCLAKAGVQGYL VGSPGGAKRFLFSERTGFSFKL AAMSSWLGLGSLGQSLGQV GGLASLTGQISNFTKMDLMEG TEEVEAEIPDSRTKEIEAIHAIL RSENERLKKLCTDLEEKHEASE IQIKQQSTSYRNQLQQKEVEISH LKARQIALQDQFLKLQSAAQSV PSGAGVPATTAASSFAYGISHP SAFHDDDDMDFGDISSQEQEINRL SNEVSRLESE
6293	36661	A	6343	3810	5310	SQGTCTVPRPCNVSG*RI/SIEEI EAGRIPNPHLGPVEERLALHVL QQQGLVPEHVESRPLYSPLQPD IEQAFPSFGRKSRWIRVIPPRFF LRCIWNTNRDVLDDLSLTGEK MSDIYVKGWIMIGFEEHKQKT VHYRSLGGEGNFNRWIFPFDFY LPAEQVCTIAKKDAFWRLDKT ESKIPARVVFIQWINDKFSFDD FLDPYAIVSFLHQSQKTVVKN TLNPTWDQTLIFYEIEIFGEPAT VAEQPPSIVVELYDHDITYGADE FMGRICQPSLERMPRLA WFL TRGSQPSGELLASFEIQLREKPA IHHIPGFESEDTLPYPPQREA NIYMPQNIKPAQRATAIEILA WGLRNMKSYQLANISSPSLVVE CGGQTVQSCVIRNLRKNPNFDI CTLFMEVMLPREELYCPPI TVK VIDNRQFGRRPVVQGCTIRLSLES FLCDPYSAESPPQGGPDDVSL LSPGEDVLIDDDKEPLIPQNYA
6294	36662	A	6344	1	527	
6295	36663	A	6345	5251	5711	PPQRGPSSSCYSRSQRVSRCR SRHRPSAASPRGRPSGRSGLLA GLRLWAGAGCFQCPCLQRL FSPEALRPQAPAHKGLFSGSLW PQQRSHQGLRAAATS*DRRAAG ALCKWCPRPSGTPRGEHLS*EN ESLPP**RWAHQTAPEQSQTS
6296	36664	A	6346	1	924	
6297	36665	A	6347	1	894	
6298	36666	A	6348	1	525	
6299	36667	A	6349	6	343	
6300	36668	A	6350	1	2693	
6301	36669	A	6351	26	353	
6302	36670	A	6352	1	9182	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
6303	36671	A	6353	1	8655	EA AKDLADIAAFFRSGFRKNDE MKAMDVLPILKEKVAYLSGGR DKRGGPILTFPARSNHDIRIQE DLRLRLISYLACIPSEEVCKRGFT VIVDMRGSKWDSIKPLLKILQE SFPCCIHVALIIPDNFWQKQRT NFGSSKFEFETNMVSLGLETKV VDPSQLTPEFDGCL EYNHEEWI EIRVAFEDYISNATHMLSRLEEL QDILAKKELPDLEGARNMIEE HSQLKKKVIKAPIEDLDLEGQK LLQRIQSSESF
6304	36672	A	6354	1	1338	
6305	36673	C	6355	152	404	
6306	36674	A	6356	137	1278	MDSQPNSTRGQSGRR/MEIKGI QLGKEEVKLSLFADDMIVYLEN A/TSQPKISLS**ATSAKSQDTKS MCKNKHHSYTPITDKQRAKS* VNHSQLLQRE*NT*ESNL*GT* RTSSRKTTHNCMSMK*KRIQTNG RTFHAHG*EESIS*KWPYCP*F IDSMPPSSSYQ*LSSQNWKRL SSSYGTTKEPASPQS*AKRTKL EAS/LLPDFKLYYKATVTKTAW DMDEAGNHHSQQTITRTKNQT PHVLTHRWELNNENTWTQEGE HHTPGLVVRSPDPEQNFKAVR CLDLPD/PSSSFLAVLTFHFKA FLQSLR*DKPRS/SPALGTWHP *KITPKKQ/HQAITKPNTYEYRTA VKPSVVGALPDINSFLKLGGLH RITNGCLLD

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6307	36675	A	6357	1	2569	MRTKTQHTRISWDAFKAVCRG KFIALNAHKRQERSKIDTLTS QLKELEKQEOTHASKASRRQEIT KIRAELEIETQKSLQKINESRS WFFERINNDRPLARLIKKEKREK NQIDTIKNDKGDIITDPTEIQTIT REYYKHLVANKLKNLEEMDKF LDITYTLPRLNQEEVESLNRPTIG SEIVTIINSLPTKSSPGPDGFTAE FYQRYKEELVPFLKLQFSIEKE GILPNSFYEAIIIPKPGRDTTK KENFRPISLMNIDAKILNKLAN RIQQHIKKLIIHDDQVGFIPGMQ GWFNIRKSINVIQHVNRADKDN HMIISIDAEKDFDKIQPFMLKT LNKLGIDGTYLKIIIRAIYDKPTA NIILNGQKLEAFPLKTGTGRQGC LSPLLFNIVVEVLASAIRQEKEI KAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFIIASKRIKYLGIQLTRDVKDLF KENYKPLIKEIKEDTNKRKNIPC SRVGRINIVKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKRAHIAKSILSKQKNKAGGITLP DFKLYYKATVTKTAWYSYQNR DIDQWNRTEPSEITPHIYNLYIF DKPEKNKQWKGDSLNFNKGW ENWLAIWRLKLDPPFTPTTKI NSRWIKDLNVRPKTIKLEENL GITIQDIGMGKDFMSKTP/TSNG NKRQN*QMGSNETKELLHSKR
6308	36676	A	6358	1702	2252	FLSLFFISLASSLSILIIHIMNSW IPHSPIFDLNVESRLCPLGDIM M*IPLTWYLIVTCTHLSREITTV PRGLARLWSFTRICPRTHCKPIP AIVLLRAGCPPSCWWDQDTHS QLPSKRSSYLFFCTVTEYPFLO *WP*NHGTPC*TAPLWSMF/PCS CWYPVTGPGVSCSPSCVQVFS FISHL*VRTCGVWFFVLAIVC*E *WFPASSMSQAVLVTVL*YSL KSGSVMPA/FSFGLGLTWRCR LFFGSIRTLK*IFPIL*RKSLVA* WGWH*YKLRWAVWPFSSRY*F FLPMSM/VMFFHLFVSSFISLSS GL*FSLKRSFMSLVSWIPKYFIL FEAIVNGSSLMIVLWVCLLLLH KNACDFCTLILYPETFLKLLISL RRFVAETMGFSRYTIMSSANR DNLTSFFPN

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6309	36677	A	6359	207	1209	IPRHHPPKTKPGRS*/TP*IDQ*Q ALKLRQ/CINSLPTKKSPGPDGF TAKFYQSPSLTGKNDKEPEILPY FHADFLVVPGTHQASVLMVL GHKSPHRNSPPSVCMANFFQT KPPSQSIHNAVNTHTDPLFLVL LKDRGLLVIWCHESQGDLELWH LVLLDSKCCFGSMTHRMEWSG PSAAGLLEFAGGPLQTLFAVVS AVEAAEQRIILLNSKCCCLIPLE ALSQRGIW/PWQGSVPVRPWTTT TLWPVRNQTQQTSLMPCQL EGKEPLALPTKEAEIEGRRTGEI KKVERDSNTNKEELLLDLAFK VSSFLDKLEEVVELLVIGELQL YPSK
6310	36678	A	6360	544	678	AFHHVSFGCINVFF*EVSVHML CPLFDGVVFFLVNLEFFVDSG
6311	36679	A	6361	7	94	VRTSGVWFFVLAIVC*E*WFP SSMSLIY
6312	36680	A	6362	381	431	ATKQDSVSKKKEEEEEEEEEEE EEEEEEEEEEEEEEEEKEK/GNK ERKK/DKGKARQVQARQIYLLS LHLGRIRKVPNNKA*SSCP
6313	36681	B	6363	1	603	
6314	36682	A	6364	1	987	
6315	36683	B	6365	1	444	
6316	36684	A	6366	977	1177	RTSISSPVSTCSPLVMTLLPQP TVPWRMWRPCTQ*RNAITFSP AVAMGLPVEAVICLSV*DSPA
6317	36685	A	6367	1148	1395	
6318	36686	A	6368	33	663	VHVLGDDTDETNHHSQQTIA RTKNQTPHYLTHRERLSLRGL HSCAYSLHRWLGAHQKGS NTKGGCGGQGPRTSERGPASGEF SENCTSLGQRGVFSPPRRALL HSPSDGSPVPLGAVDSSP/PASTR RDWSHWAVGKPSPEREPAGKV T*TTTQLQPASP*REHPLLSQH GHCLKISLPLLLPTVLSPPPLSLC SNVTFSTRPLT
6319	36687	A	6369	1	1314	
6320	36688	A	6370	120	410	
6321	36689	A	6371	1	492	

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6322	36690	A	6372	3	945	EEVPRSMKSKKKRKRKRKRKR EEEEEEEEEEEEEEEEEEEE EERRVEGEVEEEEEEGEKEKID PSHLEKMYVRNKNTMYEVCLM PIGIKQVNVGAMQCILVAPYIS PIVGVINFNDQVNSQGGGSKME DGIHFRGKVMHLHVGRKRQRVK KGLGYAFISSMKTNEYTKLVVP EWGLAEKIPKNVEATLELGNRR SKKTGGILPLLWNFELERDEL GYLVEEISKQPSIQMTWLLK AFRFQEAEPKSSLENLNDNVIE KKNPFSEGGKFLAAEICISNEE WNGVNPQDYGKWLQGMA EVFTATPSITGLEA
6323	36691	B	6373	1	792	
6324	36692	C	6374	348	884	
6325	36693	A	6375	1	588	
6326	36694	B	6376	1	5339	
6327	36695	B	6377	520	3146	
6328	36696	A	6378	1	2044	
6329	36697	A	6379	1	585	
6330	36698	A	6380	1	2433	
6331	36699	B	6381	53	441	
6332	36700	A	6382	2	425	
6333	36701	A	6383	1386	2569	FLRKHRESGKDEEMTALCSFPG VAGEDELQVIQPEKSVSVAAGE SATLRCAMTSLIPVGPIMWFRG AGAGRELIYNQKEGHFPRVTTV SELTKRNNLDFSISISNITPADAG TYYCVKFRKGSPDDVEFKSGA GTELSVRAKPSAPVVSQPAVRA TPEHTVSFTCESHGFSRDLTK WFKNGNELSDFQTNVDPAGDS VSYIHSTARVVLTGRDVIHSQV ICEIAHITLQGDPLRGTAANLSEAI RVPPTELVTSQPIRAENQANVT WQVSNFYPRGLQTLWLENGNV SRTETASTLIENKDGTYNWS WLLVNTCAHRDDVVLTCQVEH DQQQAVSKSYALEISAHQKEH GSDITHEPALAPTAPLLVALLLG PKLLLVVGVSAIYICWKQKA

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6334	36702	A	6384	1	2453	MEPAGPAPGRLGPVLCLLLAAS CAWSASRQLPAVQVLRGDVTC GSDHVFLLAYIKHLAVAGRRA LKATVHVHQRTLRLPGGCGSV PGKRAVTLISKSDGQPAFPGA PAGNTNTFLVCSCGFPDLQSSR GPERALCAFIQCLMVRPEQRE KNWPGPRGRSMARPGWNAKPP VVQAKAFKNWAVLELSTVSAR NLTGSRJPRENTKVILIGTIWVL CFLGSLGVCDPGGTHSLAM HVVIFPGVGSNNPSIVIIIRPIL QIKSQRSRVGETTFPGVSWVAEL ESKSKHTFSQCALLQPWGRK LSSCSQRTYNLLVCIQSMNVI DKHLRKHGRSVAGEEELQVI QPDKSVLVAAGETATLRCTATS LIPVGPQWFRGAGPGRELIYNQ KEGHFPRVTVSDLTRNNMD FSIRIGNITPADAGTYCVKFRK GSPDDVEFKSGAGTELSVRAKP SAPVVS GPAARTPOHTVSFTC ESHGFSPRDTILKWFKNGNELS DFQTNVDPVGESVSYSHSTA KVVLTREDVNSQSF*GPTVT LQGDPLRGATANLSETIRVPPTLE VIQQPVRAENQVNVTCQVRKF YPQRLQLTWLENGNVSRTETA STVTENKDGTYNWMWLLVN VSAHRDDVKLTCQVEHDGQPA VSKSHDLKVSAPKPEQGSNTA AENTGSNERNIYIVVGVVCTLL
6335	36703	A	6385	1	405	
6336	36704	A	6386	91	2926	PACPSPLPFTNTDTHIDTSSPA SRSTRCLCISTHGVLAQSGGSSG GPAVPTVQRGIKMLVSGCAIIV RGQPRGGPPPERQNLNIRAGN LARRAAATQPDADKTPDEPWA FPAREFLRKKLIGKEVCFTIENK TPQGREYGMIIYLGKDTNGENIA ESLVAEGLATRREGMRANNPE QNRLSECEEQAKAAKGMWSE NGSHTIRDLYTIENPRHFVD SHHQKPVNAIIHVHRDGSVVRA LLLDPYYLVTV
6337	36705	A	6387	2	448	
6338	36706	A	6388	1	645	
6339	36707	A	6389	1	294	

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6340	36708	A	6390	23	321	RGREHTQGIPGAGKRWH*FKV LLTQ/CW*SEFSVIRQFKAGPGG LDQFRDRSK/RWLRDLRGLLG SLNASLVLRALFSGNWGLTAN QL*LAVGAKGDPEA
6341	36709	A	6391	1	1599	
6342	36710	A	6392	1	561	
6343	36711	A	6393	1	1833	STLASSEGQGGFWRGPRLAILL LLFLGPCHARSHDGKYSREKN QPKPSPKRESGEFRMEKLNQL WEKAQRQERYPCRRRRRVKQV AAGTPRVFLKTPEMGVFELCRP SGPHYLISNAGVRLDLLNSPVL SIPESLRGKVNDLQNKKELLER KGRGETGLARPMHDLTAAQGG YGCALVHGAQVEGAGAGQGWA GTVHATCRGETGTACQEAALVT ATACSSCQRGQTRAPQGOHTL ESMGLNCLPQGAASGSDHHCG PRISDLPGSAARTSRWPASSELH LPPVRLAELHADLKIQUDELA WKKLKL DGLDEDEGEKEARLIR NLNGHWRAEDAHQDGGVYNK WDIPTVVGVGVAIALVAVKL FFLPINIRCVLSSEPATLHSLQV ASVLWSLEFLPYGSRSPVVIQET VILAKYGLDGKKDARQVTSNS LSGTQEDGLDDPRLEKLWHKA KTSKGFSGEELDKLWREFLHH KEKVHEYNVLLLETLSRTEVHPG PQDGVASTGREHSPMETLQFEE LKHFEAKIEKHNNHYQK/QLEIA HEKLRHAESVGDRRSV*SASPR ESTPCLEGRTKGAGLPR*KKHL QDLSGRISRARHKRTLKALGS
6344	36712	A	6394	1	185	DFFDNSAQVTIAGIPCDIRHVSP RKIECTTRAPGKIV*GSPPLSQA EGFFLKLEMLLRDWN
6345	36713	A	6395	1	1512	
6346	36714	A	6396	117	268	QSLLELYLHLYLHLCYLHLANK QELTLTWYKE*CTFFLPSPV*NPF HQNLA
6347	36715	A	6397	1	500	

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6348	36716	A	6398	1301	2565	TLLTILPFYLFKNRSTL.TGYLR WILSTKLFLCSTLWLAPTFLFLIP/ LPDPHDCISLIHLAFTFPFHTSFF PIPHPDHTWFDGSSTWPNRHSP AKVGYAIVVSSTSIIEATLPPS TTSQQAELIALTRALALAKGLH VNIYTDKYAFHILHNAVIWA ERGLSTQRSSIIASI.KTLLKA ALLPKEAGVIHCKGHQKASDPI AQGNAYADTKFLDLAFPLR LSFTCQITQAVSQALGIQWNLH TPYRQSSGKDWTVFLPLALHR IRARPREATGYSPELLYGRFTL LSPNLVPDTSPLGDYLPVLWQA RQEIHQAAANLLSTPDSQLYED TLAGRSVLIKNLTPQTLQPRWT GPYLVIYSTPTAVRLQDPHVV HRSRIKLCPSDNQPNLSSSWKS QVLPSTSLKVTLISEEQ
6349	36717	A	6399	581	2517	LFLGYSHTSLLPFPVQSLHL PLYLHTLTHKYGIPLPPWRPIM HPLPSH*NLITLTLNANIPSCST L*KD*SLLSLTCYSMAF*/QPIN PYNSPILSVQKPKPYSSFRVY SLFVESPTITIVPGPDFNLASHIIP DITPDYDCISLIHLTFTFPHVS FFPVPHPFHTWFDGSSTRPNCH TPAKAGYAIVSSTSIIEVTTLPHS TTSQQAELIALTRTLAKGLC VNIYTDPISTCTMLFYGLKCFLT MQGSSIIASLIKTLKAAALLPK EAGVIHCKGPKQKASDPIAQDNT YADKVAKKAASVPTSIHSSFS PSHLVTPTYSPETSTYQSLPTQ GKWFLDQGYLLPASQAHSILS SFCNLFHVGKPLARLSELLISF PSWKSILKEITSQCSICYSATPQ GLFRPPFPKHQAWGFVPTQD WQIDFTHPQVQKLLYLLVW VDITFGWVEAFTGSEKATVVI SSLLSDVIPRFLCPTSQSNNGLA MISQITQAVSQALGIQWKLCTP YHPOSSGKVKWANGLLKTHLT KLSLQKKDWTVLLPLALLRIR ACLRNATGYSPELLYRCSFLL GPSLIPDTRPTWTAPPKTWHPY YLLSSHTPIHRSQLLIHALLFTL PVYTVSPSHHS

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6350	36718	A	6400	281	1095	DCSKNRHSQVIAEGNICKIQE VRRKEDTQGEKDPESLLPL LAPGPT/YSTYYNISVAKAELL NKLKDQPEMAEIGLGEEDVDH ELAQQKIQLIESIRKLSVLREA QRGLLEDINANSALGEEVEANL KAVCKSNEFEKYHLFVGDLDK VVNLLLSLGRLARVENALNSI DSEANQEKLVLEKKQQLTGQL ADAKELKEHVDREKLVFGMV SRYLPODQLQDYQHFKMKS LIJQRELEEKILGEEQLKCLR ESLLGPSNF
6351	36719	A	6401	1	972	
6352	36720	A	6402	514	736	
6353	36721	B	6403	446	991	
6354	36722	A	6404	521	903	NIKPASQISPG*/*VHSSPTQRLS APPSAA/GRLLSLSLPAGLVGGD TARCIPAGRLRLPCSWLDPGKL LHLSLKSXGSGRSGAGTLQEG NQSVCIQAEKPLKPAIQTSQ MNVLCRAYSWVIDWD
6355	36723	A	6405	11	545	
6356	36724	A	6406	3	2920	
6357	36725	A	6407	1	2388	
6358	36726	A	6408	275	479	
6359	36727	A	6409	1	3810	
6360	36728	A	6410	7	1047	
6361	36729	A	6411	1	705	
6362	36730	C	6412	304	638	
6363	36731	A	6413	99	759	WAYLDFWM*HIPHLGVLL/SAH LLSDLNSCF*MGSRTEGSATG PGSCSAALPLGPYDPAAPMVLE VSMADRDASPHDPLAKFLFPVP MTLHLSALLEVLVPEGGTLPPGD TTTIPLNW/IVKIAT*TLWVPTF KFTGCRNLNTMWKLPRLGASTL *SNSLRCTLTFSHDWSGWDAG HQVIRPHGFAGYNTCGCFHRL MLSACGFSRQMVQAVNGSTTL GSGG
6364	36732	A	6414	1	685	
6365	36733	A	6415	1	1359	
6366	36734	A	6416	3	7714	
6367	36735	A	6417	1	723	
6368	36736	A	6418	1	528	

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6369	36737	A	6419	38	530	HSPRRSAASLLSQRDHEPHQKE ETPNTSEHQKEKTPDTPPLRTV TLTVRVHGFIVSETKNPPIPD TKLRG/ERLQGFGLAGERSE/GC RPSP*VLQLIKAVVTQRLGGR WDWAPWSRRWCSSGRLRPHR NQWSGWEAQAWGLQVPEPCP AGRQLRPGEKSSTAP
6370	36738	A	6420	1	649	
6371	36739	A	6421	1	987	
6372	36740	A	6422	1	924	
6373	36741	A	6423	1	435	
6374	36742	A	6424	1	147	
6375	36743	A	6425	1	1107	
6376	36744	A	6426	3	913	
6377	36745	A	6427	1	159	
6378	36746	A	6428	313	1083	
6379	36747	A	6429	1	1245	MAQELRDTCTSFSSRFQDQVEER VMVIEDQINEMKQEEKFREKR VKRNKQSLQEIWDYVKRPNLR LIGVPEKNLEETDKFLDITYTLPR LNQEEVESLNRPTDSEIEAIINS LPTKKSSGPDGFTAIFYQRYKE ELP/RQRHNKKREF*TNIPDEHR CKSPQ*NTGKPNPAHQKAYPP *SSGLHPWDARLVQHTQINKRN PAYKQNGQKPHDYLSRCRKG L*QNSAALHAKNSQ*IRY*WDI SQNNKSYL*QTHSQYHTEWAK AGSIFPENWHKRGMPSLTTPIQ HSVGGSGQNGQAGERNKGYSI RKRGSQIVPVYR*HNCISRKPH HLSPKSP*AGKQ/SSAKSQD/DKI NVQKSQAFIHTNNRQTESQIMS E/APIHNCYKENKISRNPYKGC EGPLQGEQTTAQRSKKGHKQI
6380	36748	A	6430	39	314	KSECLITYTKGSQRLASNGTKLD GE*L**VDRIRLQKIGNDKLLPA KGGCSNPQRS*KPRKKIRQMA N*NKQHRGDLK*PDGAENHGT RTT
6381	36749	A	6431	213	843	VDRSRLQKVSNNKLL*AKGEC NPLQGS*KP*KKIRRMAN*NKH CREDLK*PDGVENNGTRTS*FM HKLQ*PI*SSGRKGISD*R*N*N KIHQG*NEGKSVKGSQRESSY PQRKAHQTNSSGLSRNPSTQKK VGANIQHS*RKEFSTQNFISSQT KLHK*RRNKIFYRQADAERFCH HQACVTRAPEGSTKHGKKQPV PAPAKTGQIV

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6382	36750	A	6432	1	2112	MRAFVVLMDVSKLPSEGGPG LRSNQQHMRMFLTSVDRGSVS LLADAVAAATPQGKTSQPRGPS NLAAADLRVAEESGMENFLK MSFDSIRPAQDGGCTPEISMVTP SPGWSVHTGDLGDHPLPRMVS AHRRSRWSPPPQDGGCTPEISM VIPSPGCSVHTGDLGDHPLPRM LSAHRRSRWSPPPQDAQCTPEIS MVTSPGWSVHTGDLGDHPLP RMVSAHRRSRWSPPPQDAQCT PEISMVTPSPGCSVHTG
6383	36751	A	6433	1	648	
6384	36752	A	6434	1	1539	MLVSFVSLGSLCLQPGSQTLLE KNRTVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE/ SAN*NQCCREDLK*PEAEIHGT RTS*HMHKLQ*PI*SSGRKGVSD *GSNQ*NK*WGEWNQVGKHS A GYYPGELPPSKAGQSHNSNGNT ENTTKILLEKSNPKTHNCQIHQ G*NEGKSVKGSQRERTREARA NKFKS*QKARYN*DOCRTERD RNTENPSKN**IQEPVF*KDQQN **NASKTNKEEKREESNRNRKK **KNRTVKPHVSFTLLPALSHVS EKNEAESMNSLIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFDELTEVGFRRSVITNSSK LKEDVRTHCKEAKNLEKRLHE WLTRINSVEKTLNDLKLKMSMA RELHDTCTSFNSRFDQVEERVS AIEDQTNEINNGENGTLENTL QDIIQENFPNLARQANIQEIERR TPQRYSSRKATPRHIIVRFTKVE MKEKVLRAAREKGLERQEQTN SKASRRQDITKISAELEIETQK TLQKINEFRSRFFKKINKIDKTL ARLIKKKREKNQTDAIKNDKR DITTDPTIEIQTITREYKHL YAN KLENLEEMDKFLDTYTLPRLNQ EEAESLNRTITGSEIEAINS LPT
6385	36753	B	6435	137	586	
6386	36754	A	6436	129	506	
6387	36755	A	6437	1	237	
6388	36756	A	6438	182	1034	

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6389	36757	A	6439	203	650	SAIVCGSPRLRLRMQAVSSRINSA HSRGAIYSQASSAAACPSVSI AF LRR*IEANVS/WIRTLSTLCTPK CGPGFKHRIVLCKSSDLSKTFPA AQCPPEESKPPVRIRCSLGRCP PP RWVTGDWGO/CDSRDFRPGRR RRDFCRNCRAGAGAH
6390	36758	A	6440	207	426	AECTRCAPK/HSCYPVLLIVVS P*KKQNCSLGELSCWRRRES CRS SWSNKALPSLTRCLRGFV CGLS CYKGSS
6391	36759	A	6441	524	783	TAVLAARISNQWILSCWS/AVG CTPKCGPGFKHRIVLCKSSDLS KTFPAAQCPPEESKPPVRIRCS LG RCPPPRWVTGDWQGLSPTREK
6392	36760	A	6442	1	1524	
6393	36761	A	6443	1	8738	
6394	36762	A	6444	1	642	
6395	36763	A	6445	1	549	
6396	36764	A	6446	8	434	
6397	36765	A	6447	1	2922	
6398	36766	A	6448	18	1158	FLDFDCPYGSAHITGLRFWLPW YRKRQRYWGSNGCMPPPSLR VPERCPSHTEPRNL TGA*ELL LLL GLSEDELPILAGLSLSMYL VT VLRNLLISLAVSSDSHLHT PMC FFLSNLCWADIGFTSAMV PKMI VDMQSHSRVISYAGCLT QMSLF AIFGGMEENMLLSVM AYDF VAIChPLHYPVIMNPHL GVFLD LGAFFLLDSQLHSW IVLQFTF FKNVEISNFV*DPS QLNLACSD SVINSIFIYLD SIMFGFLPISGILW SYANNV PSILRISSSDRKSKAFS TCRSHLAVVCLFYGTGIGV YLT SAVA PPLRNGVVASV TYAVVT PMLNPFYISQR NRDIQSALRRLR SRTVESH DLLHPFCVGGKKQA
6399	36767	A	6449	2	1535	
6400	36768	A	6450	1	635	
6401	36769	A	6451	222	1040	
6402	36770	A	6452	2	1135	
6403	36771	A	6453	1	576	

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6404	36772	A	6454	2	694	QCGGIQRSHGWSWSEASDSVW QLQSMWMLDKLTGVFAPRPST GPHKLR/ECLSRIFLRNRLKYA LTGDEVKKNCMQRFIKINDGKV RTVDITYPVGFMDVVISIDKTGR EFPVLIYDTKG/RAFAVHRITPE EAQVPSCAKVRRDLCSAQKGIP HLVTHDARTIPLRSPSSKVNDV TIQNDLEDWARFT*FSSKFDNW *TCCMGDWEGA*P*GRNVVLI HQQRRRAPWDLF
6405	36773	A	6455	1	243	
6406	36774	A	6456	3	766	
6407	36775	A	6457	1	741	
6408	36776	B	6458	500	8643	
6409	36777	A	6459	1	7863	MKPRTLTVRVLTALKVARLESV PSDVQMCSEFLPSDSAQLASP SGSRRTGAAGGAAYQSCAVLPH SSALWVVDGTRCRGAGGSAHQ GGSATQEPTEVERVEGSGMAGCR SRVLPHWKAANVLGMSVESAP AVEEEKGEELEQKEKEEEDTS GNTTHSLGAEDTASSQLGFGVL ELSQSQDVEENTVPYEVDKQL QSVTTNSGYTRLSDVDANTAIA HEEQSNEDIPAEQSSKDIPVTA QPSKDVHVVKQNPPTA
6410	36778	A	6460	2	669	ERRRRRLTIPCPPPHAPPTGGQ ACRENAEGIL*AANTSEPGKDA EK*KIKV*LAP/CSHSGSSLQSDP HFGCSLGPS/DPALGLSGCILPPC SGSYLAAPNRSRIKPKPLPW/H /ESYLPASAVRPHGTQAPGLWPE RGL*PAGFLRPEPVRAASER/Q EAVSPER*VPRPPKAQQLHGQS PDPSSLCTALRQDHTHWLDARS VYPDWRGQWPPLHQDCGHG GWR
6411	36779	B	6461	241	369	
6412	36780	A	6462	1	510	
6413	36781	B	6463	1	630	
6414	36782	A	6464	229	561	SCRGYSRILLFHKKSSWCSQVIS IFRYNIICSRLPKSWKWRLPVY MNLW*YHWFQYHSSINFISFR SMWFIHINFKRSPAFILSGSWIS IARWQIFVFFTFGSRITKV

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6415	36783	A	6465	1271	1710	TEGLGHRSETPGGAALDALTG ERPRVACFPAARGRLRPRRL MIGPFETGGGQRLTLRPRRRR QRRRP/WQGLERPHVRNWGIEL ETLRDAFRPQPSVWRTARGEA GKRKGRLVECLGSQRKVLGV LLYAVTRGSPFNLFTRD
6416	36784	B	6466	1	772	
6417	36785	A	6467	1	1272	
6418	36786	A	6468	3	236	
6419	36787	C	6469	1	457	
6420	36788	B	6470	148	324	
6421	36789	A	6471	1	1407	
6422	36790	A	6472	1	651	
6423	36791	A	6473	619	835	
6424	36792	A	6474	52	535	
6425	36793	A	6475	319	647	LCRIYMYFCVMKNWMQSLW KLCTNKR*RIDKPTLHQVVVRK *LTPLMKNQVDSLELLETRSL KKDPVELGSKSLRCCQTEPV NLLPHVSIKTKI*SRILRLQRP
6426	36794	A	6476	39	515	
6427	36795	B	6477	1	807	
6428	36796	A	6478	3	247	GANICCW*GLQE/VFHSW*KTQ EPSWLHLVDPTTGLQVELPASP APFARIPQPLGGRWDWAPWSR GWCSSGRLGQHRSPWSG
6429	36797	A	6479	27	363	
6430	36798	B	6480	1132	1268	
6431	36799	A	6481	1628	2008	
6432	36800	A	6482	953	1087	
6433	36801	A	6483	2	443	QLAGRCGGRGMSGNRGC/WGA CGPAGVPGG/CWAWCALHSEE PASPALRSISRALLAAPPGRAR DLQPAMPEPTPSVGSAAQAS PTSAAPCSMAPSIDHPRAEECV ARRGTGRHDELIVALPFMMIPW HSSIQPFTHPFNWNFG
6434	36802	C	6484	175	423	
6435	36803	B	6485	122	608	
6436	36804	A	6486	644	1149	KTMHWKAPLMSWHMRASSQ KQTRTGTQT/MEAQLQLQRY QEALLQVLRKGEKAFNMGN SEVLQRADESCSQFYERLYEAF QLCSPFDPEATENQCMVNAV VGQTQGDIRRLKLECFMG NVTVQVLEVATKVYTNCEETQ GKGQFAGGSTYKGGCECPKTK
6437	36805	A	6487	1	2847	
6438	36806	B	6488	329	742	
6439	36807	A	6489	1	1035	

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6440	36808	A	6490	13	630	INPPPPFRPEPPSSNSPKMTDH KGERGEATRYMFSRPFARKHG VVPLGPHICRIYRKGDIVDMKG MGYCSKKGIATKCYHGNLE GVLPMLPQHACWPFVYNQFVL GQSFFPRELMCRJEHI*ALLRAR DKLPETVLKENDSEKERSPNEK GTWGSNLKRHPGSTPEEAHFV RTQWGRSLELAGTLFPMFMFG IIGVKEIK
6441	36809	A	6491	1	1020	
6442	36810	A	6492	1	330	
6443	36811	C	6493	250	372	
6444	36812	A	6494	1	345	
6445	36813	A	6495	2	335	TVRAYNVQHAVGIVVNRQVK GKIPAKRINVGIKHKHSTS*EN FLKRMKENDQKKKEAKEKVT WIQLKHQSAPPRE/AQCERTNG KEPELLEPLPYEFMHNTHYIHIYV CVH
6446	36814	A	6496	2	490	
6447	36815	A	6497	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQ/RKAPGKNLVYISLVLRAL L*G*DLTHHIIILFPFFLL**PAPP REAHFVRTNGKEPELL
6448	36816	A	6498	54	553	
6449	36817	A	6499	131	803	TMFCQTGSSVRRVGGPWAEN RTAMLRPCGGTFARKTRLSRLG NSPKMNEQQRGKRRGTPIIMFS KGLLRKHGVVPLAHIFMRVYK KGDIVRHRPRGMGYLVPKREL PQSCYPWPKPGRSLTNVTPAML VGHLL*NKQV*GQRFPLKRN MWRI*APFRHFLRSPRLASLKT CGRENGSRKKERPKPGGKVTVW GFQLKRRHLGFPQEEATFLK EPIGREGP
6450	36818	A	6500	1	489	

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6451	36819	A	6501	29	2028	ENEEEGEKMASTDYSTYSQAA AQQQYSAIYTAQPTQGYAQTT QQAYGQQSYGYGQPTDVSYT QAQTTATYQGTAYATSYGQPP TGYTTPTAPQAYSQPVQGYGT GAYDTTATVTITTQASYAAQS AYGTQPAYPAYQQPAATCPT RTED*ANKPTETSQSQSSTGGYN QPSLGYGQSNYSYPQVPGSYP MQPVTAPPSYPPTSYSSTQPTS DQSSYSQQNTYGGPSSYGQSS YGQSSSYGQPPPTSYPPTGGSY SQAPSQYSQQSSSYGQSSFRQ DHPSSMGVYQGESGGFSGPGE NRSMSGPDNRGRGRGGFDRGG MSRGGGRGGRGGMGSAGERG GFNKGGMDEGPDLDLGPV DPDESDNSAIYVQGLNDSVTL DDLADFFKQCGVVKMNKRTG QPMIHIYLDKETGKPKGDATVS YEDPPTAKAAVEWFDGKDFQG SKLKVSLARKKPPMNSMRGGL PPREGRMPPPLRGPGGPGGP GGPMGRMGGRGGDRGGFPPRG PRGSRGNPSGGGNVQHRAGDW QCPNPGCGNQFNAWRTECNQC KAPKPEGFLPPFPFPPGGDRGRG GPGGMRGGRGGLMDRGGPGG MFRGGRGGRGGFRGGGRGMD RGGFGGRRGGPGGPPGLME QMGGRRGGRGPGKMDKGEH
6452	36820	A	6502	1	693	
6453	36821	A	6503	3	657	
6454	36822	A	6504	1	434	
6455	36823	A	6505	208	443	

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6456	36824	A	6506	3	2650	LLPAFLLLCSDSHLQFCSQFAP RKTQGSQSVNNIQANIHKKN NHLMKKNDQKFKDLPMAGH PIHHQAQGGGAKNPQEQRRP MGQTTLPAEQEESRVKCKNCG AFGHSARNKTCPIKRWGALPL QVLGSHKEKENLKPAKALPFT TPGPFTTNDREKERSPSSTMNPS EMQRKASPRRWKHHNQTPSIH KVNKMVMSEEQMKLPSTKKA EPPTWAQLKKLTQLPKKSLEN TKVTQTPENTLLAALMIVST/A GAAAAANYTYWAYVPFPLIRA VTWMDNPIEVVYVNSAWVPGP TDDRCDDKPEEEGMMINISTGY RYPPICLGRAPACLMPIQNL VEVPTVGTTSRFTYHTGLLTFR DVAIEFSQEEWKCLDPAEDSY TRRKANSCKGPKYKNECGKAF TQNSNLTSHRHSGEKPYKCS ECGKTFTVRSNLTIHQVIHTGE KPYKCHCEGKVFHNSYSLATH RRIHTGEKPYKNECGKAFRGH SNL.TTHQLIHTGEKPFKNECG KLFTQNSHLISHWRIHTGEKPY KNECGKAFSVRSSLAHQTIHT GEKPYKNECGKVFVRGVRGVS GTTCLLSVFQVITVSSRSRAS ENRATQSILILAPPTSRGSGPGP ASVLRRLAQTRKMAWTESCT AACAAPSCLVLLYRGRGVPTDL QVPAPLFTSQSKLRPGSRTKSS
6457	36825	A	6507	54	360	CSTMNPSEMQRAPPRRQRHRS RAPSAHKMNRMMSEEQMKL PSTKKAEPPTWAQLKKLTQLA KKKLENTKVTQTPENMLLAL KTVSTVSAGVPSSEESD
6458	36826	A	6508	525	3656	SSTMNPSEMQRKAPPRRRHR NRAPLTHKMNMVTSSEQMK LPSTKKAEPPTWAQLKKLTQLA TKYLENTKVTQTPENTLLAAL MIVSMVVSLLPMPAGAAAAANY TYWAYVPFPLIRAVTWMDNPIE VYVYNSA WVPPTDDHCPAK PEEEGMMINISTGYRYPPICLGR APACLMPIQNLVEVPTVGT TSRFTYHTIDLMTEKVVVLA EVLLRFLKPGEDPTARYVSNK KCQPSVDWPTTISQRRGY
6459	36827	A	6509	1	246	
6460	36828	A	6510	1	246	

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6461	36829	A	6511	1	279	
6462	36830	A	6512	1	363	
6463	36831	C	6513	109	245	
6464	36832	A	6514	2	429	LMTFCWDTPRQSGVPRRMPH TGTWRTVGIRCPKKKLRANS MMRGKVQFPFP/DIQA YGAAPF EDLQVDFREMPKCGGNKYVLV LGRTYSGWVEAYPTRTEKTR VTPVLLRDLIRFRPPLWIGSDN GPAFLAALVQKTAK
6465	36833	C	6515	31	895	
6466	36834	A	6516	2	4735	
6467	36835	A	6517	263	418	
6468	36836	A	6518	120	295	YDPLPTWILGKISQRGAEEPAQ HPGCQL*LPPP/SPRTSSSPSCA GLTSVSPRPRFPR
6469	36837	A	6519	1	1758	MKIRRRFPSSLQLSADLQVPVR KAPRQGVSQEKRTKPSLELMIS GTISQEDIRNNVTRGCTPPAIQR VISSPPLLAIRNNVTEGVYTPCD TGGRVHLPVILLISRDGGHDIS FNIAVDVHSPCDTDPNIQGVY DMTPNIAMNVQPPGISQKRCT LPAILGLISYASSVNIRSNITGWL YIDRYVGSHVILYPLGIRMGVT GEMKGERRRGLHAATKWLEE HAPADYQNPQEYGRGTQLPGTQ PQLDPHEREDMQLNRDREAL LEGFKRGAQKATNVNKVSEVI QGKEESPAQFHQRLCEACAKQ VLVNGDAVSREEKRKENERQA RRNADLLVSCSNQSGPPKEARE ELWTKDYRPGQDLRLLSQATL TFHPTVPSPTLLGLLPAEDSWF TCLDLKDAFFPIRSAPESQKLFA FQWEDPESALAKTVRQRCVSC RQHHA/GKVQFPFP/DIQA YGA AAFEDLQVDFTEMPECCGNKY LPVLGRTYSGWVETYPTRA EK AREVTRVLLRDLIPRLELPPRIG SDNGPAFVADLLQKTATVLGIT RKLHAASRPQSSGKGIQNNRTG GVVYTPCDIESHVILFRSGY
6470	36838	A	6520	1111	1342	MFVPHIGFQNTAALCLRLGLGVL FP*PVGFPAGSCLL*WNRHWH VPDFSCVTTPOEWCGGVSDVC CGHPHAEPHLQ

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6471	36839	A	6521	1	1144	MIRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFVNRDAVSRKENGKENG GQARRYADLFSRTKNYQPVD LRLHQAQLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRALAATAALLVQEANKLTG QKLNKASRAVVTLMNTKGHH WLTNATLTDYQTLLENPRITIE VCNTLHPATLLPVSKSPVKPGC VEVLDIDSSRPDLWDQPWASV DWELYLDGSSFFNPQGEVEG/S RGDTSELPPCWVCGIPALTQRL EKQHLPPSGHQGSLKHLIWDLL LLTKKRTFSSMI
6472	36840	A	6522	1	554	
6473	36841	B	6523	63	620	
6474	36842	A	6524	1	796	SRTKNYQPVDLRLHQAQLT FHPTVPNPSTLLGFPPAEDSWFT CLDLKDAFFPIRLAPERQKLFAF QWEDPESGWPPCWRALAATA LVQEANKLTGQKLNKASRA VVTLMNTKGHHWLTNATLTD YQTLLENPRITIEVCNTLHPAT LLPVSKSPVKPGCV EVDIDSS RPDLWDQPWASVDWELYLDG SSFFNPQGEVEGSRGDTSELPP CWVCGIPALTQRLKQHLPPSG HQGSLKHLIWDLLLLTKKRTFS
6475	36843	A	6525	3	2640	
6476	36844	A	6526	2745	3732	IRIGKNYFKVHMEPKKSPHRQV NPKPKEQSWRHHTT*LQTLQG YSNQNSMPGPTQPSTPAPGG NLRNPQSSDLLQVTKQQGQAL AIQREAPLHRIPAEIPWYFQP QPATQLGSPVPDPSSAMM/SR RAHRSRGPDROGYPLQGD*PGE PRPQEH*RGHSQERLPSSEKQTP ICPPAQATQHPEEPDAHQPYKH LFQVCAHQGHVPAQRRN*PGY WERYHSAEDPELQPILAGLSLS MYLVTVLRNLLIS
6477	36845	A	6527	1	1860	
6478	36846	A	6528	1	1458	
6479	36847	B	6529	1	1503	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6480	36848	A	6530	3	515	TISQKRCTLPAILGLISYASSVNI RSNITGWLYIDRYVGGSHVILYP LGIRMGVGTGEMKGERRRGLHA ATKWLEEHAPADYQNPQEYGR TQLPGTQPQLDHEREDMQRL NRDREALLEGFKRGAQKATNV NKVSEVIQGKEESPAQFHQRCLC EAYRMYTPLDHDSPENQRMHI MALVRQSAEDMRRLKQKAG LAGMNPSSQLLEIASQVFVNRDA VSPKENSKEGGQARRHDDLF SPVEPDCVEVLDSIHSSRPDLRD QPWPSGDW/RTICGWEQLLQPP RRERCRCVCSDNPGH/WLLKPHR CPRPLQARKLNSLLSLGP*NSTR DCVRPIVCILPLITIALKISA
6481	36849	B	6531	96	2524	
6482	36850	B	6532	61	2025	
6483	36851	A	6533	674	2913	
6484	36852	B	6534	120	1849	
6485	36853	A	6535	1	426	
6486	36854	A	6536	2	475	
6487	36855	A	6537	1	501	
6488	36856	A	6538	15	593	SMWWNSAREPCPWRIVDDCGG AFTMGVIGGGVFQAIKGFERNAP VCRLLSEAPLFIYSCSRVSPTV NVSSERAESRPTLFMAVSLHMA WCLAHIGIRHLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA/LTGA VLAAARSAPLAMI/VGSAMMGGI LL/ALIEGVSILL/TR*TATV
6489	36857	A	6539	2	557	RRFRASAMEEYAREPCPWRIVD DCGGAFTMGVIGGGVFQAIKIG FRNAPVGIRHLRGSANAVRIR APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA/LTG AVLAAAR/SGPLAMGGLQQ*WG GILFAPHLRAFGILLTRYTAQ/Q FRNAPPFLEDPSQLPPKDGTPA VTGYPSPYQYH
6490	36858	A	6540	223	2274	

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6491	36859	A	6541	2795	3762	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISV MED EMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTI.QHIIQENFPN LARQANVQIQEIQRTPQRYSSRI AIPRHIIIVRFTKVEMKEKMLRA AREKGRVTLKGKPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEEIKYLTQDK MVRDFVTTTRPALKELLKEALN MERNNRYQLLQNHAKF
6492	36860	A	6542	245	1293	TGAVPIRPSWQWGNRTEKL ETLKRRAPLLQRNAVPHQQQ NKAGWRMLTS*EKKASDDQIT LSYGRFTKPK/DKEVENFEKNL EECITRITNTEKCLKELMELKTK APELREECRSLRSRCDQLEERV SAMEDEMNMKREGKFREKRI KRNEQSLQEIWDYVKRPNLHLI GVPESDVENGTKLENTLQDIIQ ENFPNLRQANVQIQEIQRTPQ RYSSRRATPRHIIIVRFTKVEMK EKMLRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK YFIDKQMLRDFVTTTRPALKELL KEALNMERNNRYOPLQNHAK
6493	36861	C	6543	116	283	
6494	36862	A	6544	51	281	KSQNQLLSSKGEYADGQQDQV SIPAPSPYTLSPQTQSCVPVRPE LGL*GASSAVQAPAVRYLTRFL LFVMSNLHSP
6495	36863	B	6545	1	897	
6496	36864	B	6546	91	8030	
6497	36865	A	6547	126	362	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
6498	36866	A	6548	936	2064	ERADCLFKRKTNNQKGHLHRK PICTSPSSKTKSR*NHKDGEKTE QKNWKL*NAERLSSS/IRNAV HQQQNKAGWRMILTS*EKKAS DDQITLSYGRITFKPK/DKEVENF EKNLEECITRITNTEKCLKELME LKTARELHEECRLSRCDQL EERVSAMEDEMNMKREGKFR EKRIKRNEQSLQEIWVYKRPN LRLIGVPESDVENGTKLENTLQ DIIQENFPNLARQANVQIEIQR TPQRYSSRRATPRHIIVRFTKVE MKEKMLRAAREKGQVTLKGG PIRLTADLSAETLQARREWGPIF NILKEKNFQPKISYPAKLSFISEG EIKYFIDKQMLRDFVTTRPALK ELLKEELNMERNNRYQPLQNH
6499	36867	A	6549	1	767	MAGAPPPASLPCCSLILDCCASN QRDSVGVGPSEPGVGYSLVVR RFLSRSEKRNIRVGVTRFSSEM NPVPQMEMQKSPSSASLTGA VDRSCSYSAILAPPLGFCFYPLY ENSTLQSAKKRDAELANGALGI IELNNDYTLKKVMKPLITSNTV TDEIERANVFKMNGKWYLFDT SRGSKMTIDGINSNDIYMLGY/D IKLFNRPLQAAEQNRACAANGS *SKRCDIHLSLRSAASQRQQC GYHKLHDKQRLLRG
6500	36868	B	6550	50	327	
6501	36869	A	6551	333	1301	FLHFHLRNAVPHQQWNKAGW RMTLRS*EKKASDDQITLSYGR TFKPK/DKEVENFEQNLEECITR ITNTEKCLKELMELKTKARELR EECRSLRSRCDQLEERISV MED EMNMKREGKFREKRIKRNEQ SLQEIWVYKRPNLRLIGVPES DGENGTKLENTLQHIIQENFPN LARQANVQIEIQRTPQRYSSRI AIPRHIIVRFTKVEKMEKMLRA AREKGRVTLKGGPIRLTADLSA ETLQARREWGPIFNILKENNFQ PRISYPAKLSFISEEIKYLTOKQ MVRDFVTTRPALKELLKEALN MERNNRYQLLQNHAKF
6502	36870	A	6552	352	2304	
6503	36871	A	6553	1	1617	

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6504	36872	A	6554	1	257	MGPPIHKISHYVYANISKSEKVL KSEHFRSQAFQPGQSETVSEK KKKTRKKRKKRKKRKKKKK KKKKKKKKKKKKKKKKKKKK SE*DRLGKKKEDEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
6505	36873	A	6555	5	156	RKKGGG/EREEEGEGEEEEEE EEEEEEEEEEEEEEEEEEVVL LTPGTGAEDFKKH
6506	36874	A	6556	1	279	
6507	36875	A	6557	3	120	TEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE
6508	36876	A	6558	3	123	
6509	36877	A	6559	239	432	CLWLFQEEEEEEEEEEED*EE EEE/EEEEEEEEEEEEEEEE EEEEEEEEEEKIFLGHVRGI
6510	36878	A	6560	1	588	
6511	36879	A	6561	1	204	
6512	36880	A	6562	75	234	
6513	36881	B	6563	100	2510	
6514	36882	A	6564	47	4976	
6515	36883	A	6565	3	4755	SCRCRRRRRGPAPAMAQILPVR FQEHFQLQNLGINPANIGFSTLT MESDKFICIREKVGEQAQVITI MSDPMPIRRPISAESAIMNPAS KVIALKAGKTLQIFNIEMKSKM KAHTMAEEVIFWKVWSVNTV ALVTETAVYHWSMEGDSQPM KMFRHTSLVGCQVIHYRTDE YQKWLLLVGISAQQRVVGGA MQLYSVDRKVSQPIEGHAAAF AEFKMEGNAKPATLFCFAVRN PTGGKLHIIIEVGQPAAGNQ
6516	36884	B	6566	47	482	
6517	36885	A	6567	1	555	MNARPHKVD/GRVVEPKRAV* EDSQRPAFVAGIKEDTEHHILR DYFQYQYGMVEIIMTDRGSG KKRGFAFVTFDNHDSVDKTVV QKYHTANDHNCEGRKALSKQE MASASSQRGHSSGNFRGGHG GGFGGNDIFGYGENFSOHGGFS GSCGGGGYGSSGGGYNEFGND GSNTGGGGSYNDFGN
6518	36886	A	6568	1	645	

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6519	36887	A	6569	2	944	GRGLRKLFIGGLSF*FIDESLKS QVGEWGLTDCVVMRDPNTK RSRGFGFVYATVEEVDAAAMN ARPHKVDGRVVEPKRAVSRED SQRPGAHI/TLVKKIFVGGIKED TEEHHLRDYFEQYGKIEVIEIMT DRGSGKKRGFA/VTFDDHDSV DKIVIQKYHTVNGHNCEVRKA LSKQEMASASSSQRGRSGSGNF GGGRGGGFGGNDNFGRGGNFS GRGGGGSRRGGGYGGSGDGY NGFGNDGNSFGGGGSYNDFGN YNNQASNFGPMKGGNFGGRSS GPYG/GGGQYFAKPR/NQGGY GGSSSSSYGSGRRF
6520	36888	A	6570	1	1512	
6521	36889	A	6571	2864	3677	RCQLDHLPLCHLCCCCHRR/CIPSL RDPQQAAGSTRLSRAPHIESRV GRKPPEEPANPTMNSLTLRDKQ /HDASTC/DWKRAL*VPESGLPR ALLKYIRCPNMSSAQKPRELSK RRN*K*PCVKRTPFRPT*E/DLP YSGKKTGVKGLICPVPGTAVK APQRPPGPPQPPAPQASSETA WFPVADRRVFSENPGWTA AKT LGTLSPPCQAGAGVGRQDGP GQELTSQEKPWVGRKIPEHAV ADKGYRQCCGAGEARGGPVF WAAAPRTSWQQASYT
6522	36890	A	6572	1	666	
6523	36891	A	6573	2926	3304	EYSLGHRHYNWKC*ALGQKDQ VTFATKFAPTSHRTRKQPELWR /QDPGSYGEKQPAWCSVPPGRF SGGLVGLGFLDGGIVVQPLRRP CCQDCVCGFPLRSSTKTSTEL GPSFLPCERQGETISVT
6524	36892	A	6574	1	665	

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6525	36893	A	6575	3	1121	SSTFRMPWRLVTSWTAYIPEL EGSTSDPSPAVAQKGEKPVKL GNSLWGSHTPEVPRPGTGPRPL SFVHRLPTMDPHKVNALRAV KMCKQDLSVLHTKEMHFLRE WVESMGKLSPATQKVKSEEN TKEEKPDSSKKVEEDLKADEPSS EESNLLIDNEDVIEPDPAPQEM GDENAEITEEMMDQANHKKVA AIEALNDGELQKAIDLFTDAIKL NPQLAILYAKRASVFIKLQKPN AAIRDCDRAVEIYSAQPYKWR/ GKYEKREEREIKERIERVKKA REEQERAQREEEARGQSAQY GSFPDGLPGGMLEMRGGMPGK PGITGLNEIFSDPEVLAAVQDPK VMV/AFQDVAQNPNANMSQYQ GNPKVM
6526	36894	A	6576	3	1351	PEAGGERERERAQREEDSTRQS RAQYGSFTGGFPGMPGNFPG GMPGMGGPSARSRAQRSLSE PDRSPSYAHHLPMTDPRRVNE LRAFEKMKCKQDPSVLHTEEMR FLRECVESMCGKVPPATHKAM SEENTTEEKPDSEKAEDLQAD EPSSEESDLRKLKEGVIEPDT APQEMGDENAEIPEEIMMDQA NDKKVAAIEALNDGELQKAIDL FTDAIKLNPRLAILYAKRASV VKLQKPNAAIRDCDRAIEINPD SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDYDEASAML KEVQPRQAQIAEHRKRYERKR EEREIKERIERVKKAREEHERA QREEEARRQSGAQYGSFPGGFP GGMPGNFPGMPGMGGGMPG MAGMPGLNEILSDPEVLAAMQ DPEVMVAFQDVAQNPNANMSK YQSNPKVMNLISKLSAKFGGQ
6527	36895	A	6577	2	433	GPPLNLSSPRGGILKTYGCELGG KRFLDSLRLRMHLLAHSAGAK AFVCDQCGAQFSKEDALETHR QTHGTDMAVFCLLCGKRQFQA QSALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHGTGDH PYECEFCGSCFRDE
6528	36896	A	6578	1	687	
6529	36897	A	6579	2	449	

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6530	36898	A	6580	852	1084	TDAGCYAARQCGTAVPSRDV HIRHQGTVPVQF*TAPLRARS/E VSPARRRRARMLSSSASFASANIT TSSAWSDTLQP
6531	36899	A	6581	1	681	
6532	36900	A	6582	1	483	
6533	36901	A	6583	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG/SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
6534	36902	A	6584	1	678	
6535	36903	A	6585	3	634	
6536	36904	A	6586	4	479	CSAKTAIRGVSECLIHGHGIPHS TASDQGTHTFAKEVWQWAYA HGIHWSYHVLHHPEEA/GKER WNLGKLSQLQCQLGDNLTQGG* GKVLQQAQVYVLN*HPIYGTVP IARIH/GSRNQGV/ETELTPTITP SDPLAKFLLPVPTLHSAGLEIL VPEGEIR
6537	36905	A	6587	1	1539	MVGKAKWKPLELPLPRKMVSQ KQYRILGGTAEISVTIKDLKDA RVVIPSTSPFYSPWVQKIDGS WRMTEDYRKLNVVVTPTAAA VPDVVSLLEQINTSPGTRYAAID LTNAFFSIPFHKAHQKLFASF WQGGQYTTFTVLPWGDINSALCH NLIRRDPCFSLPQDITLVHHID DIMLTGSREQEVADTRDFLVKD KLLHLAPPTTKQAQHLVGLF GFWRQHIIPLGLLQPIYRVTQ KVASFWSQEQKTALQQVQAA VQAVLPLGPYNPADPMVLEVS VADRDVCSLWQAPIGESQWR PLGFWKALPSSADNYSPPFERQ LLA/CHKVGHAQQHSISKWK*Y IHDRAQADYHPWTQACLIHCQ GIPHSIASDKDAHFTTKEVWQW THAHEIHWCYHVLHHPEAAGL TERWNRLLKSQQLRQLGDNLT QSGGKVLQKAMYALNQHPYIG TISPIARIHGSSNQGVVAPLTIT PSDPLAKFLLCVPTTLRSAGLD VLVPEGGMTQQQFH

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6538	36906	A	6588	1	566	MGRNQSRKAENSKNWSASSPP KDHSSLPAMEQSWMENDEF TEVGFRRSVITNFSELKEHVLTY CKEAKNVEKRIYRSRNQGMVEV KVAPLTITPSDPLANFFASVPAT LHSAGLEVLVPEGGTLPLGDTT MIPLNWKLRLRTGYFGLLLRLS QQAQKKGAMVLA/GVVDPDYQ NEISLLHN*GKTHDH
6539	36907	A	6589	221	357	
6540	36908	C	6590	228	342	
6541	36909	A	6591	745	849	
6542	36910	A	6592	1	240	
6543	36911	A	6593	2	495	FVRLVGRGDCDPLLSVCLTTMP LYEGLSGGGEKTAVIDLGEA FTKCGFAGETGPRCIIPSGIKRA GMPKPVRRVVQYNINTEELYSYL KEFIHILYFRHLVLPNPRDRRVV IIESVLCPSIHFREDTHSCFFFKY FEVPSVLLA/PSHLMALLTLGI NSWHGPRL
6544	36912	A	6594	1	579	
6545	36913	A	6595	1	621	
6546	36914	A	6596	1	351	
6547	36915	A	6597	1	447	
6548	36916	A	6598	114	880	
6549	36917	A	6599	1	2625	
6550	36918	A	6600	1	1674	
6551	36919	A	6601	1035	2235	QTHSQYHTEWAKTGSIPFENW HKTGIPSLTTPIQHSVGSSGQGN QAGEGNKGYISIRKRGSIQVPC RRHD/VYI*KTPLSQPEISLS**A TSAKS/LGYKINVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIKPSWVGRIN IVKMAILPKVIYRFNAIPIKLPM PFFTELEKTTLKFIWNQKRARIT KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNILFDKPEK NKQWKGKDSLFNKWCWENWLA ICRKLKLDPLFTPYTKMNSRWI KDLNVRPKTIKLEENLGITIQD IGMGKDFMSKTPKAMATKAKI DKWDLIKLKSFTAKETTIRVN RQPTK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6552	36920	A	6602	369	1917	AGEKNKGYSIRKRGSQIVPVC RHD/VYI*KTPLSQPKISLS**AT SAKS/LGYKINVQKSQTFLYTN NRQTESQIMSELPFTIASKKIKY LGIQHTRDVKDLFKENYKPLLK EIKEDTNKWKNI PCSWVGRINI VKMAILPKVITYRFNAIPIKLPM TFFTELEKTTSKFIWNQKRARITK SILSQKNKAGGITLPDFKLYYK ATVTKTAWYLYQNRDIDQWN RTEPSEMTPHITYNYLIFDKPEK NKQWGKDSL FNKWCWENWLA ICRKLKLDPFLTPTKINSRWIK DLNVRPKTIKLEENLGITQDI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR QPKKWEKIFATYSSDKGLISRIY NELKQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAHQKSGNNRCWRGCGEIGTL LHCWWDCKLQVHILTHRWE L NNEITWTQEGEYHTLGT VVGW GEGGGIALGDIPNAR
6553	36921	A	6603	1	2781	

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6554	36922	A	6604	1320	2403	LQTLQVYSNQNSMVLVPKQR YRSMQNRALRNNAATYQLQSD L*QT*EKQAMGKGFP1**MVLG KLASHM*KAETGSLPYTLKYK QFKMD*RLKR*T*NSKKQSPSP PPKERSSPATEQSWTENDFDE LREEGFRSNYPFLREDIQTKG KEEIQTIREYYKHLANKLEN LEEMDKFLNTYTLPRLNQEEVE SLNRPTGSEIVAVINSLPTKKSP GPDGFTAEFHQRYKVELVPFLL KLFQSIEKEGILPNSFYEASIIIP KPGRDTIKKENFRPISLTNIDAKI LNKILANRIQQHIKKLIHYDQV GFIPGMQDWFNIRKSINVIQHIN RTKVKNHMIISIDA EKAFDKIQ QRFMLKTLNKL AQNLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVGRLNIVK MAILPKVIYRFNAIPIKLPMTFF TELEKTTVKFIWNQKRACITKSI LSQKNKAGGITLPDFKLYYKST VTKTAWYWYQNRDIDQWNRT EPSEIMPHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLD PFLTPYTKINSR WIKDL NVRPKTIKLEENLGITIQDIGV DKDFMTKTPKAMATKPKIDKW DLIKLKSFC TAKETTIRAFDELD DVHPHEEIEACRVWQNYGTHP
6555	36923	A	6605	2202	2515	KSLQCEHSSHQDLP LACLGLR KHYMVAQYL*HSHS/ASGGGSR YDVLKISVSCSSTIDI*LA FVSLG *DKRTS**TNLAESSPNFFHWV WIFLASKKFC SVPAR
6556	36924	A	6606	1934	2077	AIPFRIQA WARTSCPKHKKQWQ QKPKLTNGI*FN* RASAQKKL PSE
6557	36925	B	6607	1	2325	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6558	36926	A	6608	1524	2877	IRKRGSQIVPVCRRHD/VFV*KT PSSQPKISL**ATSAS/LGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASRKRIYLGQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPKLPMTFFTELEKTTL KFIWNQKRARIAKSILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNRDIDQCNRTPESEIMPH IYNYLIFDKPERNKQWKGKDSLF NKWCWENWLAICRKLKLDLPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGITIQDIGVGKDFMSKTP KAMATKDKIDKWDLIKLSFC TAKETTIRVNRQPTTWEKIFAT YSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSSSLAIRERQIKT TMRVHLTPVRMAIHKKSGNNR DMDEIGNHHSQ
6559	36927	A	6609	1	2226	
6560	36928	A	6610	1	674	MGKKQNRKTGNSKTQASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKE VQNFENLEECITRITNTEKCLK ELMELKTKARELREECRLRSR CDQLEERSAMEDEMNMENKRE GKFRKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIHQEN/CPQSSKAGQRSD SGNTENATKILLEKSNSKTHNC QIHQS
6561	36929	B	6611	1	5175	
6562	36930	A	6612	1666	2032	LQTLQGYSNQNSMVLVVKQR YRSMQNRALRNATY/LQLSD L*QT*EKQAMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKH*T*NHKNPRRKP RHYHSGHRHGGQLHV
6563	36931	A	6613	1596	2169	AGEGNKGYSIKRGSQIVPVC *HD/VYI*KTPLSQPKISL**ATS AKS/LGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASRKRIYL GIQLTRDVKDLFKENYKPLLKE IKEDTNKWKNIPCSWVGRINIM KMAILPKVIYRFNAIPKLPMTF FTELEKTKVHMEPKKCPHHQG NPKPKEQSWRHHTT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: In USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6564	36932	A	6614	1667	3103	AGEGNKGYSIKRGSGQIVPVC *HD/VYI*KTPLSQPKISLS**ATS AKS/LGYINNVQKSQAFLYTNN RQTERQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYKPLLQE IKEDTSK WKNVPCSWVGRINIV KMAILPKVIYRFNAIPKLPMPF FTELEKTILKFIWDQKRARIAS ILRQKNKAGGITLPDFKLYYKA TVTKTAWYWYQNRDIDQCNR TEPSEITPHIYNYLIFDKPEKNK QWGGKDSL FNKWCWENWLAIC RKLLDLPFLTPYTKINSRWIKD LNIRPKTIKLEENLGITIQDIGM GKDFMSKTPKAMATNAKIDK WDLIKLSFRTAKETTIRVNRQ PTKWQKIFATYSSDKGLMSRIY NELKQIYKKKTNNPIKKWAED MNRHFSKEDIYA AKKHMKKCS SSLAI REMQIKTTMRYHLTPVR MAHKKSGNNRLTLNNHNNPQ PLISIKEPREKEELNLQV
6565	36933	A	6615	3134	3288	
6566	36934	A	6616	1	2630	
6567	36935	B	6617	877	7936	
6568	36936	A	6618	2	1589	
6569	36937	A	6619	1	240	
6570	36938	A	6620	200	486	
6571	36939	A	6621	1	558	
6572	36940	A	6622	1	3885	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US/N 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6573	36941	A	6623	1	2302	KLPVTNRAAHGLCASLGPDFM TFKVPSSWRHSDSICREWFTLA GAPSRDVLVSAIITVLSLVTVV LCGLCHWCQRKLGKRYKNSLE TVGTDPDSGRGRSEKKAIVSRP CPPPAKASATHPTCKSPRSQEK VESPGDLDRDFWNNNESTVQQ KWSSYPPEFILNISPYAPYGDP RLSLNGLTLLSGAKVAAAAGLA VEREGRLGEKAPVPPPGEDAL RSGGAAPSEPGSGGKAGRGRW RTVQSHLAAGKLNLSNFEDSTL STATLESIPSTGEPKCCQRPRT LMRQQLSQQLSQHQRGRQPS QPTTSQSLGQLQAHMASAPGP NPRAVGRGQARQGTSAQSKYR AAGGRSRSPGSDWHVVGQIR NRGLDMKSFLTSSRAAKWNF TNSETVPALDLDSAVVLIPWISS KEDTGDSDHYGRVAIYHKGLSFS SDGLVYPGAKGREGRMVVLSL VLGLSEQDDFANIPDLQNPQTQ QNQNAQGDKRLPAGGKAVNT APVPGQTPHDESDRRTEPRSSV SDLVNSLTSEMLMEDWPPAVF SSGWAIAHTAPASLHSPGYSF LAARGGLLFEADFCWCKRSG STFPDCDGVANLAATEMALSQ LRFSEKATAMRESLVMLSPGSEE DEAHEGCSRENLGRIQFSVGYN FQESTLTLKIMKAQELPAKDFS GTSDPFVKIYLLPDKKHKLKTK
6574	36942	A	6624	1	576	
6575	36943	A	6625	1	155	
6576	36944	A	6626	4746	5258	DAGAQPSPRYLIYHQPSRFFRI TSTVTPFSKPISLLWLV*/GLHG DILL/RLQS*RC*CRSHPEYHSG PPGRWQGPSPAPQKCSRSTSR RSSR*HPPPPRPGGSAPSSPASYS WTPPRTVPGSWARRWRRHLSR PSWATQPSWTATLWSQPLWRL KWEDCLSPGRSRLQ
6577	36945	A	6627	1	588	

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6578	36946	A	6628	444	1056	GPLLREPHQLCHFPVAGFVLDA GLPEAAAAPHDRGPFLAGPQA AGQHPAQVAHQPRAAAQQRQ GRRAREEAGAAQEEPRGPQE RRRRLAEGLRRQCGHPAGRDG RGGYRRAAQPARGGRTPEWQ QSGGARRTPSVGHPRRARADW CLTGANDALSCSSPTCGKFLKT VSKVPV/CRRLAVNRKEAEGR SSESPTSSATFQSPALSWMLVS QRLLLPHMIGAQSSPGKRPNG TLRKWLTPSVRRSSGKADGH VKKLAHKKHKSREVRKSADAG SQKDDSDSAATPQDETVEEDTV AQPRGRREGAGRQSGSRAAGP GRRASAIRGGHARTDVGKRN GTRTRKELMPLHGKRDAAEH DEPTSASRPAGERPELTLAAVQ TEYNCSFPS
6579	36947	A	6629	128	1103	
6580	36948	A	6630	1	602	
6581	36949	A	6631	3	1618	
6582	36950	A	6632	1	602	
6583	36951	A	6633	3	1618	
6584	36952	A	6634	1	912	
6585	36953	A	6635	195	396	VLPLHRQI**LLH*SKKHNHYK GKQQDLR/CSSTVPRRPQILPII SFSNVVPGSRRLKAPLVFIGPG

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6586	36954	A	6636	2	1813	FNTPLSTLDRSSRQKVNKDIQD VISALHEAGLIDYRTLHPKSTE YTFFSAPHHTYYKIDHIVGSKA LLSKCKRTEITNCLSDDRAIKL ELRIKKLTQNYTTTWKLNLLLL SDYVWNEMKAEIKMFFETNE NKDTMYQNI.WDTFKAVCRGK FIAVNAYKRKQERSKIHTLTSQ LKEPEKEQETHSKASRRQEITKI RAELKEIDTQKTLQKISVSRSW FSERINKIDRLIARLMKKKREK NQIDAINDKGDITIDPTEMQTT IREYYKNLYANKLENLEEMDK FLDTYILPRLNQEEVELPNRPIT GSENEAIIINSLP/TKKSPGPDFT AKFYQRYKGLARAIRQEKERE DTQLGKEEVKLLFAEDMIVYL ENPIVSAONLLKLINNFskVSGY KINVQKSQAFLHTNNRQTESQI MSECPLTIASKRIKYLGIQLTRD VKDLFKENYKPLLNKIKEDTN KWKNIPIRSWLGRNNIVKMTILP KVI/YKKTTLNFIVNQERARIAK TILSKKNKAGGITLPDFKLYYK ATVTKTARYWTLTIKKGSVWPI SLKSEKRHRTRPLWKLCHND VQGELL.KTIQFLFGSPLGHSSLD
6587	36955	A	6637	1	2988	MPPHSEQPHSPSTRQKRKVPLF VRQCPFSFVIQAPKAKMDTFDGR KKQFTRFLFLFSMDQLGQGRFS MQTLSFALAVYRKDSPLVACQ VQALGNLEPSSVEAHVSSHGIAI DRKGWHVSLFSIQPGDCFPKAL VEDSPRDRARRQSSKEEGWC RDRRRLKFHSKKGA AIVVKS KKYESPSFGVCFESLNNPRLTS RREKTISSSKRCRQCHAEETT VFWAKESQTGEQTGRGAGQRR MGMIICKACSMPLAE
6588	36956	B	6638	362	1463	
6589	36957	A	6639	1	1061	
6590	36958	A	6640	1	1581	

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6591	36959	A	6641	46	862	AAFPAPRTLFFLSRPLRPTACAA FRPEFWRLNMKLPARVFFTLGS RLPCGLAPRRFFSYGKILYQN TEALQSKFFSPLQKAMLPNSF QGGKVAFITGGGTGLGKGM TTL LSSLGAQCVCVIA SRKMDVLKAT AEQISSQTGNKVHAIQCNVKYP DMVQNTVSELKVKQHPSTVIT N*STERSSISFLLPTIYA*DWFRF CSTQVLLPKQVWKPMKSLAA EWGKIWNAIQC
6592	36960	A	6642	1	2902	MVKGSLQQUELTILNIYAPNTE APRFKQVLRDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKINKD TQELNSALYQADLDIYGT LHP KSTLEYTF/SAPHHTYSQNWTT IVGSKALLSEHKRTEIITNYLSD VHSAVKLELRKKLTQNRSATW KLNNLLNDYWVHNDMKA EI KMFFETKVENKIDTTYQNLWDT FKAVCRGKFIAKNAHNRKQEV RSKIDTLTSQLELEKKEQTYL KASRRQEI
6593	36961	A	6643	1	5127	
6594	36962	B	6644	1	3570	
6595	36963	A	6645	1	3663	
6596	36964	B	6646	143	3122	
6597	36965	A	6647	1	3235	
6598	36966	A	6648	1	3249	
6599	36967	A	6649	1	3297	

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6600	36968	A	6650	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEVESLNRPIITGAEI GAIHNSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIIIPKPGRDITTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIIISIDAEKAFDIQQPFMLKTL NKLIGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTTRQGCPL SPLLNFNILLEVLARAIQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSQY KINVQKSQAFLYTSNRQTESQI MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITSILSQKNK AGGITLPDFKLYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLLKD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQDIGMGKDFMS RTPKAMATKAKIDKWDLIK SFCTAKETTIRVNRQPTTWKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKHKMKKCSSSLAIREMQI KTTMRYHLTPVRMAIHKKSGNN
6601	36969	A	6651	1	3402	
6602	36970	A	6652	1	3288	
6603	36971	A	6653	1	3168	
6604	36972	A	6654	1	3516	
6605	36973	A	6655	1	3693	

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6606	36974	A	6656	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF NNLSC*KLSIN/IVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADD MIVYLENPVISAQNLKLLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSQWVGRINIVK MAILPKVIYRFNAIPKLPMTFF TELGKTALKFIWNQKRARITKSI LSQKNKAGGITLPDFQLYCKAT VTKTAWFPSPGDVGLEADFSPSH TLKTQFFSCLAEFAAASCFFQR MNGFGMAMTTTYSTGAESPL PSCSIDQGGDTKLHRRASPGRT FPAAAGIPAAAAADGPPSLLLH KLWFPVELGGRALPRAESHGE VAALGVMVVAQGKNGQEEA RSTPWL RPTSHLPPCSSSAWW TEQTD AHLPLLCLGIYLLNA LSNLSMVALVRSDGALRSPMY YFLGHLSLVDVCFCTTVTVPRLL AGLLHPGQAISQACFAEMYFF VALGITESYLPAAMSYDRATAA CRPLRYGALVTPWALRLAARY DRLASVYAVITPTLNPFINSLR NKEVKGALKRGLRWRAAPQE
6607	36975	A	6657	1	3514	MELKTKARELREECRLSRSCD QLEERVSA MEDEMNEMKREG KFREKRIKRNEQSLQEIWYVK RPNI RLIGVPESDVENGTKLEN TLQDIIQENFPNLAQANIQIEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKDRSTRQK VNKDTQELNSALHQADLIDIYR TLHPKSTEYTFSPHIIITYSKT DHIVGSKALLSKCKRTEIITNYL SDHSAIKLELRJKNLTKSRSTTW KLNNLLNDYW
6608	36976	A	6658	3	3316	
6609	36977	A	6659	1	4794	
6610	36978	A	6660	1	3570	
6611	36979	B	6661	1	3384	
6612	36980	A	6662	1	3429	
6613	36981	A	6663	1	3780	
6614	36982	A	6664	1	3894	

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6615	36983	A	6665	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDFAKAVC RGKFIALNVYKRKQERSKIDTL TSOLKELEKQEQTHSKASRRQE ITKIRAELEKIETQ
6616	36984	B	6666	1	3145	
6617	36985	A	6667	1	4398	
6618	36986	A	6668	523	3852	
6619	36987	A	6669	1	3934	MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRLSR CDQLEERVSAEDEMNEMKRE GKFRKRIKNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMQRYSSRRATPRHIIVR FTKVEKMEKMLRAARQKAPH HTYSKIDHIVGSKAL
6620	36988	B	6670	1	5215	
6621	36989	A	6671	1	7171	
6622	36990	A	6672	3	493	
6623	36991	A	6673	1	729	
6624	36992	A	6674	3	800	
6625	36993	A	6675	1	327	
6626	36994	A	6676	2	462	KSSWLEEDDDPVVARVNRMQ HITGLTVKTAELLQVANYGVG GQYEPHFDFSRPFDSGLKTEG NRLATFLNYMSDVEAGGATVF PDLGAAIWPKKGTAVFWYNLL RTGEGDYR/TRHAACPVLVGCK WVSNKWFHES/GQFLRPGST EVD

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6627	36995	A	6677	3	717	RHRLRNRLKDVGGAEFYPLLE DDQSNLPHSNSNNELSAATLP LIIREKDTEYQLNRJILFDRLLKA YPYKKNQIWREARVDIPLIRG LTWAALLGVEGAHAKYDAID KDTPIPTDRT/QLKWDIPRCHSV R*TVIIHAPEGHAKFRRLKAW VVSHPDLYVWQGLDSLCAPEL YLNFNNEALVYACMSAFIPKYL YNFFLKDNSHVIQEYLTVFSQM IAFHDPELSNHLNEIGFIPD
6628	36996	A	6678	1	508	
6629	36997	A	6679	1	888	
6630	36998	A	6680	2	584	
6631	36999	A	6681	2	152	QVAKGMDALLQHLEDCGYR/S SKKKAQICRQQVTKWGDGSAL MGTSSTASL
6632	37000	A	6682	733	894	
6633	37001	B	6683	1	1626	
6634	37002	A	6684	1	1971	MAQVWANDNPPGLAVNQAPV LIDVKGPAQPIRQKQYPVPREA LKGIQPGTKDYQPQDRLRVN QATVTLHPTVPNPYTLGLLLA EDSWFTCLDLKDAFFSIRLAPES QKLFAFQWEDPQSDLGICLLLY VDDLLGHSTAVECAKGMVDL LQHLEDCRYKMSKKKAHICRQ QVRYLGFTIRKGRS/WEREKM AVGVLTQTVGWPWRPVAYLSK QLD/EVSKGWPLCLRTLAATAL LAQEADKLTGQNLNIKAPHA VVTLMITTEGHHWLTNARLTKY QSLPCENPHITIEVCNTLNPITL LPVSESPGEHNCVEVLDSVYSS RPDLRDQPWASSVDWELVMD GSSFINSQGERCAGYAVVTLDA VIKAKLWLQGTSAQKAELIALT RAVELSEGOESLEELLGRYFYV SHLPFAKAVAQLCITCRQHNA RQSPTVSPHIAQYGAAPFEDLQ VDFTEMPKCGGNKYLLVLTCT YSGWVEAYPTRTEKPYKKGKN DPSCTKGQCNPLELVITNPLNP HWKKGERTVLGIDRARLDPRV NILVRGGEVYERSPEPVFQTFY DELNVVPPEIPGKTRNLFQLA ECVAQPLNVTSCYVCGGTVTG YQWPWKARELVPDVPVPEFL AQKNYPDNFWVLKPSITGQYCI
6635	37003	A	6685	1	1461	
6636	37004	A	6686	1	1005	

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6637	37005	A	6687	1	174	
6638	37006	A	6688	519	588	
6639	37007	A	6689	2	4527	GRAGLGWSSGGGRGRACSEGP AEARGREGDKGSAALSPPLPLT LGEEMAAERGARRLLSTPFWL YCLLLLGRRAPGAAAARSGSAP QSPGASIRTFTPFYFLVEPVDL SVRGSSVILNCSAYSESPKIEW KKDGTFLNLVSDRRQLLPDGS LFISNVVHSHKHNKPDGYYQCV ATVESLGTIISRTAKLIVAGLPR FTSQPEPSSVYAGNNAILNCEV NADLVFVVRWEQNRQPLLLDD RVIKLPSGMLVI
6640	37008	A	6690	1	879	
6641	37009	A	6691	407	594	
6642	37010	A	6692	1	3621	
6643	37011	B	6693	1	609	
6644	37012	B	6694	1335	1599	
6645	37013	A	6695	1	354	
6646	37014	A	6696	181	683	SRYFILLRKPTFPAMALLPVLFL VTLLPSLPAGGKDPATALLT TQLQVQREIVNKHNELKAVSP PASNMLKMEWSREVTTNAQR WANK/CTLQHSDPEDRKTSTRC GENLYMSSDPTSSWSSAIQSWY DEILDVYGVGPKS/PQYCPAG NNMNRKNTPTYQQTGPCG
6647	37015	A	6697	199	969	
6648	37016	A	6698	1	564	
6649	37017	A	6699	153	427	
6650	37018	A	6700	1	978	
6651	37019	A	6701	3	419	
6652	37020	A	6702	9	255	VRAPAQGPLAGGRRRCGSGA SCTPSRGPASWSRSAAQVPRS SRWRAGSASS*/N/GRQAPPTSQ PPRAQFFAQPPGPWPLS
6653	37021	B	6703	96	283	
6654	37022	A	6704	172	365	PTYHLYPCHFYQHRTRRIPRK SERLFTPPQLSWKGTWDY*1 CLCCNDSEGRDVLVRLVK
6655	37023	A	6705	3	1171	
6656	37024	A	6706	2	740	
6657	37025	A	6707	256	461	
6658	37026	A	6708	1	414	
6659	37027	A	6709	1330	1386	YIDSILPK*NHDTLSQYCRYMH SRQRAAS*PLSTGKLQCLGLD LVLC

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6660	37028	A	6710	207	1173	GGDRDRMTANHESYLLMASTQ NDMEDWVKSIRRVINGDLSCGG IFGQKLEDTVRYEKRYGNRLAP MLVEQCQDFIRQGLKEEGLFR LPGQANLVKIELQDAFDCGEKP SFDSNTDVHTVASLLKLYLREL PEPVIPYAKYEDFLSCAKLLSKE EEAGVKELAKQVKSLPVVNYN LLKYICRFLDEVQSYSGVKNKMS VQNLA TVFGPNILRPKVEDPLTI MEGTVVVQQLMSVMISKHDCL FPKDAELQSKPDGVSNNNEIQ KKATMGQLQNKENNNTKDSPS RQCSWDKSESP/TEKQHEQWIP HSSIRQQNQPKQEQWSQAI
6661	37029	A	6711	173	881	
6662	37030	A	6712	1605	1844	
6663	37031	B	6713	123	699	
6664	37032	A	6714	1	462	
6665	37033	A	6715	1	2607	
6666	37034	A	6716	1	918	
6667	37035	A	6717	1	549	
6668	37036	A	6718	1	687	
6669	37037	A	6719	1	258	
6670	37038	A	6720	90	1621	HGLDLRTMNRSRQVTCVAWV RCGVAKETPDKVELSKGGVKR LIAEAEELQEEGGSDDEKGTG SPLEEGMQSARTQARP/REPLE/ DGDPE/DRTLDDDELA EYDLD KYDEEGDPDAETLG/ESLLGLT VYGSNDQDPYVTLKDTEQYER EDFLIKPSDNLIVCGRAEQDQC NLEVHVYNQEEDSFYVHHDILL SAYPLSVEWLNFPSPDDSTGN YIA VGNMTPVIEVWDL/DIVDSL EPVFTLGSKLSKKKKKKGKSS SAEGHTDAVLDSLWNKLIRNV LASASADNTVILWDMSLGKPA ASLA VHTDKVQTLQFHPFEAQT LISGSYDKSVALYDCRSPDESH RMWRFSQGIERTVWNHFSPOCH FLASTDDGFVYNLDA/SDKPIF TLNAHNDEISGLDLSSQIKGCL VTASADKYVKIWDILGDRPSLV HSRDMKMGVLFCSGCCPDLPFI YAFGGQKEGLRVWDISTVSSV NEAFGRRLRLVLGSARNSSISGP FGSRSSDTPMES
6671	37039	A	6721	1	549	

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6672	37040	A	6722	1	1318	AKQQLNLRTHMADENKNEYA AQLQNFNGEQHKHFYVVIPIQY KQLQEMDERRTIKLSECYRGFA DSERKVIPIISKCLEGMILAAKS VDERRDSQMVDVSFKSGFEPFG DFFPEDYSQHIYRTISDGTISAS KQESGKMDAKTTVGKAKGKL WLFGKKPKQSPPLTPTSLFTSS TPNGSQFLTFSIEPVHYCMNEIK TGKPRIPFSRSLKRGWSVKMG/ AALEDFSHLPPEQRRKKLQORI DELNRELKQESDQKDALNKMK DVYEKNPQMGDPGSLQPKLAE TMNNIDRLRMEIHKNEAWLSE VEGKTGGRGDRRHSSDINHLVT QGRESPEGSYTDDANQEVRGPP QQHGHNEFDDEFEDDDPLPAI GHCKAIYPFDGHNEGTAMKE GEVLYIIEEDKGDGWTRARRQ NGEEGYVPTSVIDVTLEKNSKG
6673	37041	A	6723	1	741	
6674	37042	A	6724	1	1063	MPFYISDLICGDRILRALCPQD LPTYSLHSRGMKMRASCRRKFLD NNSSRLVSCNMGALISIWGTTT PPLHATILDSQPTVHPPLAKDCL PCGLQASASDLRALQRLCQ QLPWVGSQPHTRSPSPQRGGKT GLFAGLASSVSMRPASPPSPAA DSCSACRFFARRPPLRVTWVKP SSALALCVSISDSPGNLKALPA ETRAQLHHAASLSQPPLQLRP FPKTSQAGDLQDLGPYYVCVRK AVGKGDKQIRAVVKEHSVRSQ ERIWHPGITTANMPGHLGQNT ESGRDKLPMFGVWFPGRFWG LWVWRLP*LKLAAPCRPSRSLR SSPISRRASSTRCLTVSGCPAAP
6675	37043	A	6725	25	573	
6676	37044	A	6726	1	483	

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6677	37045	A	6727	1	996	MVGKAKWKPIELPLRRKIVNQ KQYHIPGGVAKISATIKDLKDV GVVPTTSPFNSPIWPVQKTDGS WRK WLS*QGQQT/FTVLPHG YINSLALCHNLIRRLDHFSLPQ DITLVHYIDDIVLTGSSEQEVAN TLDLLTSLDWALVETECLTMG HQVTMQPELTIMNWALSDPSN YKVGCAQQHSIIKWKWYIRDQ ARAGTTCKWTAALQPLSRTS LKDSGERKSSQWAELEAVHLI MHFAWKEKWPDVQLYTDSWA VANGSAGWSGTWKNHWDKIA TTVIAQWAHEQSSHGSRNGGY TWAQQHGLPLTKADVATATDE CPICQQQRPTLSP
6678	37046	A	6728	2	1380	CLAGLFGFWSPCIPHLGLVLLQSI YLVTQKAA/SSEWGPEQEKALQ EVQAAVQAAALILEPYDPAGPVV LEVSLADRDVWSLWQAPIGE SQQRPLGFWSKALPSSA/DHKA CHAAQHSIIKWKWYIHDRARA GPEGTNSSARYAATM*KWTAS ALQPLSRKSLKDSSEKSSQWA ELRAVHLAVHVAWKEKWPDV RLDTSWAVANGLARWSGTW KEHDRKIGDKEVWGRGTRIELS EWSKTVTIFVSH/VLLPRLPSIRG LTECLIHQHGPHSIASDQGTHF TAKELQQWAHAHGIHWSYHVP HHPGWGWKVLQAVYALNQRPP IYEWKEESCLHTGVADALRGN WAEGRHREKALWGLWSTWS QHPLRSLKTRHHPLGLGVLS ICEAGGATELSRASGFATGYG KRKEDTKKHKQHSVSDIIEQQH SLGLTEKTVKGTPTQGISMRRP LYHKATEFQE
6679	37047	A	6729	1	2229	
6680	37048	A	6730	1	789	RDLQPFTSVTVHCRKGNDDTF GGPLDAGSELTLIPGDPKHHCG PPVKVGYGGQVINGVLAHPL IWL VQKTDGS/WRMTVDYCKL NQVVIPAAAVSDVVSILEQINT SPGTWYAAIDLANAFFSIPVHK AQKQFAFSWQGOQYTFVLPL QWYINSPALCHNLIRRLDCFS LPLDITLVHYIDIMLIGSSEGE VANTLDLFRHLRARGWEINPT KIQGPSTSVKFLGFQWCGACQA IPSKMRDKLLHLVPPPTTKKEAQ

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6681	37049	A	6731	1	553	MTVDYCKLNQVVIPIAAVSD VVSLLLEQINTSPGTWYAAIDL NAFFSIPVHKAQQQAFSWQG QQYTFTVLQWYINSALCHNL IRRDLDLDCFSLPLDITLVHYIDDI MLIGPRQLLACY/WALVETEHL TISHQVTMRPELPMNWVLFDP SSHKVGCAQQHSIIKWYVH DWARAGPEGT
6682	37050	A	6732	3	266	
6683	37051	A	6733	3	582	
6684	37052	A	6734	3	403	
6685	37053	A	6735	1	2712	
6686	37054	A	6736	875	1506	LSIYLVTVQKAA/SSEWGPQEKE ALQEVQAAVQAALILEPYDPA GPVVLEVSLADRDVWVSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQQHSIIKWYIHD RARAGPEGTNSSARYAATM*K WTASALQPLSRKSLKDSSEGK SSQWAE LRAVHLA VHVAVWKE KWPDVRLDTSWAV/ANGLAR WSGTWKEHDRKIGDKEVWGR GTRI
6687	37055	A	6737	1	633	MTVDYRKFNQVVTPTMAA/AVP DAVSLLEQINTFGTWYAAIDL ANAFFSIPVHEAHQKQFALPQ GYINFALCHNLIRRELDFFLLL QDITLVHYIDDIIGSSSEQEVV NTLDLIHKRSKEAEHTAASRRIR VSCLPEQKSHEQLTPWEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
6688	37056	A	6738	2	1103	DLWPFTRTVTLHRGKRNDQTFQ GLLDGTGSELMIPEDTKHHCGP PVKVEAYGGQVINGVLAQIQLT VGPVGSSTHPVVIYPVPECIIGI GILSSWQNPHGSLTSRKTDGS WRMTVHYHKLNMVTPIAAAI PDVVSLLEQVNTSPGSWYAAID LANAFFSIPVHKAHQKQAFSW QQQYTFTVLQWYINSALCH NLIRRDLDLDCFSLPLDITLVHYID DIMIGSSSEQEVANTLDLFRVRL LRARGWEINPTKIQGPSTSVKFL GFQWCGACQAIPSKMRDKLLH LVPTTTKKEAQLQLLACY/W ALVETEHLTISHQVTMRPELPI MNWVLFDPSSHKVGCAQQHSII KWKYVVDHVARAGPEGT

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6689	37057	A	6739	1	2058	
6690	37058	A	6740	2	1173	WEVRQYFTFTVPQGHINSLVLC HDVVRRLDGHFFLPQDITLVHY IDDIMLIGSTPPTKKKAQLVVG LFGFWRQLVPHLGVLLWPIYQ VTQQAASFEWGPEKEKALQQV QAAVQAAALPLGPYDPADPMVL EVSVADRDVAVWSLWQDPGES QWRSLGFWSKALPSSADNYSPP ERQLLACYWVLVETERL/QWV TPAEEDFNNQVDRMTHSVDDTT QPLSPATHVITQWAHEQSGHG GRDGGYTRVQQHGLPLTKADL ATAGKVFFQKAV*ALN*HSIYGT LSLIARIHRSRNGQVEVEVAPLT ISPSDPPAKFLLPVPTLRSAGLE FLVPEEGMLPSGDTTVPLNWKL RLPPGHFGLLFLPHQQANKGVT VLVGVTDLQDEISLLPHNG
6691	37059	A	6741	823	2487	KELKLWKNRHKLLSYPTVGAA VTQLQNLTAGVIGSHGARGQ VVALNRQRQGLDQPFTRVTVH WGKG/NMQIFGGLDGTSELTL IPGDPKHHCPPVKVGAFFGQ/Q VINGALARVQLIVGPVGPWAHP VVISPVPECIIDISSLSSWQNP SLTGRVRAIMVGKAKWKSLEL PLPRKIVNQKYHIPGGIVEISA TIKDLKDAGEVPIPTTFPLNSPI WPVRKTDGCWRMTVDYCELN QVVTPTAATVPDVVSLLEQINT SPGTWYADIDLANAVFSIPVHK AHQKQFAFSWQQQYFTVLP QEYINSLGLCHNLIQRDLDFSL LQDITLVHYIEDIMLIGSTEQEI NTLDLLFMAKEVWQWAHAHG IHWSYHVSHPEAAGLIEWWK GLLKLQLQCQLGDNTLEGWGK VLQKTVYALNQHPYGTVSPIA RIHRSRNKGVEVAPFTITPSDPL PQFLLPVPATLCSAGLEVLAP GGTLPPGDRTTPLNWKLRLPP EDFGLLPSLSQQAQKGYTVLAG VIHPDYQDEISLLHNGCKEDL
6692	37060	A	6742	3	350	
6693	37061	A	6743	1	3339	
6694	37062	A	6744	1	2271	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6695	37063	A	6745	3	1377	AHLAADDFTK*GWVSGLPQG LDKL.TPGANLEMQPENLKED LVYLKKNHEELSMAIKRNESM AKGLQRALLQQQFEDDSKCFP RPQDLIRLYDIILQLTLEDREGK GLSFSFACVDKDVSVKMDTVP GVNLSCLINEMRDQDKKLVEK SCKDAQGWFFSLKALLEGSLVE TEVCYRTQLAQLQGLIRSMEEQ LCELCCDAEHQDHEHQVLLDV KTQLEQEIATYSRLLEVEDAQL ATQYSLSLASQPTREDLEKAIL KFIWNQNRQAIAKTILSKKSKA RGIMLPFSKIYYKTTVTKTAWC WYKNRHIDQWNRIENPEIRPHT YNHVIFDKPDKRKQWGKDSLF NKWCWENWLAICSKLTDPFL NPYTKVNSRWIKDLNLOPKTIK ILKENLGNAIQDTGKGKDFMTK MPKAIAATKAIKIDKWDLIKLSF CTALRNYQSKPTTYRMGENF
6696	37064	A	6746	1	882	
6697	37065	A	6747	13	1402	STGSTHACDLLFSPSPVCLPPAA ATMTTSIR/QFTSSS/SIKGSSGL GGG/SSRTSCLSGGLG/AGSCR LGSAGLGLSTLGG/SSYSSCYSF GSGGGYSSFGGVDGLLA/GGE KA/TMQNL/NDIRLGSYLDKVP PWKEANTELEVKIRDLVTRGR APGPARDYSQYYRTIEELQNKI LTATVDNANILLQIDNARLAAD DFRTKFETEALRLSVEADING LRRVDELTLARADLEMQIENL KEELAYLKKNHEEEMNALRGQ VGGEINVEMDAAPGVDLSRLN EMRDQYEKMAEKNRKAEDW FFSKTEELNREVAATNSELVQSG KSEISELRRTMQALEIELQSOLS MKASLEGNLAETENRYCVQLS QIQGLIGSVEEQLAQLRCEMEQ QNQEYKILLDVKTRLEQEIATY RRLEGE DAHLTQYKKKEPVTTT QVRTIVEEVQDGKVSSREQVH
6698	37066	A	6748	2	452	FLLPSSFSCTHSLLSPTITIVGPG DFNLASHIIPDTTPDPHDCISMIH LTFTFPFHISFFVPHPDHA*FID GSSTRPNRHTPAKAGYAIAQAT IPPLRTSHFLSIVEIYPQGNNSFV FHVLFYSSGHHQAPSLPYTLRR DRRPGTSRA
6699	37067	A	6749	1	1791	

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6700	37068	A	6750	1	219	
6701	37069	A	6751	2	528	TLTVESKSIKAYKLSLQPHFTC PKTGHALQVSSGFVESPTVITVP GLDINLASHTIPDNTPEPHDCIS LIHLTFTPPHVSFFPVPHPDHT WFIGDSSSTRPNCHSPAKTGYAI VSSTLIIDATALPPSTTSQQAEI ALTRALTLAKGLPINIHTDSKY AFHILHHHAVI* AER
6702	37070	B	6752	1	1744	
6703	37071	A	6753	1	1376	MCKRMPGLQASQTVCPFYDKN YLDLKRKGTEIKRRERLKCCKG IERRKRLRDSERLEKRIKRGCLP DLKLSTEIQINRLRGLYTLLRKE RRFGLQETINYAEVTGIYVKELI EDREHLNSGKYIFNIFDIKVP VFGLIDPYMLWEKKEGTKEGJK EGMKRESQKRIKWERSFITFI NTADRTLMSAGCYRKQVKIHI DALPPNSQTLKKRGGASLIISF RRQSGPSAAGLWEFARGPFQTL FAWLSPAAEAQORLLPASSAE SFIAEGDPPDAGQSSPPSSLHAA AATALLLEALKITNYAQLTLY SSPNFQNLFSSSHLLTHLSADWL LQLYSLFVESPTITIVPGPDFNPA FHFIPDTPDPHDCISLIHLTFTF FPHISFFPVPHPDHTWFIGDSS RPNRHTPAKAGYA/DGRNTSYC VLPVPGNSPLVPNPGSARCTEG GLLYARA
6704	37072	B	6754	400	820	
6705	37073	B	6755	1	1190	
6706	37074	A	6756	1	1002	
6707	37075	B	6757	1	3216	
6708	37076	A	6758	1	4020	
6709	37077	A	6759	1	1155	
6710	37078	A	6760	2	346	SSYLMHILSAPNLLQLYSLFVES PTITIVPGPDFNLASHIILDTTPD PHDYLSDDPDHIS/TFP/DISFFPV PHPGHTWFNDGSSSTRPNRHSPA KAGHAIVFSTSIIEATALPPSTT
6711	37079	A	6761	189	1201	
6712	37080	A	6762	1	231	
6713	37081	A	6763	1	834	
6714	37082	A	6764	470	479	PRNPSSFLQVQVQHRFLQLFVP FHFVFLLASLYVMVTLTTFWR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT
6715	37083	A	6765	21	706	
6716	37084	A	6766	1	158	

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6717	37085	C	6767	78	401	
6718	37086	A	6768	536	694	
6719	37087	C	6769	1	1410	
6720	37088	B	6770	1	1836	
6721	37089	A	6771	306	487	VGFLGILF/CFEAIVNVSSLMIW LSVCLLSVYKNACDFCTLILYP ETLLKLLJSSSLYLW
6722	37090	A	6772	714	1096	FFLPMSMECSSICLYPL/CISLRS GL*FSLKRSFTSLVSWIPRYFILC KSQGMRWLGLGSEA*YSCLLIL IRKITQNSVEVLGRKFLGGGM EREWVFLRAASSGIRGSVGT NFKSESRIQISCASV
6723	37091	C	6773	1	2796	
6724	37092	A	6774	126	490	FFLPMSMECSSICLYPLFPAGAV VCSSP*RGPSHPL*VGFLGILF/C FEAIGNGSSLMIWLSVCLLLVY KNACDFCTLILYPETLLKLLISL RRFWAETMGFSRYIIMSSANRD NLTSSFPN
6725	37093	A	6775	1	550	
6726	37094	A	6776	578	865	MCPRDYGMCLCSHCFKEHLY FCLHFVMPVVIQEQQVQFPCS *AVLSEFLNPEF*FDCTVV*ETV CYNF*SFTFAEKSFTSNVSVNFG IGVVWC
6727	37095	A	6777	1	2091	
6728	37096	C	6778	1	1458	
6729	37097	B	6779	1	504	
6730	37098	A	6780	70	511	NHASPGIRNLFHPRGLRAITIA VFCKQNTYIRLEPFKINVLEQIT KHIEKLQCGGVVKLSRRGNN QHISSTYDINRADTQVRAVNN YDIIV*ATVSMASRSIRCGSVGS LPSSNLPIINSVIRCARQEGIM SSPGQQVGFA
6731	37099	A	6781	3	306	
6732	37100	A	6782	1	3567	MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRSLRSRCDQLEERVSV MEDEMNMKQEGKFREKRIRK NEQSLQEIWDYVKRPNLRIGV PESDGENGTCLKNTLQDIIQENF PNLARQAKVQIEIQRMPIQRYS LTRATPRHIIVRFTKVE
6733	37101	A	6783	386	550	
6734	37102	A	6784	1	594	

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6735	37103	A	6785	1	1324	MGKKQSRKTGNSKRQASPPPKERSSSPAMEQSWMENDFDELREEGFRRNTYSELQEQIGITKGKEVKNFEKNLDECITRITNTEKCLKELMELKAKARELREECRLRSRCDQLEERHHTTPIPKLTTYLEVKLSPANVKEQVITNCLSDHSAIKLELRIKKPTQNPSTTWKLNLLNDYVWNKEMKSEIKMFFE TNENKNTTYQNLWDAFKA VCRGKFIALNAHKGKQERSKIDTLTSQLRELEKQEQTHSKVSRREQEITKIRAEPKEIETQKTLQKINESRSWFFERINKIDRRRLARIKKKREKNQRDAIKNDEGDITDPTIEQITIREYYKHLYANKLENLKEMDKFLNTYTLPRNLQEEAESLNRPIAGSEIVAIHNSLPTKKSPGPDGFEAFYQRYKEKLVFGAGYFGMWALAALPSNLLKLSQLCQEEAEVNVLVQFVCIC*SCLNSVRRQ
6736	37104	C	6786	1	1719	
6737	37105	B	6787	1	1098	
6738	37106	C	6788	1	1782	
6739	37107	A	6789	3095	3217	CRCLQMAM*WS*AIALSMKISMSPRKPEV*IKVLAGLCLL
6740	37108	A	6790	1	5364	
6741	37109	C	6791	1	2505	
6742	37110	A	6792	37	1214	KLLQDLPFSSINSSAVEKISMSTTGQVIRCKAAIILWKPAGPFSIEEVVAPPKAKEVRJKVATGLCGTEMKVLGSKHLDLLYPTILGHEGAGIVESIGEGVSTVKPGDKVITLFLPQCCECTSCNLSEGNFCIQFKQSKTQLMSDGTSRFTCKGKSIYHFGNTSTFCEYTVIKEISVAKIDAVAPLEKVCILSCGFSITGFAAINAKVTPGSTCAVFGLG/VGGLSVVMGCKAAGAARD/IIGVDVQOGRKF*GRAQELGATEC/LNPIQALKKPHFKEVLFDMDTDAGIDFCFEAIGNLDVLAALASCSNESYGVVVVGVLPASVQLKISGQLFFSGRSLKGSVFGGWKSRQHIPKLVDADYMAEKLNDPLITHTLNLDKINEAVELMKTKKW
6743	37111	B	6793	1	2280	
6744	37112	A	6794	1498	1764	LVLYKVMGRMEPSWKTLCRLIRSRRTSANLSKAGQCSDSNGNTENTTKILLKKSNSKTHNCQIHQS*N EGKNVKGSRQERSGYPRGRPS

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6745	37113	A	6795	3	640	
6746	37114	A	6796	1	996	
6747	37115	A	6797	1	933	
6748	37116	A	6798	74	1128	LLLDL*VD*SPSRPLEMRFRV*P MKRCTTLKKNYLSFLVVISRNL *NRVKAIM/VGKAEWKIETPL PRKTVNQKQYRIPGGIAEISTTI KELNNAGMVIPTTSPFNSPIWP VQKIDGSRWMTVDYCKLNQV VTPIAATVPYVVSSELEQIN/TSPG T/WNRKRCNRSRLHKLCHL GHMTQOI*CFRLCQWHIGMLF GPEICGCTLSGQKL/WKIFVSH AASFWSPEQEKALQQVQAVV QAALPLGPYPDPADPVLLEMSV ADRDVAVWILWQAPISESQWRPP GFWSKALPSSADNYSFPERQLL ACYWTLVETERLTMGHQVTIPP ELPIMNWVFSDLSSPKMCHPQQ
6749	37117	A	6799	1	229	
6750	37118	A	6800	1	1011	MVSTPATLPSLPKALMASWG VPYDQLTKEEKTRVWFTDGS RYAGTTQKWTAVALQPLSRST LKDSSEGKSSQWAEQAVYLV VHFAWKEKWPDPGLYTDSWA VANLAGWSETWEKQDWKIG DKEIWGRGMWMDLSEWSKAV KIFVSHVSAHQRVTSAEFEFNN QVDRPL/PVFTQWAHEQSGHSG RDGGYSWAQQTGLPFTKADL AMATAECPCQQRPTLSPLYS TIPQGDQPATWWQIDYIGPLPS WKGQKFVLTVIDTYSRYFAY PAHNASAKTTIHGLIECLIHCY IPHSIASDQSIHF/TTKEVQ*WAH AHGIHWSYHVSHHPEAAGL
6751	37119	A	6801	2	739	HKMGHAQQHSIIKWK*YICDW ARAGPKGTTAPMASWGVLYD QLTEEEKTRWFTDGSARYAG TTQKWTAALQPLSRSTLKS GEGKSSQWAEQAVHLVVHFS WKDKWPDVRLYIDSWAVANG LAGWSGTWKKHDWKIGDKEI WGRGMWMDLSEWPKPVKIFG SHVSAHQWVISAEEEDFNNQVD KMTCSVDITQPLSPATPVITQW AHKQSGHGGRDGGYTWAQQH GLPLTKTGLAMATAECPI
6752	37120	A	6802	1	354	
6753	37121	A	6803	3	592	

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6754	37122	A	6804	126	365	QLAEPHWWLPD*KGAGFEWGP EQKKALQ*VQAAVQAAALPLGP YDPADPMVLVVSVADKDAVWI FHLGSDRWRRTRYRCL
6755	37123	A	6805	1	636	MEFNDSMHNTFDHIWRTKEYD EAGWLLSSLDKAMKENDEL DSNSQIQKQILSLQSSKILNLTE GTVVTLQNLNSVGIIGSQGGR GQVAALSLQRQGASFEWSPEQ EKALQQVQTAVQAAALPLGPYD PSDPMVFEVSADGNVWSLW QAPIGELQWRILEFWSKALPSS ADNYSFGRQLLACYWALVET EHLTVDHQVT/M*PELPI
6756	37124	A	6806	1	672	
6757	37125	A	6807	308	470	
6758	37126	A	6808	1	1908	
6759	37127	A	6809	1	1218	MGIIGSRGGRGQVAALKRQRQ VTKKAASFEWGPEEKALQQV QAAVQAAALPLGPYDPADPIVLE VSVADRGA VWSLWQVPIGESQ QRPLGFWSKALPSSADNDSPF RQLLACYCAI.VETERLDMGHQ VTMRPEVLIINCVLSDPSSH/QG WRLCMSATWTSTYQ/A*PGY GHC*VPLPAEETNDPSIWHH S/YG*LASYLVIG*LHWTSIME GAEVCPHWNRLRLI*VCLST QCFCED/SHPWIHE/ASYLPSWH ST*HCL*SRHSPYS*RSVAVGSC SWNSLVLPSPSS*SSWINRMV EWPFEVTITMPTR*QYSAGLGK SSSEGCVCESASNIWYCFRSQ DSWVQESRGGSGGTIIHHF** PTSKIFASCFDLMFCWT*GCS/S *WRNAATTRHNNFI
6760	37128	A	6810	901	1142	GPEDLQGLFILSFQDPLL/SHPV CLEALAPFPSPVVPISFPHPVA GEFWLYPSGAA/RASSDAQSWT VIAVSPLRGLNSWG
6761	37129	B	6811	1	1452	
6762	37130	A	6812	122	1838	
6763	37131	A	6813	101	249	MTHVTALRTSSNLMRN*RKVG EAKSQEH*S*QACHL.KSRMSS SRLWIN
6764	37132	A	6814	1	1074	
6765	37133	A	6815	310	397	LTIWQDSNPGSCL*GCSVCAHA /CVGQGHMVC*PSYSLYLKSE PKEGTGRNKDPDLNSQNRKGF LEQIHQ
6766	37134	A	6816	1	583	

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6767	37135	A	6817	1	486	
6768	37136	A	6818	2	1001	
6769	37137	A	6819	1	2307	
6770	37138	A	6820	3	393	
6771	37139	A	6821	1	1776	
6772	37140	A	6822	1	1140	
6773	37141	A	6823	1	558	
6774	37142	A	6824	2	798	PRVRIFFSITWYSLRVLTEISLW GGLLLVVIITQYDMTRTRNKYL HTNSLVLANMSAQFRSLHQY AA\QRIIRLFSLLSKKHNVLEQ ATQSLRGSLSNDVPLPDYAQD LNVIEEVIRMMLEIHNSCLVTNS LHHNPNLGITPWLQRRSLWN NFRVTHPSFQINGKIIWVIF/LS /SRLQGLAGKLGAEISVERVLEI IKQGVRI/S/LPKDRLLKFPPELKF YVEEEQPEEFFIPYVWSLVYNF SSRPVLGIPQDIPAVSPWVSD
6775	37143	A	6825	3	206	PSASRPWAHPALHPSVPVARG WQPPITGLHPLREQRGLGQHM* QSSGQQPQGGVGPESHFPAL WAQL
6776	37144	A	6826	200	601	EMGSCDQWQRPCVPWEAVVM PRDP/LKMALAVVWPMMKAPR VTKRTP*LTSTHQLAGLTSSISE SLA*MRHSPGKTKMKQAARPP MTEITLPMGSMKS/VQQQGEQE PDQRLQHSPPPLPPHVLLHWWP LVAQFQA
6777	37145	B	6827	25	1407	
6778	37146	A	6828	1786	1795	HC*LNALPSGETWGQKRGPLG TQLPLPL/VPLRAPKGRSPKGSK GPTHHTWALSSFSLTSPQVTVG TEDQATSASGRPWLRIGTGPGG GRVWAGRDSIRGVPALTVLHV LSSLGRETP*RPCLRGPTAPAGP KRAPGKWLPWSQAPPCGCCPR *LSHVL*DRNRCAW*KGGGRG L/LRAPTPVPELAHPHCPGAPTL SKPLSSPNMPAQGLTQE*PGSV ANLPPYPGALLCLGRREWDER GQVG*VPTSEME*RRTEPLKT PGDCSAAASKIPSFSSNRTPFPPL CPHKNKLGKT
6779	37147	A	6829	1	311	
6780	37148	A	6830	1	402	
6781	37149	A	6831	1	750	
6782	37150	C	6832	130	450	

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6783	37151	A	6833	1	875	MRLRLRLKLVKEQHVELYQKYS NNSWRYLSNRLAPSDSPEWLS FDVTGVVRQW/VWSRGGEIEGF RLSAHCSCDSRDNTLQVDINGF TTGRRGDLATHGMNRPFLLFM ATPLERAQHLQSSRRHRLDTK YCFSSTEKNCCVRQLYIDFRKD LGWKWIHEAPKGYHANFCLGP CPYIWSLDTQYSKVLALYNQH NPGASAAPCCVPQALEPLPIVY YVGRKPKVEQLSNMIVRSCKC NLGPAPPRPAPAGPAPRPAPV ALPMGAVFKDTRAPSPGAPLK MERGKKKKKK
6784	37152	B	6834	162	635	
6785	37153	A	6835	2	1846	
6786	37154	A	6836	322	2104	
6787	37155	A	6837	1	352	
6788	37156	B	6838	92	1774	
6789	37157	A	6839	260	1016	
6790	37158	A	6840	479	1937	DVEHVGMKRRRWRRRVVVAD GNVVKPMSCAGDLQ/PFTRVTV HWGKGNDQTFQDLDLTGSELT LIPGDPKRHCAPPVKIGAYGGQI INGVLAQVQLTVDAVGPWTHP VVIFPVPECIGIDMLSSRQNPHT GSLTGRVWTIMVRKAKWKPLE LPLPRKIVNQKYHIPEGIVEIS ATIKDLKDAVVVPTTSPFNPI WPVQKTGSGWRMTVGYCKLN QVVTPIAAAVPDVVSLEQINT PPGTWYAAIDLANDF
6791	37159	B	6841	20	26	
6792	37160	B	6842	2	207	
6793	37161	B	6843	187	405	
6794	37162	A	6844	451	770	LFLFLLSSHPRSSASWYRHRH PHHPAARLPVADSASSSSPSS SSPSPSSSSSSPSSSSSFVYPHC QPPAPHFPH*HSR*QGRLFHFLP LPQLPSSPLSPWW
6795	37163	A	6845	1	417	
6796	37164	A	6846	191	314	
6797	37165	A	6847	129	212	

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6798	37166	A	6848	1	192	CALNAGL/IGENEAKRRRSKVT QEADFPMSMDGASNFVRGDAI AGILIMVINIVGGLLVGVLQHG MSMGHAAESYALLTIGDGLVA QIPALVISTAAGVIVTRVSTDQD VGEQMVNQLFSNPSVMLLSAA VLGLLGLVPGMPSLVLLFTAG LLGLAWWIRGREQKAPAEPPK VKMAENNTVVEATWNDVQLE DSLGMATGLLT*PIFRAQWTGQ VTLFAAMPSPGSSSWSLTSLAG CWSACCNMA
6799	37167	B	6849	65	1129	
6800	37168	B	6850	46	1038	
6801	37169	A	6851	2	413	PSFQGPVSLPSITVVSIDSQASKP LKTPTQLWCQLRQYSFKHSFLV VPTCPVPLL*DTLTKLSASLTI PGLQPHLIATHLNPQVEDTSIPS LATYHAPLTISLKPNIHPPSQC QYPIQHALKGLKPVITHLLQH
6802	37170	C	6852	35	346	
6803	37171	C	6853	239	484	
6804	37172	A	6854	1	1020	
6805	37173	A	6855	3	131	
6806	37174	A	6856	1	956	MAGALPPASLPPCSLISDCCASN ERSSMGIGPSEPCAGYNLLVCR LTKKKRIRSTNKVWDYVVRPN LRIIGVPEEEENSKSCENILGEIIE ENFPSLATDLDIQIEAQRTPOK FITERSLPRYIVIRLSKVKTAKERI LRAVRQKHQIFLTQRLKNTAQ SPQKLPGPSQTLVLTREITIVP GLDFNPASHIADTTPDPHDCIS LIHLTFIQPHISFFVPHPDHTW FINGSTRPNRHSPAKAGYAIVS STSHIETTLPSSTTSQAEFIAL TQALILAKGLCINIYADSKY/AF HILHHHAVIWAERDTFTG
6807	37175	A	6857	1	1269	
6808	37176	A	6858	1	741	
6809	37177	B	6859	411	1257	

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6810	37178	A	6860	438	3997	SPLPHSTPISHPAACFKKIKACY HLPATAWPKAYKLSLQFPHT CPKTRQGLQHNSHKNTALPD YRLRLISQTPIPSTKQQLSFLG MVSKVRILTQELGPRPIAFLSKQ LDLTVLTQPSCLHAAAAAAIL LKALKITKYAQLTLYSSHNFNQ LFSSSYLMHILSAPWLLQLYSLF VESPTITIVPGTDFNPASHIILD TPDPHDCISLIHLTTFPFRISFFP VPHPNHIWFDIGSSTRPKCHSPA KAGY
6811	37179	A	6861	245	505	
6812	37180	A	6862	346	522	PAPEFWVHG*NVSPLSL*SKEQ EDRGFISQGRSPDLSHGTFKHV RPCEETTKQALCEQH
6813	37181	A	6863	3	879	SGDLPEINPSSYTLLCEKDPP TISGPQTNQPKHILTNFKSETK ETRFIRGPTTPAPVTDWEGSLPL VFNHSRDTSLIHPGFRGVRPRR DACLGPSLAASPTFLGKGPA PRQTELGPNSSASAPPPYNPFI ASPPHTWSGLQFPMSPTPPPA QQFTLKKVAGAKGIVKDLINLT FKVYNNRKKLQFLASTVRQTP ATSPAHKNFQTPELQQGPVPPE PPPRGACYKFQKSGHRAKECLQ PRIPPKPHPICVGPWHKSDCP THLAATPRAPGTLAGGSLTPSQIFL
6814	37182	A	6864	143	331	DTSTPSLVTDHASLTISLKPNIH YPD*CYPIQHALKGLKPVITC LLQHGLLKPINSYPRA
6815	37183	A	6865	1	783	
6816	37184	A	6866	32	415	WRHALKGLKPVITRLLQHGLL RPINSYPNSPFLVLEPDKPYRK RK*ISPPNRHILASVEVLKNQVN SHEFERSALIHTLSGLAPCSLH KMCSKLPKRSFLSVGSGTGKEAR SKILTFRTASRHLVL

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6817	37185	A	6867	1	1374	MSELPTIASKRIKYLGIQLTRD VKDLFKENYKPLLEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTTFTELEKTT LKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKPTETKTAW YWYLNRRDIDQWNRTEPSEITPH TYNYLIFDKPEKNKQWGKDSL FNKWCWENWLAICRKLKLDPPF FTPYTKINSRWIKDLNVRPETIK TLEENLGITIQDIGVGKDFMSKT PKAMATKDKTGKWDLIKLSF CTAKETTIRVNRQVAALLNSA VFQNAVEVVVWPSSEVHVKFL FCKIISCAQKQPIKFDGSSSL GVATAMMSATIAHLKRIKACY RSPVTAWTFKAYKLSLQFPHFT CPKTGQALQ*HT*KGLKPVIAH LLQHGLLPINSYPNSLILPVQK PDKPYRKLESFTSKAIKWHQIPS VPGKHLC*GS*RSPVTAWTFKA YKLSLQFPHFTCPKTGQALQEA GVIHFGKHGMASDPITQGNTYA NKVAKEAASVLTSPVHGQFFSF SSVTPTYFPTIEDFTYMPQVRKL KHLMV
6818	37186	A	6868	122	281	
6819	37187	A	6869	2	2144	
6820	37188	A	6870	224	418	LSQWRHALKGLKSVITRL*HG LLKPINSYPNSPIPVLPKPKDITY RKVESFTAKTIKRCQIPLL
6821	37189	A	6871	5	289	
6822	37190	A	6872	1	2205	
6823	37191	C	6873	1	2082	
6824	37192	B	6874	1	1614	
6825	37193	A	6875	1	2067	
6826	37194	A	6876	1	1152	
6827	37195	A	6877	1	798	
6828	37196	C	6878	488	788	
6829	37197	A	6879	90	765	NTVFLGVVLPLELKLRIFLRLD VRSVLSLSAVCRDLFTASNDPL LWRFLYLRDFRGRNDIYSWT TKDFEYYINLVDKTEARFEKVD SDFESFTVGKMPSNSIACTEKSF MKGRVSQCDKKPVITRLQLHG LLKPINSYPNSPILPVLPKPKPY KLVDLHRINQVLPHPGCAQP HTLFCPQYLPQLTIPVPLKDA FFTIPLQPSQVPLFAFT*TPDPT

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6830	37198	A	6880	1824	2286	PRVLRPNSPRNISPISNRIFSD*R CPIASEASWTITDALG/RLLQWR HGLLNPNISPYNSPILPVQKPKD PYRLVQALLSLPQLPLFLAWTSI WPPTLFRITLLNPMPTVSL*ST*H SLHFPMFPSFLTLTLITLGLLMA VPLGLIATHQQRAML
6831	37199	A	6881	930	1289	LSQWTDGLLKPMSNPYNPILP VLKPKDPYK*VQDLRLINQIVL PIHPVVNPYPYTLSSIPPSTTHY SVLDLKLAFFTIPLHPSSQPFFAF TWTDPDTHQAQQIT*AVLPQSF SDSPHE
6832	37200	A	6882	2	196	IHGCKFIQCKRILSNFTEVADHV HDQIRL*TGIRLLTQPQRLSCR HQVAQHSVCRYLCQLPLL
6833	37201	A	6883	2	1441	LNQEEGESLNRPTGSEIEAIINS LPTKKSPGPDGITAIFYQRYKE ELVPFLVKLFQSTEKEGILPNSF YEASIIIPKPRDRTTKKENFRPI SLMNIDAKILNKILANRIQQHIK KLIHNGQHINRTNOKSHIISIDA EKTFGKIQQPFMLKTLNKLIGID GTYLKIIIRAIYDKPTANILTGQ KLEAFPMKTGTREGCPLSPLL NIVLEVLARAIQKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLRLISTFSKVSGYKINVQ KSQAFLYTNNRQTESQILSELFF TIASKRIKYLGIQLTRDVKDLFK ENYKALLNEIKEDINKWKNIPC SWVGRINIVKMAILPKVIYRFN AIPIKLPMFTFTELEKTTLKFIW NQKSARIAKSILSQKNKAGGIM LPDFKLYYKATVTKTAWYWY QNRDIDQWNTTEPSEIMLHIYN Y/LIFNKPEKNKKWGKDSL FNK WCWENWL

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6834	37202	A	6884	69	2415	DKTSRGTIRQQRLRFTNIRCSAA TAADIQANRVWRGPPANSNR AAVRVLTVRRKTNKQKGHPHQ KPICTSPSSNTKEIQTIREYYKH LYANKLENAEERDKFLNIYTL RLNQKEVESLNRPTGSEIEAIK SLPTKKSPGPDGFTAKFYQRYK EELVPFLKLFQSEIEGILPNSF YEASIIIPKPRDRTTKENFRPI SLMNIDARILNKILANLIQHHK KLIHHDQVGFIPGMQGFNICK SINIIQHMRNTKDKNHMISIDA EKPFDKIQPFMLKTLNKLDD GTYLKIVRAKYDKPTANIILNG QKLEAFPLKTGTROGCPLSPLL FNIVLEVLAREIRQEKEIKGIQL GKEEVKLSLFVDDMIYLENPIV SAQNLLKLISNFSKVSQYKISVQ KSQAFLYTNNRQTESQTMSELP FTIASKRIKYLGIQLTRDVKDRF KENYKSLSEIKEDTNKWKNI CSWVGRINIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI NQKRARIAKSILSQKNKAGGIT LLDFKLYYKATVTKTAWYWY QNRHVDQWNRTEPSEIMLHIY NYLIFEKPDINKQWGKDSL FNK WCWENWLAICRKLKLPFLTS YTKINSRWIKDLNVRPKTIKTLE ENLGNTIQDIGMGKDFMSKTPK AMATKAKLDKWDLIKLSFCT AKETTIRVNRQPTGWEIFATY
6835	37203	A	6885	1	2358	
6836	37204	B	6886	1	1443	

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6837	37205	A	6887	452	2913	KMGLAREWILRFLVLILQEIRS MRQKENKDIQDLNSALHQADL IDIYRTLHPKSTEYTFFSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKTQ/NRS ATWKLN/MLLNDY/WVHNEMK AEIKMFFETNENKDTTYQNLW DTFKA VCRGKFIALNAHKRKQ ERSKIDTLMSQLEKEKQEQT SKVSRRPISSEIEAIIINSLPTKKS PGPDGFTA E FYQRYKEELVPFL LKLFSQIEKEGILPNSFYEASILI PKPGRDTEKENFRPISLMNIDA KILNKILANRIQQHIKLLHHDQ VGFIPGMQGWFNICKSINVIQHI NRTSDKNHTIISIDA E KAFNKIQ QLFMLKTLNKLGTNGMYLKIV RAIYDKPTANIILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVL RAIRQEKEIQGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLLKLI SNFSKVSGYKINLQKSQAFLYT NNRQTESQIMSELPFTTASKRIK YLGQLTRDVKDLFKENYKPLL NEIKEDTNKWRNIPCSWVGRIN IVKMAILPKVTYRFNAIPKLP M TFFTELEKTILKFRWNQKRAHI AKTILSQKNKAGGIRLPDFKLF YKATVTKTARYWYENRDIQ WNRTEPLEIMPHIYNHLIFDKPD KNKQWGKDSL F NKWCWENWL AICRKLKLDPFLTSYTKINSRWI
6838	37206	A	6888	I	1677	

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6839	37207	A	6889	2	2400	SMRQKENKDIQDLNSALHQAD LIDYRTLHPKSTYETFFSAPHCI /RTYSKIDHTLGSKALLSKCKIT EIITDSQTTVLSELRIKKLTQINR SATWKLN/MLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDTFKAVCRGKFIALNAHKKR QERSKIDTLMSQLKELEKQEQT HSKVSRPPIPSEIEAIINSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEAII LIPKPGRDITTEKENFRPISLMNI DAKILNKILANRQQHIKKLLIIII DQVGFIPGMQGWFNICKSINVI QHINRTSDKNHTIISIDAEKAFN KIQQLFMLKTLNKLGTNGMYL KIVRAIYDKPTANIILNGQKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIQGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINLQKSQA FLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWRNIPCSWV GRINIVKMAILPKVTYRFNAIPI KLPMTEFFTELEKTILKFRWNQK RAHIAKTILSQKNKAGGIRLPDF KLFYKATVTKTARYWYENRDI DQWNRTEPLEIMPHIYNHLIFD KPDKNKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLTSYTKIN SRWIEDLNVRPKTIETLEENLG
6840	37208	A	6890	1	1515	
6841	37209	A	6891	1	1428	

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6842	37210	A	6892	150	1920	NYQCREVLKGPDGAENHGTRI T*RMHKLSSQFSQLEERVSGM EDQTNETKDTLRLKIKGWRKIY QANGKQKKAEEAAILVLDKTD KPTKIKGDKQGHYIMVKGSIQQ GQLTILNIYAPNTGASRLIKQVL RDLQRDLDSHTIIMGDFNTRL TLDRSTRQRLNKDIQELNSALH QVDLIDYRILHTKSTEYTFSSA PHITYSKIDHTVGSKALLSKGK RTEITNRLSDHSAIKLELRJEL TQNRSTTWKLNLLNDYWNL WDTFAVCRGKFIALNIQKRK QERSKIDTLTSQFKELEKQEQ HSKASRRQEITKIRAEKERETQ KSLQKISESRWFFKINNIDTP LARLIKKKREKNQIDTIKNDKG DITTDPTIEITIRQYYKHLN KQENLEEMNKFLDYTYLPRLN WEEAESLNRPTGSEFAIINSLP IKKSPGPDGFTAKFYQSYKEEL VPFLKLKFSIEKIGLPNSFYE ASIILIPKPRDITTKDNFRPISL MNIDAKILNKILANKIQHSHK LIHHNQVGFIPGMQGWFTCKS INIHQHNRTKDKNHMISIDA AFDKIQQPSC
6843	37211	A	6893	1	1797	

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6844	37212	A	6894	2	1880	APNTGAPRFFIKQVLSDLQRDLDSHTIIMGDFNTPLSTLDRSMRQKVNKDIQELNSALHQADLIDYRTLHPKSTEYTFFSATHHTYSKIDHIVGSKALLSKCKRTEITNCLSDHSAIKLELRJIKLLENSTTWKLNLLNDYVWHNEMKAEIKMVFETNDTLPRINQEEVESLNRPKTGSEIEAIINSLPTKKSPGPDGFTAEFYQRYKEELVPFLLKLFQSIEKERILPNSFYEASILIPKPGRDTTKK/EENFRPISLMNIDAKILNKILANRIQQHIKKLIHIDQLGFIPIGMQGWFNICKSMNVQHINSPKDKNHMIIISVDAEKAFDKIQQPFMLKTLNKLIGDGYLKIRAIYDKPTASIIILNGQKLEAFTLKTGTRQGCPLSPLLFNIVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIIVYLENPIISAQNLLKLIGNFSKVSQYNTINVQKSQAFLYTNNRQTESQIMSELPFTIASKRIKYLGIQLTRDVKDFPKENYKPLLNEIKEDKNKWKNI PCSWVGRINIVKMAIPPKVIYRFNAIPKLPMTFGMIFLSQKYGHVTLFRLLQWLLNVARNNNKVFYKIYKVGHKLSSAYVCLCTCSHFSVSFL
6845	37213	B	6895	13	1506	
6846	37214	A	6896	1	6635	MTPESRDTTDLSPGGTQEMEGIVIVKVEEEDHDFQKERNKVESSPQVLSRSTTMNERALLSSYLVA YRVAKKMAHTAAEKIILPACMDMVRTIFDDKSADKLRTIPLSDNTISRRICTIAKHLEAMLITRLQSGIDFAIQLDESTDIASCP TLVYVRYIPLKRLGLLQPEKPIVLKVESRDGTQYNSQQHINLSAAWLKTA VQGREAPGKQPSKQ QHSAKRKTHRTQLKKESGDGPHPKFGGNNLASP
6847	37215	B	6897	1	3045	

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6848	37216	A	6898	1	2764	MARELHDKCTSFSSRFDQLEES LSAMEDQMNMEMMRREEKFKREK RRKRNEQSLQEIWWDYVVRPNL HLIGVPESDRENGPKLENTLQDI IQENFPNLARQGNIQIEIQRM QRYSSRRATPRHIIVRFTKVEM KEKMLRAAREKEIQTTIREYYK HFYANELENLEEMDKFFETYTL PRLNQEEVESLNRPIITGSAIEAII NSLPTKKSPGPDGFTAEFYQRY KEELVPFLLKLQFSIEKEGILPNS FHEASILIP
6849	37217	B	6899	1	3549	
6850	37218	A	6900	387	541	
6851	37219	A	6901	1	545	
6852	37220	A	6902	71	370	RRCKVRPSARGVLRVAVCVCV CVCVYPCVHVCTCVRMCLCVC VCVC/CSVEIHCGGQGCARCIC LQPQEGGCTEQAVAHCAAQL WRNRLKLMKQPVARV
6853	37221	A	6904	1	738	
6854	37222	A	6905	1	567	
6855	37223	A	6906	1	1416	
6856	37224	A	6907	3	1267	
6857	37225	A	6908	1	552	NALPGRKSRVFGVCSADTWK PPSSAKVTETKGASPAFLRAGQ PRLVPGETLEKSLGPKDPQVE PQHVPVHLPGISSEGFWDGFNE QTPKDLPNRDGGAWVLGYRA GPACPFLLHEEREKSNRSELYL DLHPDHSLTEQDDRTPGRIQA VWPPPKTKDTEEKVGLKYTEA EYQAAILHLKRE
6858	37226	A	6909	1	561	
6859	37227	A	6910	219	1343	RRLCHTQPTLGMRESELVNV CVHSVFSPLSPVQAMQEKDEAK AETIQALYHQTFLEALQTLKAL FIEDPTPAGLKSILEALGPWMNS GKAHERARAVNTNVSVLNMH LLTLFFMPLGFPALGLLRLI LHIGDPDEIGCEALDGIHILYTI LELQKRARDKEETNKELYES NKHFLGYPYVSPCQNLRVIEE FGDFLGPQIKDLLLLAALEGLK GSSEAPGKDSREMMQLASEVM LSSVLEWYRHRALVEIPEIMQGI YMQLSHIQEPRAQVALLPVSL LASSFMTEVVVALLMCPLPLNR QPAACASSCPSTAAWAV*GAST LSCSWPCSFRTSASTCLAAW LLPRTPRRRVHSPSYLCAGW

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6860	37228	A	6911	3	730	
6861	37229	A	6912	2	1218	ERKCMQGGKYAGAMESEPCVCT EADFDCCDYG YERHSNGQCLPA FWFNPSSLSKDCSLGQSYLNST GYRKVVSNNTDGVREQYTAK PQKCPGKAPRGLRVVTDAGKL TAIEQGHNVLTLMVQLEFGDVQ RTLQVDFGDIASVYVNLSSM EDGIKHVYQNVGIFRVTVQALV RLPPHISQCDVFRFFEAPEDV NPPKDQALLGELGPAVELCLK EERFADAILAQAGGTDLLKQT QERYLAKKTKISSLLACVYVQK NWKDVVCTCSLKNWREALAL LLTYSGTEKFPELCDMLGTRME QEGSRALTSEARLCYVCSGSVE RLVECWAKCHQALSPMALQD MHVISTDENQVFAAVQEWQON DTYNLYISDTRGVYFTLALENV QSSRGPEGNIMIDLYEVTI
6862	37230	A	6913	1	1659	
6863	37231	A	6914	540	824	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNMKREGKF REKRIKRNEQSLQEIWDYVKDQ IYVRLVYLKVTGRMEPSWKTL CRILSRRTSPI
6864	37232	A	6915	1	939	
6865	37233	A	6916	285	458	QVFSQLEGRIALGKFORPSSLPT GKWTQRQWGAQWE*D*LFG LHGWWVRPIAGFP
6866	37234	A	6917	32	171	
6867	37235	A	6918	294	461	
6868	37236	A	6919	2	255	LIPCPATVNNVSDIMGMYMKE CSASLITREMQRITTMRHHLTS IGTEMIRK/SKNNECWSGRECQ TVGAGQCVRAPCASRSARH
6869	37237	A	6920	2	393	
6870	37238	B	6921	87	633	
6871	37239	A	6922	78	260	TQYLRWKCRNHLRLRRSCWEL *TRAVPIRPSWLQNRVQGTSRF CVCFEESGTPSTQLEI
6872	37240	A	6923	1	369	FVLHEKCLGPFWITGNTNDEM VKKICAPT*TKHVW*LES*M WEEPRWPNGKAPVYSSQREQR RRRVISAFPPSEGVLPTFKNKKF TVKQPQVGRSVGIPEGIVIGD GQLQGCLLPLKTF
6873	37241	A	6924	3	201	LKEMQINTTMRVHSTPSRTS*I KKTDDNNKFWMRMTEKLETSY CWWECEMTQPRWKVSLQYLL PLI

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6874	37242	A	6925	1	2064	
6875	37243	A	6926	95	752	
6876	37244	A	6927	2237	5072	RAKSPANIHMTGSNSHITLTNLVNLGNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDKPTKIKRDKEGHYMMV KGSIQQEELTLNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFSSAPHHYSKIDHILGSEA LLSKCKRTEITNYLSDHSAIKL ELRIKNLTSQR
6877	37245	A	6928	3	331	
6878	37246	A	6929	364	853	
6879	37247	A	6930	2	531	RPRVRELVGSAIQALKEWNTT GKLRINH*KRCGSTQHGHGSKYA TDKEERPDACPLQPPQIQNG PMNGCEKDSSTDSANEKPALI PREKKISILEEPSKALRGVTPGNI EKSAKDLQRCVSLTRYRVMIK EEDVSSVKKITAFAELHNCIID KEASLMAEMGTVNEQAMRC
6880	37248	A	6931	1	456	ISILEEPSKALRGVTEGNRLQ OKLSLDGNPKPIHGTTERSDGL QWSAEQPCNPSPKPAKTSPVKS NTPAAHLEIKPDELAKKRGPN EKSVDLQRCVSLTRYRVMIK GEVDSSVKNKAACAEFPICIID KEVSLMAEMDKVKGRKPW
6881	37249	A	6932	333	964	
6882	37250	A	6933	240	691	
6883	37251	A	6934	1	2076	
6884	37252	A	6935	14	485	RRSLESVLSRKLNP*KATGTSR SESAVVAIIDAVSSPQKRLDSE FIDPLMNKKARISHLNRPVPTL NGHLNPTSEKSAAGLPLPAAA AIPTPPPLPSTYLPISHPPQIADS HSPAAPVQGIQPFLLTADQYWLE NRYPSQHLRSVTASRARHQT
6885	37253	A	6936	1	643	
6886	37254	B	6937	1	408	
6887	37255	A	6938	2	197	
6888	37256	A	6939	103	298	CLWLFQEEEEEEEEEEEE*EEE EEE/EEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEKI FLGHRVGI
6889	37257	A	6940	117	257	

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6890	37258	A	6941	46	219	LKECNCIVCNSKNKCLKG*KKK EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEGRRRGRRRR RRRRRRKKK
6891	37259	A	6942	1	1314	MVSRISWISWIAQCPLCRPSGT YGPGEAALLWLCIEAAAAA AARSTTPIITNHQSNITAEQNP PRIHENGDPKTYIIHVLAEQVLE RLPHGVALRHDPLAPVVSRA GVGHQRCAADDALQPLLQGRP EPGLAERHGVQDNLILKVSHTH TQKSAEKRAVSDPSSTVHRPQP LPPSTVHQSTIPSNPDSSAYCL PSTRHGFSSYTDSFVPPSGPSNP MNPTIGNGLSPQRVHYQHLPTH AGGKRNAALEYGVPRKYHYM LKITASDYKTKPFQVGDVVM GSGWRKVGMMQT*FL*LKKEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEENSLSLTE
6892	37260	A	6943	1	160	
6893	37261	A	6944	1	306	
6894	37262	A	6945	1	933	MWLARELEESLAVSLQGEPGL LAGAGRLQGSFSPHMEPGRQS ETLSQKKKKKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE DQLDTMFGTHQQTSPQRSAR RRPCSVOGPRS*SPFSPHMEPGR QSETLSQKKKKKEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EEDQLDTMLWDSSTNLNTAL SKEKTMFSSRAKIVKPNGEKPD EFESGISQALLEMLNLDLKAQ LWELNITAAKEIEVGGGRKAIH FVPVPLKSFQKTQVQLRRILP KPTQKSCNTNNKQKLPRSCITLA VHDAILEDLVFPSEIVGKRIHV LDGSHLIKIHLEAQQNNVEHK VEPFSGVYKMLMGKDVNFEP
6895	37263	A	6946	1	1365	
6896	37264	A	6947	416	610	EFKKPVLEGG*RGEGGSPCV WSFFDPVHFNYQAGLFRVALP GEQCRTGRLVARVYTGISGASF
6897	37265	A	6948	1	846	

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6898	37266	A	6949	3	620	HVTLLIVVTQSHLVIHNLFEGLMI WFIIVPISCVICNDIMAYMFGFFF GRTPILKLSKKKTWEGFIGGFFA TVGFGLLLSYVMSGYRCFVCP VEYNNDTNSFTVDCEPSDLFRL QEYNIPGVQSAUGWKTVMRY P/QIHSIALSTFASLIGPFGGFF ASGFKRAFKIKDFANTIPGHGGI MDRFDCQYLMATFVNVYIACV LRPL
6899	37267	A	6950	50	554	
6900	37268	B	6951	446	625	
6901	37269	A	6952	1	2149	
6902	37270	A	6953	1	1704	
6903	37271	A	6954	1	1853	
6904	37272	A	6955	1	1305	MVKGSIQEEILTILNIYALNTGA PRFIKQVLRDLQRDLDSHTIIMG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADIIDIYRTLHPKST EYTFFSAPHHTYSKIDHIVGSKA LLSKCQRIEITNCLSDYSAIKLE LRIQKLTQNCSTIWKLNNLLN DYVWHKEMKAEIKMFFETNEN KDTTYHHLWDTFKA VCRGKFI ALNAHKRKQERFEMDTLTSQ KELKKQEQTTHSKASRRQEITKI RAERKEIETQKTLQKINESGSW FVEKINKIDRPLARLIKKKREKN QIDAINKDKGVITTDPTIEQTIRE EYKHLIYANKLENLEEMDKFL DTYNLRLNQGEVESLNRPIGT SEIEAIINSLP/TKKS PGPNGFTA KF*QEELTILNIYALNTGAPRFI KQVLRDLQRDLDSHTIIMGDFN TPLSTSDRSTRQKVNKDIQELN SALHQADIIDIYRTLHPKSTEY FFSAPHHTYSKIDHIVGSKALLS KCQRIEITNCLSDYSAIKLELRI QKLTQNCSTIWKLNNLLNDY WVHKEMKAEIKMFFETNENKD TTYHHLWDTFKA VCRGKFIAL NAHKRKQERFEMDTLTSQLE LKKQEQTTHSKASRRQEITKIRA ERKEIETQKTLQKINESGSWFV EKINKIDRPLARLIKKKREKNQI DAINKDKGVITTDPTIEQTIRE YYKHLIYANKLENLEEMDKFLD
6905	37273	A	6956	1	1926	